

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 37.6727 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-1  
Perfect score: 42  
Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	4 AAB72500	Aab72500 Colostrin
2	42	100.0	7	4 AAB59324	Aab59324 Ewe colos
3	42	100.0	7	4 AAB72246	Aab72246 Colostrin
4	42	100.0	7	4 AAB72532	Aab72532 Colostrin
5	42	100.0	7	5 AAO14577	Aao14577 Neural ce
6	42	100.0	7	5 AAM51036	Aam51036 Colostrin
7	42	100.0	7	5 AAE20228	Aae20228 Colostrin
8	42	100.0	7	8 ADN60295	Adn60295 Constitue
9	42	100.0	7	8 ADS74400	Ads74400 Ovine col
10	42	100.0	8	4 AAB59354	Aab59354 Ewe colos
11	39	92.9	9	8 ADK10336	Adk10336 Human pap
12	39	92.9	10	8 ADK10337	Adk10337 Human pap
13	39	92.9	10	8 ADK10338	Adk10338 Human pap
14	37	88.1	8	8 ADK10335	Adk10335 Human pap
15	36	85.7	12	7 ADC36090	Adc36090 Chemokine
16	36	85.7	12	8 ADR42838	Adr42838 Modulator
17	34	81.0	12	6 AAE32821	Aae32821 Human CEA
18	34	81.0	15	3 AAY8491	Aay8491 Human ced
19	34	81.0	16	3 AAY85494	Aay85494 Human ced
20	33	78.6	7	4 AAM46973	Aam46973 H11 bindi
21	33	78.6	10	2 AAW06853	Aaw06853 Peptide b
22	33	78.6	11	3 AAB21127	Aab21127 Src homol
23	33	78.6	12	2 AAW06845	Aaw06845 Peptide b
24	33	78.6	13	2 AAW38072	Aaw38072 PPPPY mot
25	33	78.6	13	7 ADB49333	Adb49333 Biotinyla

26	32	76.2	6	2 AAR91753	Aar91753 Prolyl en
27	32	76.2	7	2 AAR60997	Aar60997 Fragment
28	32	76.2	7	2 AAR91752	Aar91752 Prolyl en
29	32	76.2	7	4 AAM46827	Aam46827 H11 bindi
30	32	76.2	7	4 AAM46861	Aam46861 H11 bindi
31	32	76.2	7	4 AAM46876	Aam46876 H11 bindi
32	32	76.2	7	4 AAM47027	Aam47027 H11 bindi
33	32	76.2	7	4 AAM46856	Aam46856 H11 bindi
34	32	76.2	7	4 AAM46871	Aam46871 H11 bindi
35	32	76.2	7	4 AAM46851	Aam46851 H11 bindi
36	32	76.2	7	4 AAM46866	Aam46866 H11 bindi
37	32	76.2	8	2 AAR71945	Aar71945 Human 3BP
38	32	76.2	9	7 AAW01573	Aaw01573 Mouse Pnn
39	32	76.2	10	2 AAR77371	Aar77371 SH3 bindi
40	32	76.2	10	2 AAW06861	Aaw06861 Peptide b
41	32	76.2	10	2 AAW38097	Aaw38097 PPPPY mot
42	32	76.2	10	2 AAW38074	Aaw38074 PPPPY mot
43	32	76.2	10	4 AAB86131	Aab86131 Prolin-e-r
44	32	76.2	10	4 AAB86149	Aab86149 Prolin-e-r
45	32	76.2	10	4 AAB70933	Aab70933 Polyoma v
46	32	76.2	10	7 ADB49372	Adb49372 Biotinyla
47	32	76.2	10	7 ADB49335	Adb49335 Biotinyla
48	32	76.2	11	3 AAB21129	Aab21129 Src homol
49	32	76.2	11	3 AAB21132	Aab21132 Src homol
50	32	76.2	11	3 AAB21126	Aab21126 Src homol
51	32	76.2	11	5 ABB99165	Abb99165 Formin-2
52	32	76.2	11	5 ABB99166	Abb99166 Formin-2
53	32	76.2	11	7 AAW01570	Aaw01570 Mouse Pnn
54	32	76.2	11	7 AAW01571	Aaw01571 Mouse Pnn
55	32	76.2	12	2 AAW03154	Aaw03154 Potential
56	32	76.2	12	2 AAW05101	Aaw05101 Prolin-e-r
57	32	76.2	12	2 AAW25457	Aaw25457 SH3 domai
58	32	76.2	12	3 AAB18002	Aab18002 FC-TNF al
59	32	76.2	12	6 ADA50131	Ada50131 Mad2 bind
60	32	76.2	13	2 AAR84641	Aar84641 Grb2-SOS
61	32	76.2	13	4 AAB70928	Aab70928 Polyoma v
62	32	76.2	13	6 AABU10225	AabU10225 Human cyt
63	32	76.2	13	7 AAE39883	Aae39883 Human cyt
64	32	76.2	13	8 ADQ48407	Adq48407 Cytochrom
65	32	76.2	14	2 AAW05490	Aaw05490 SH3-bindi
66	32	76.2	14	2 AAW38067	Aaw38067 PPPPY mot
67	32	76.2	14	7 ADB49257	Adb49257 Biotinyla
68	32	76.2	15	2 AAW39034	Aaw39034 Peptide r
69	32	76.2	15	2 AAW39005	Aaw39005 Peptide r
70	32	76.2	15	2 AAW39050	Aaw39050 Peptide r
71	32	76.2	15	2 AAW38988	Aaw38988 Peptide r
72	32	76.2	15	2 AAW39035	Aaw39035 Peptide r
73	32	76.2	15	2 AAW38959	Aaw38959 Peptide r
74	32	76.2	15	2 AAW39015	Aaw39015 Peptide r
75	32	76.2	15	2 AAW39040	Aaw39040 Peptide r
76	32	76.2	15	2 AAY41635	Aay41635 Mammalian
77	32	76.2	16	2 AAW25411	Aaw25411 Crk N-ter
78	32	76.2	17	2 AAW38977	Aaw38977 Peptide r
79	32	76.2	17	2 AAW38963	Aaw38963 Peptide r
80	32	76.2	18	2 AAR91750	Aar91750 Prolyl en
81	32	76.2	18	2 AAR91746	Aar91746 Prolyl en
82	32	76.2	18	2 AAW38923	Aaw38923 Peptide r
83	32	76.2	18	2 AAW39010	Aaw39010 Peptide r
84	31	73.8	12	3 AAY56628	Aay56628 Virus-lik
85	31	73.8	12	3 AAY56271	Aay56271 Human cat
86	31	73.8	13	2 AAW05447	Aaw05447 SH3-bindi
87	31	73.8	13	2 AAW37655	Aaw37655 PPPPY mot
88	31	73.8	13	7 ADB49202	Adb49202 Biotinyla
89	31	73.8	13	7 ADB49281	Adb49281 Novel WW
90	31	73.8	14	3 ADC16813	Adc16813 Human sin
91	31	73.8	15	2 AAW38905	Aaw38905 Peptide r
92	31	73.8	16	2 AAW38947	Aaw38947 Peptide r
93	31	73.8	17	2 AAW38104	Aaw38104 Peptide r
94	31	73.8	17	7 ADB49204	Adb49204 Biotinyla
95	30	71.4	7	4 AAM47005	Aam47005 H11 bindi
96	30	71.4	7	4 AAM47010	Aam47010 H11 bindi
97	30	71.4	7	8 ADP17755	Adp17755 Prion pro
98	30	71.4	9	2 AAR60998	Aar60998 Sequence

Kam.C.  
10/69/157  
Seq IDs 1-8





DR WPI; 2001-202804/20.  
XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator.  
XX  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX  
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
CC have immune response modulatory activity, and are capable of inducing  
CC cytokines. Colostrinin and its derived peptides are useful for inducing  
CC cytokine production, for modulating an immunological response and for  
CC inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies  
XX  
XX Sequence 7 AA;  
SQ

Query Match 100.0%; Score 42; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQPPPLP 7  
DB 1 MQPPPLP 7

RESULT 5  
AAB72532  
ID AAB72532 standard; peptide; 7 AA.  
XX  
XX AAO14577;  
XX  
XX 27-MAY-2002 (first entry)  
XX  
XX Neural cell regulatory colostrinin peptide 1.  
XX  
XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
XX neural cell formation; proline-rich polypeptide aggregate; colostrum;  
XX neural cell treatment.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 7 /note= "Optional C-terminal amide"  
FT  
XX  
XX WO200213851-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022777.  
XX  
XX 17-AUG-2000; 2000WO-US022777.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Boldogh I, Stanton JG, Hughes TK;  
XX  
XX WPI; 2002-269152/31.  
XX  
XX Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog.  
XX  
XX Claim 7; Page 21; 37pp; English.  
XX  
XX The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention  
XX  
XX Sequence 7 AA;  
SQ

Query Match 100.0%; Score 42; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQPPPLP 7  
DB 1 MQPPPLP 7

RESULT 6  
AAB72532  
ID AAB72532 standard; peptide; 7 AA.  
XX  
XX AAB72532;  
XX  
XX 09-MAY-2001 (first entry)  
XX  
XX Colostrinin peptide #1.  
XX  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
XX colostrum.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200112651-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 17-AUG-2000; 2000WO-US022774.  
XX  
XX 17-AUG-1999; 99US-0149633P.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Boldogh I;  
XX  
XX WPI; 2001-226545/23.  
XX  
XX Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating damaged  
PT neural cells in a patient.  
XX  
XX Claim 6; Page 21; 35pp; English.  
XX  
XX The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
XX  
XX Sequence 7 AA;  
SQ

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ID  AAM51036 standard; peptide; 7 AA.
XX
AC  AAM51036;
XX
DT  30-MAY-2002 (first entry)
XX
DE  Colostrinin constituent peptide.
XX
KW  Colostrinin; colostrum; immunomodulator; cardiovascular;
KW  blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Modified-site 7 /note= "optional C-terminal amidation"
FT
XX  WO200213849-A1.
XX
PD  21-FEB-2002.
XX
PF  17-AUG-2000; 2000WO-US022775.
XX
PR  17-AUG-2000; 2000WO-US022775.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (REGE-) REGEN THERAPEUTICS PLC.
XX
PI  Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX  WPI; 2002-269150/31.
XX
PT  Modulation of blood cell proliferation in a patient involves use of blood
PT  cell regulator selected from colostrinin, its constituent peptide and/or
PT  analog.
XX
PS  Claim 1; Page 34; 54pp; English.
XX
CC  The present sequence is that of a colostrinin constituent peptide that is
CC  preferred for use as an immunological regulator and as a blood cell
CC  regulator in claimed methods of the invention. It is classified as having
CC  a beta-casein homologue precursor. Methods are claimed for: inducing a
CC  cytokine in a cell by contact with an immunological regulator, where the
CC  cell is present in a cell culture, a tissue, an organ or an organism, and
CC  the cell is mammalian, including human; modulating an immune response in
CC  a cell by contact with the immunological regulator under conditions
CC  effective to induce a cytokine; modulating an immune response in a
CC  patient by administering an immunological regulator under conditions
CC  effective to induce a cytokine, where the immunological regulator is
CC  administered topically or as part of a dietary supplement, and where the
CC  immune response is specific or non specific, an interferon response or an
CC  antibody response; modulating blood cell proliferation by contacting
CC  blood cells with a blood cell regulator, where the blood cells are
CC  present in a cell culture or an organism, are mammalian or human, and
CC  where the blood cells are increased in number or differentiated; and a
CC  method for modulating blood cell proliferation in a patient. A claimed
CC  cytokine-inducing composition comprises a pharmaceutical carrier and an
CC  active agent such as the present peptide. Cytokines induced by this
CC  peptide in human leucocyte cultures include interferon-gamma, tumour
CC  necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
CC  interleukin-12. It was one of the best overall inducers in almost all
CC  cytokine and blood cell proliferation experiments conducted
XX
SQ  Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 8

```

ADN60295  
 ID ADN60295 standard; peptide; 7 AA.  
 XX AC ADN60295;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Constituent peptide of colostrinin SEQ ID NO:1.  
 XX KW modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
 KW DNA damage; beta-amyloid; retinoic acid; cytosolic; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.  
 XX OS Synthetic.  
 XX PN WO2004037851-A2.  
 XX PD 06-MAY-2004.  
 XX PF 22-OCT-2003; 2003WO-US033423.  
 XX PR 22-OCT-2002; 2002US-0420369P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (BOLD/) BOLDGOH I.  
 XX PA (STAN/) STANTON J G.  
 XX -PA (GEOR/) GEORGIADIS J A.  
 XX PA (HUGH/) HUGHES T K.  
 XX PA (KRUZ/) KRUZEL M.  
 XX PI Boidogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
 XX WPI; 2004-365494/34.  
 XX DR Use of colostrinin for e.g. modulating an intracellular signaling  
 XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 XX PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 XX PT a cell.  
 XX PS Claim 6; SEQ ID NO 1; 46pp; English.  
 XX CC The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 42; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQPPPLP 7  
 DB 1 MQPPPLP 7  
 RESULT 9  
 AAB59354  
 ID AAB59354 standard; peptide; 8 AA.  
 XX AC AAB59354;  
 XX DT 21-MAR-2001 (first entry)  
 XX DE Ewe colostrinin peptide fragment derived sequence #14.

ADN74400  
 ID ADS74400 standard; peptide; 7 AA.  
 XX AC ADS74400;  
 XX DT 16-DEC-2004 (first entry)  
 XX DE Ovine colostrinin peptide.  
 XX KW Colostrum; colostrinin; sheep; peptide purification.  
 XX OS Ovis aries.  
 XX PN WO2004081038-A1.  
 XX PD 23-SEP-2004.  
 XX PF 10-MAR-2004; 2004WO-GB001014.  
 XX PR 11-MAR-2003; 2003GB-00005552.  
 XX PR 08-MAR-2004; 2004GB-00005190.  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
 XX WPI; 2004-677519/66.  
 XX DR Recovering peptides such as colostrinin from mammalian colostrum, by  
 XX PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 XX PT and precipitate, separating alcohol phase from precipitate, and  
 XX PT recovering alcohol phase.  
 XX PS Disclosure; SEQ ID NO 17; 41pp; English.  
 XX CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrinin using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.  
 XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 42; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQPPPLP 7  
 DB 1 MQPPPLP 7  
 RESULT 10  
 AAB59354  
 ID AAB59354 standard; peptide; 8 AA.  
 XX AC AAB59354;  
 XX DT 21-MAR-2001 (first entry)  
 XX DE Ewe colostrinin peptide fragment derived sequence #14.

XX Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX WO200075173-A2.  
 XX  
 XX PD 14-DEC-2000.  
 XX  
 XX PF 02-JUN-2000; 2000WO-GB002128.  
 XX PR 02-JUN-1999; 99GB-00012852.  
 XX  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 XX PI Georgiades JA;  
 XX WI; 2001-071058/08.  
 XX  
 XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 XX PS Claim 8; Page 27; 63pp; English.  
 XX  
 XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX  
 XX SQ Sequence 8 AA;

Query Match 100.0%; Score 42; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 Db 2 MQPPPLP 8

RESULT 11  
 ADK10336  
 ID ADK10336 standard; peptide; 9 AA.  
 XX  
 XX AC ADK10336;

XX DT 06-MAY-2004 (first entry)  
 XX DE Human papillomavirus peptide #2391.  
 XX

KW pathogenic virus; alternative reading frame; antigenic determinant;  
 KW virucide; vaccine; therapeutic agent; infection; HPV.  
 XX

OS Human papillomavirus.  
 XX

XX PN WO2004011650-A2.  
 XX

XX PD 05-FEB-2004.  
 XX

XX PF 24-JUL-2003; 2003WO-EP008112.  
 XX

XX PR 24-JUL-2002; 2002AT-00001124.  
 XX

XX PR 11-JUL-2003; 2003EP-00450171.  
 XX

XX PA (INTE-) INTERCELL AG.  
 XX

PI Mattner F, Schmidt W, Habel A;  
 XX  
 XX DR WI; 2004-169243/16.  
 XX  
 XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX  
 XX PS Claim 18; Page 199; 220pp; English.

XX  
 XX CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.

XX SQ Sequence 9 AA;

Query Match 92.9%; Score 39; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. NO. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 Db 1 LQPPPLP 7

RESULT 12  
 ADK10337  
 ID ADK10337 standard; peptide; 10 AA.  
 XX  
 XX AC ADK10337;

XX DT 06-MAY-2004 (first entry)  
 XX DE Human papillomavirus peptide #2392.  
 XX

KW pathogenic virus; alternative reading frame; antigenic determinant;  
 KW virucide; vaccine; therapeutic agent; infection; HPV.  
 XX

OS Human papillomavirus.  
 XX

XX PN WO2004011650-A2.  
 XX

XX PD 05-FEB-2004.  
 XX

XX PF 24-JUL-2003; 2003WO-EP008112.  
 XX

XX PR 24-JUL-2002; 2002AT-00001124.  
 XX

XX PR 11-JUL-2003; 2003EP-00450171.  
 XX

XX PA (INTE-) INTERCELL AG.  
 XX

XX PI Mattner F, Schmidt W, Habel A;  
 XX

XX DR WI; 2004-169243/16.  
 XX

XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX  
 XX PS Claim 18; Page 199; 220pp; English.

XX  
 XX CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a

CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope-peptide of the  
 CC invention.

XX Sequence 10 AA;

Query Match 92.9%; Score 39; DB 8; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 45;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 :|||||  
 Db 1 LQPPPLP 7

RESULT 13

ADK10338  
 ID ADK10338 standard; peptide; 10 AA.

XX AC ADK10338;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #2393.

XX KW pathogenic virus; alternative reading frame; antigenic determinant;  
 XX virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PN WO2004011650-A2.

XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.

XX PR 24-JUL-2002; 2002AT-00001124.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 199; 220pp; English.

XX CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.

XX Sequence 10 AA;

Query Match 92.9%; Score 39; DB 8; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 45;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 :|||||  
 Db 1 LQPPPLP 7

RESULT 14

ADK10335  
 ID ADK10335 standard; peptide; 8 AA.

XX AC ADK10335;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #2390.

XX KW pathogenic virus; alternative reading frame; antigenic determinant;  
 XX virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PN WO2004011650-A2.

XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.

XX PR 24-JUL-2002; 2002AT-00001124.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 199; 220pp; English.

XX CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.

XX Sequence 8 AA;

Query Match 88.1%; Score 37; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 :|||||  
 Db 1 QPPPLP 6

RESULT 15

ADC36090  
 ID ADC36090 standard; peptide; 12 AA.

XX AC ADC36090;

XX DT 18-DEC-2003 (first entry)

XX DE Chemokine binding peptide BKT-P4.

XX KW peptidic chemokine modulator; antiinflammatory; antiallergic;  
 XX immunosuppressive; antidiabetic; antirheumatic; dermatological;  
 KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;

KW antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotropic;  
 KW cytostatic; inflammation; allergy; immune response; autoimmune reaction;  
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
 KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;  
 KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;  
 KW hypertension; reperfusion ischaemia.

XX Synthetic.

XX WO2003072599-A2.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-IL000155.

XX PR 28-FEB-2002; 2002US-035999P.

XX PA (BIOK-) BIOKINE THERAPEUTICS LTD.

XX PI Peled A, Eizenberg O, Vaizel-Ohayon D;

XX WPI; 2003-671869/63.

XX New peptidic chemokine modulator, useful for preparing a composition for  
 PT treating a disease modulated through and/or caused by binding of a  
 PT chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis  
 PT or cancer.

XX Example 1; Page 28; 43pp; English.

XX The present invention describes a peptidic chemokine modulator (I) for  
 CC modulating a biological effect of a chemokine. (I) comprises a molecule  
 CC consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr  
 CC and Pro, and features at least 2 histidines spread along the molecule,  
 CC where the molecule features an overall positive charge (family 1); or (b)  
 CC the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two  
 CC neighbouring histidines, where the molecule features an overall positive  
 CC charge (family 2). Also described: (1) a composition for treating a  
 CC condition involving abnormal cell migration in a subject; (2) a method  
 CC for treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor in a subject; (3) an antibody for  
 CC binding to a chemokine-binding receptor that recognises at least a  
 CC portion of a chemokine-binding receptor or the peptide; (4) a vaccine  
 CC formed with the antibody; and (5) a method for producing an antibody. (I)  
 CC has antiinflammatory, anti-allergic, immunosuppressive, antidiabetic,  
 CC antirheumatic, dermatological, antiarthritic, antibacterial,  
 CC antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive,  
 CC neuroprotective, virucide, vasotropic and cytostatic activities. The  
 CC peptidic chemokine modulator is useful for preparing a composition for  
 CC treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor, comprising inflammation (primary or  
 CC secondary), allergy, a non-optimal immune response, an autoimmune  
 CC reaction (including rheumatoid arthritis, systemic lupus erythematosus,  
 CC multiple sclerosis and others), allograft rejection, diabetes, sepsis,  
 CC cancer and any type of malignant cell growth, acne and chronic bacterial  
 CC and viral infections, arthritis, colitis, psoriasis, atherosclerosis,  
 CC hypertension or reperfusion ischaemia. The present sequence represents a  
 CC chemokine binding peptide, which is used in an example from the present  
 CC invention.

XX Sequence 12 AA;

Query Match 85.7%; Score 36; DB 7; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQPPPLP 7

Db 5 MQPPPRP 11

RESULT 16  
 ADR42838

ID ADR42838 standard; peptide; 12 AA.  
 XX  
 AC ADR42838;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Modulatory chemokine-binding peptide BKT-P4.

XX Chemokine-binding peptide; MCP-1; SDF-lalpha; MIG; eotaxin;  
 KW interleukin-8; abnormal cell migration; vaccine; inflammation; allergy;  
 KW non-optimal immune response; autoimmune reaction; allograft rejection;  
 KW diabetes; sepsis; cancer; malignant cell growth; bacterial infection;  
 KW viral infection; arthritis; colitis; psoriasis; atherosclerosis;  
 KW hypertension; reperfusion ischaemia.

XX Synthetic.

XX US2004171552-A1.

XX PD 02-SEP-2004.

XX PF 28-AUG-2003; 2003US-00649873.

XX PR 27-FEB-2003; 2003WO-IL000155.

XX PA (BIOK-) BIOKINE THERAPEUTICS LTD.

XX PI Peled A, Eizenberg O, Vaizel-Ohayon D;

XX WPI; 2004-625117/60.

XX New peptidic chemokine modulators for modulating a biological effect of a  
 PT chemokine, useful for treating a condition involving abnormal cell  
 PT migration in a subject, e.g. inflammatory condition, or cancer  
 PT metastasis.

XX Claim 19; SEQ ID NO 112; 50pp; English.

XX The invention relates to peptidic chemokine modulators for modulating a  
 CC biological effect of a chemokine comprising a molecule composed of the  
 CC amino acids histidine (H), serine (S), alanine (A), leucine (L),  
 CC isoleucine (I), lysine (K), arginine (R), threonine (T), and proline (P),  
 CC and featuring at least 2 Histidines spread along said molecule, where the  
 CC molecule features an overall positive charge (family 1) or a molecule  
 CC composed of the amino acids H, P, T, L, R. Tryptophan (W), phenylalanine  
 CC (F), and featuring at least two neighbouring histidines, where the  
 CC molecule features an overall positive charge (family 2) and/or a molecule  
 CC comprising a peptide having an amino acid sequence from a list, given in  
 CC the specification. Also included are a composition for treating a  
 CC condition involving abnormal cell migration in a subject (comprising a  
 CC therapeutic agent for administering to the subject, where therapeutic  
 CC agent is any of the modulators cited above), a method for treating a  
 CC disease modulated through and/or caused by binding of a chemokine to a  
 CC chemokine receptor in a subject (by administering the therapeutic agent),  
 CC an antibody for binding a chemokine-binding receptor (comprising the  
 CC antibody capable of recognising at least a portion of a chemokine binding  
 CC receptor, where the antibody also recognises a peptide of the sequence of  
 CC the modulator), a vaccine formed with the antibody and a method for  
 CC producing an antibody (by inducing formation of antibody against a  
 CC peptide having the sequence of the chemokine modulator, where the  
 CC antibody is also capable of recognising a chemokine binding receptor).  
 CC The method, therapeutic agents and compositions are useful for treating a  
 CC disease modulated through and/or caused by binding of a chemokine to a  
 CC chemokine receptor, e.g. primary and secondary inflammation, allergy, non  
 CC -optimal immune response, autoimmune reaction, allograft rejection,  
 CC diabetes, sepsis, cancer, any type of malignant cell growth, acute and  
 CC chronic bacterial and viral infections, arthritis, colitis, psoriasis,  
 CC atherosclerosis, hypertension or reperfusion ischaemia. The present  
 CC sequence is a modulatory chemokine-binding peptide of the invention  
 CC binding chemokines MCP-1, SDF-lalpha, MIG, eotaxin and interleukin-8.

XX Sequence 12 AA;

```

Query Match      85.7%; Score 36; DB 8; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPLP 7
Db 5 MOPPPRP 11

RESULT 17
AAE32821
ID AAE32821 standard; peptide; 12 AA.
XX
AC AAE32821;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human CEA exon #24 encoded peptide.
XX
KW Human; carcinoembryonic antigen; CEA; cell adhesion-mediated disease;
KW prognosis; cancer; tumour; gene therapy; exon.
XX
OS Homo sapiens.
XX
PN WO200250508-A2.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-US014457.
XX
PR 07-MAY-2001; 2001US-0289179P.
PR 29-AUG-2001; 2001US-0315736P.
XX
PA (ALPHA-) ALPHAGENE INC.
XX
PI Stark KA, Weaver A, Hoffmann HM, Krauss R, Valenzuela DB;
PI Saini KS;
XX
WPI; 2003-111965/10.
XX
New carcinoembryonic antigen and polynucleotides encoding them, useful
for treating and/or preventing cell adhesion-mediated disease (e.g.
cancers, solid tumors, tumor metastasis or benign tumors) symptoms.
XX
Claim 17; Page 130; 143pp; English.
XX
The invention relates to novel human carcinoembryonic antigen (CEA).
polypeptides and polynucleotides encoding such polypeptides. CEA genes
are useful as diagnostic and prognostic markers of colon, stomach and
breast cancers. Polypeptides of the invention can be used to diagnose,
treat and/or prevent cell adhesion-mediated disease (e.g. cancers, solid
tumours, tumour metastasis or benign tumours) and to modulate cell-cell
or cell-matrix adhesion in mammalian tissues. The invention is useful in
gene therapy. The present sequence is human CEA exon encoded peptide.
CC Note: This sequence is stated to be encoded by SEQ ID NO: 52 (AAD50572).
CC However this does not appear to be the case
XX
Sequence 12 AA;

Query Match      81.0%; Score 34; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPLP 7
Db 1 MOPPDLP 7

RESULT 18
AAE32821
ID AAE32821 standard; peptide; 15 AA.
XX
AC AAE32821;
XX

Query Match      81.0%; Score 34; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 6 QPPPPV 11

RESULT 19
AAE32821
ID AAE32821 standard; peptide; 16 AA.
XX
AC AAE32821;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human ced-6 (hced-6) peptide epitope.
XX
KW ced-6; hced-6; h2ced-6; signal transduction pathway; phagocytosis;
KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;
KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;
KW cardiant; immunosuppressive; apoptosis modulator; epitope.
XX
OS Homo sapiens.
XX
PN WO9964586-A2.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99WO-EP004043.
XX
PR 11-JUN-1998; 98GB-00012660.
PR 24-SEP-1998; 98GB-00020816.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Smits E, Van Crielinge WMR, Bogaert TRAE;
XX
WPI; 2000-246285/21.
XX
Assays for determining the phagocytosis of apoptotic cells useful for
identifying a compound which influences the phagocytic uptake of
apoptotic cells and treats cancers and neurodegenerative diseases.
XX
Claim 62; Page 56; 122pp; English.
XX
The invention relates to assays involving two human homologues of
Caenorhabditis elegans ced-6 (hced-6 and h2ced-6) for identifying
compounds which function as an inhibitor or an enhancer of a signal
transduction pathway. The assays are carried out by measuring
phagocytosis of apoptotic cells. The methods are useful for identifying
compounds which can act as apoptotic modulators which are useful for
treating diseases such as cancer, autoimmune diseases, neurodegenerative
diseases such as Huntington's disease, stroke, myocardial infarction and
AIDS. The assays are well adapted for medium and high throughput
screening using a multi-well plate format. Sequences AAY85489-91
represent peptide epitopes of hced-6, used for generating antibodies
XX
Sequence 15 AA;

Query Match      81.0%; Score 34; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 6 QPPPPV 11

RESULT 19
AAE32821
ID AAE32821 standard; peptide; 16 AA.
XX
AC AAE32821;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human ced-6 (hced-6) peptide epitope.
XX
KW ced-6; hced-6; h2ced-6; signal transduction pathway; phagocytosis;
KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;
KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;
KW cardiant; immunosuppressive; apoptosis modulator; epitope.
XX
OS Homo sapiens.
XX
PN WO9964586-A2.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99WO-EP004043.
XX
PR 11-JUN-1998; 98GB-00012660.
PR 24-SEP-1998; 98GB-00020816.
XX
PA (DEVG-) DEVGEN NV.
XX
PI Smits E, Van Crielinge WMR, Bogaert TRAE;
XX
WPI; 2000-246285/21.
XX
Assays for determining the phagocytosis of apoptotic cells useful for
identifying a compound which influences the phagocytic uptake of
apoptotic cells and treats cancers and neurodegenerative diseases.
XX
Claim 62; Page 56; 122pp; English.
XX
The invention relates to assays involving two human homologues of
Caenorhabditis elegans ced-6 (hced-6 and h2ced-6) for identifying
compounds which function as an inhibitor or an enhancer of a signal
transduction pathway. The assays are carried out by measuring
phagocytosis of apoptotic cells. The methods are useful for identifying
compounds which can act as apoptotic modulators which are useful for
treating diseases such as cancer, autoimmune diseases, neurodegenerative
diseases such as Huntington's disease, stroke, myocardial infarction and
AIDS. The assays are well adapted for medium and high throughput
screening using a multi-well plate format. Sequences AAY85489-91
represent peptide epitopes of hced-6, used for generating antibodies
XX
Sequence 15 AA;

```

```

PN WO9964586-A2.
XX
PD 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP004043.
XX
XX 11-JUN-1998; 98GB-00012660.
XX
XX 24-SEP-1998; 98GB-00020816.
XX
XX (DEVG-) DEVGEN NV.
XX
XX Smits E, Van Crieckinge WMR, Bogaert TAOE;
PI WPI; 2000-246285/21.
XX
XX Assays for determining the phagocytosis of apoptotic cells useful for
PT identifying a compound which influences the phagocytic uptake of
PT apoptotic cells and treats cancers and neurodegenerative diseases.
XX
XX Example 6; Page 35; 122pp; English.
XX
XX The invention relates to assays involving two human homologues of
CC Caenorhabditis elegans ced-6 (hced-6 and hced-6) for identifying
CC compounds which function as an inhibitor or an enhancer of a signal
CC transduction pathway. The assays are carried out by measuring
CC phagocytosis of apoptotic cells. The methods are useful for identifying
CC compounds which can act as apoptotic modulators which are useful for
CC treating diseases such as cancer, autoimmune diseases, neurodegenerative
CC diseases such as Huntington's disease, stroke, myocardial infarction and
CC AIDS. The assays are well adapted for medium and high throughput
CC screening using a multi-well plate format. Sequences AAY85492-94
CC represent peptide epitopes of hced-6, used for generating polyclonal
CC antibodies
XX
XX Sequence 16 AA;
SQ
    Query Match      81.0%; Score 34; DB 3; Length 16;
    Best Local Similarity 83.3%; Pred. No. 3.1e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 7 QPPVP 12

RESULT 20
AAM46973
ID AAM46973 standard; peptide; 7 AA.
XX
XX AAM46973;
AC
XX 25-OCT-2001 (first entry)
DT
XX
XX H11 binding site consensus conforming peptide (CCP) #3244.
DE
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX CA2290722-A1.
PN
XX 08-JUN-2001.
PD
XX 08-DEC-1999; 99CA-02290722.
PF
XX 08-DEC-1999; 99CA-02290722.
PR
XX (NOVO-) NOVOPHARM BIOTECH INC.
PA

Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
Entwistle JM, Macdonald GC;
WPI; 2001-425937/46.
Composition useful for treating and diagnosing cancer, comprises stress
protein-peptide complexes associated with tumor, and isolated antigen-
binding fragments of an antibody that binds specifically to the complex.
Example 4; Page 112; 154pp; English.
The present invention describes a composition (I) comprising stress
protein-peptide complexes (SPPC) associated with tumours that is
specifically immunogenically cross-reactive with cell surface-associated
SPPCs specific to target cancer (TC). Also described is an isolated
antigen-binding fragment of an antibody that binds specifically to SPPCs
or a population of different SPPCs consisting of immunogenic cancer cell
surface-associated SPPC of TC. (I) has cytostatic activity and can be
used in vaccine production and as a tumour-specific immunogenic response
inducer. (I) is useful for treating 71 types of cancers or tumours in a
subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
ectodermal tumour (PNET). (I) is useful as cancer immunogen including
vaccines. (I) is useful for diagnostic and palliative use, for detecting
or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention
XX
XX Sequence 7 AA;
SQ
    Query Match      78.6%; Score 33; DB 4; Length 7;
    Best Local Similarity 83.3%; Pred. No. 1.8e+06;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7
Db 2 RPPPLP 7

RESULT 21
AAW06853
ID AAW06853 standard; peptide; 10 AA.
XX
XX AAW06853;
AC
XX 16-FEB-1997 (first entry)
DT
XX
XX Peptide binding the Crk-SH3 domain, used to treat cancer.
DE
XX
XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;
KW diagnosis; antibody; signal transduction; disease; disorder;
KW intracellular signalling protein.
XX
XX Synthetic.
OS
XX WO9621011-A2.
PN
XX 11-JUL-1996.
PD
XX 28-DEC-1995; 95WO-US016979.
PF
XX 30-DEC-1994; 94US-00367070.
PR
XX (UVRQ) UNIV ROCKEFELLER.
PA
XX Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;
PI Cowburn D;
XX
XX WPI; 1996-333986/33.
XX
XX New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for
PT the diagnosis and treatment of defects in intracellular signal

```





XX PPPPY motif containing peptide used to bind WW domains.  
 XX  
 DE Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KW cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction; YAP protein; dystrophin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9737223-A1.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 03-APR-1997; 97WO-US005547.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYN-) UNIV NORTH CAROLINA.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 XX  
 DR WPI; 1997-503234/46.  
 XX  
 PT Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are useful  
 PT in targeted drug selection.  
 XX  
 PS Disclosure; Fig 15B; 220pp; English.  
 XX  
 CC Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is found  
 CC in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
 CC containing this residue have been shown to bind the YAP WW domain, but  
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
 CC AAW38068-92 were biotinylated and complexed with alkaline streptavidin,  
 CC and used in a cross affinity mapping experiment. They were tested for  
 CC their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were  
 CC expressed as glutathione-S-transferase expression proteins. The present  
 CC peptide, derived from WBP-2A, does not bind to the WW domains of the  
 CC novel protein. The WW domain is a small functional domain. Its name is  
 CC derived from the observation that two tryptophan residues, one in the  
 CC amino terminal portion of the WW domain and one in the carboxyl terminal  
 CC portion, are conserved. Most proteins containing WW domains have a  
 CC function involving cell signalling and growth regulation or the  
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain are  
 CC identified by treating a multivalent recognition unit complex that has  
 CC selective binding affinity for a WW domain, with many polypeptides and  
 CC identifying those with selective affinity for the complex. Proteins  
 CC containing WW domains are used for targeted drug screening, i.e. to  
 CC identify potential modulators of specific WW domain interactions  
 XX  
 SQ Sequence 13 AA;  
 Query Match 78.6%; Score 33; DB 2; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MQPPPLP 7  
 Db :||| |  
 2 VQPPAP 8  
 RESULT 25  
 ADB49333  
 ID ADB49333 standard; peptide; 13 AA.  
 XX  
 AC ADB49333;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Biotinylated WW domain binding peptide #5.  
 XX  
 KW WW domain; drug candidate screening; drug discovery; drug modification;

KW drug refinement; immunogen; WW binding protein; WW domain.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003077577-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 28-JUN-2002; 2002US-00185050.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 PR 03-APR-1997; 97US-00826516.  
 XX  
 PA (PIROZZI) PIROZZI G.  
 PA (KAYB/) KAY B K.  
 PA (FOWL/) FOWLKES D M.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 XX  
 DR WPI; 2003-635075/60.  
 XX  
 PT Novel purified polypeptide comprising WW domain, useful for drug  
 PT discovery, modification and refinement, for discovering polypeptides  
 PT involved in pharmacological activities, or as an immunogen to generate  
 PT antibodies.  
 XX  
 PS Example; Fig 15A; 133pp; English.  
 XX  
 CC The invention describes a purified polypeptide (I) comprising a WW domain  
 CC which has a sequence (S1) selected from 11 sequences fully defined in the  
 CC specification, a sequence (S2) selected from 48 sequences fully defined  
 CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
 CC amino acids fully defined in the specification. (I) is useful for  
 CC screening a potential drug candidate, by allowing (I) to come into  
 CC contact with at least one recognition unit having a selective affinity  
 CC for the WW domain in (I), in the presence of an amount of a potential  
 CC drug candidate, such that (I) and the recognition unit are capable of  
 CC interacting when brought into contact with one another in the absence of  
 CC the drug candidate, and determining the effect, if any, of the presence  
 CC of the amount of the drug candidate on the interaction of (I) with the  
 CC recognition unit. (I) is useful for drug discovery, modification and  
 CC refinement, for discovering polypeptides involved in pharmacological  
 CC activities, or as an immunogen to generate antibodies. This is the amino  
 CC acid sequence of a WW domain binding peptide.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 78.6%; Score 33; DB 7; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MQPPPLP 7  
 Db :||| |  
 2 VQPPAP 8  
 RESULT 26  
 AAR91753  
 ID AAR91753 standard; peptide; 6 AA.  
 XX  
 AC AAR91753;  
 XX  
 DT 14-AUG-1996 (first entry)  
 XX  
 DE Prolyl endopeptidase inhibitor peptide #8.  
 XX  
 KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;  
 KW prevention; dementia; human.  
 XX  
 OS Synthetic.  
 XX  
 PN JP08059697-A.  
 XX

PD 05-MAR-1996.  
 XX  
 PF 09-MAR-1995; 95JP-00079661.  
 XX  
 PR 15-JUN-1994; 94JP-00158031.  
 XX  
 PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (NIHA-) NIPPON HAM KK.  
 XX  
 DR WPI; 1996-184809/19.  
 XX  
 PT Prolyl-endo:peptidase inhibitory peptide(s) - useful as additives for  
 PT food and animal feed and to treat and prevent dementia.  
 XX  
 PS Claim 1; Page 11; 11pp; Japanese.  
 XX  
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.  
 CC These peptides are useful as PEP inhibitors in functional foods and in  
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical  
 CC preparations for the treatment and prevention of dementia of animals,  
 CC including humans. The advantage with using these peptides, is that they  
 CC are safe and easily absorbed  
 XX  
 SQ Sequence 6 AA;  
 Query Match 76.2%; Score 32; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 .Qy 3 PPPLP 7  
 Db 2 PPPLP 6  
 .  
 RESULT 27  
 AAR60997  
 ID AAR60997 standard; peptide; 7 AA.  
 XX  
 AC AAR60997;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 14-APR-1995 (first entry)  
 DE  
 XX Fragment of the 3BP1 protein that binds to SH3 of Ab1 kinase.  
 XX CD4; T cell; surface antigen; receptor; MHC class II antigen;  
 KW protein-tyrosine kinase; p56lck; TCR/CD3 complex; PI 3-kinase;  
 KW PI 4-kinase; lipid kinase; T cell receptor complex; 3BP1; SH3;  
 KW Ab1 kinase.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9418832-A1.  
 XX  
 XX 01-SEP-1994.  
 PD  
 XX 25-FEB-1994; 94WO-US001840.  
 XX  
 XX 26-FEB-1993; 93US-00023915.  
 XX  
 XX (DAND ) DANA FARBER CANCER INST INC.  
 FA  
 XX Rudd CB, Kanteti P, Cantley L;  
 PI  
 XX WPI; 1994-293868/36.  
 DR  
 XX Method for inhibiting or reducing signal transduction - utilises peptide  
 PT or corresp. nucleic acid which decreases association of PI 3- or 4-  
 PT kinase with CD4/p56lck.  
 XX  
 PS Example; Page 32; 46pp; English.  
 XX  
 CC In order for certain T cells to make an optimal response to antigen, it

CC is necessary for the T cell surface antigen CD4 to couple to the protein-  
 CC tyrosine kinase p56lck. (CD4-p56lck is known to associate with and  
 CC functionally synergise with the Tcr/CD3 complex.) CD4-p56lck complex in T  
 CC cells associates with two lipid kinases: PI 3-kinase and PI 4-kinase,  
 CC which suggests that these lipid kinases are also involved in  
 CC intracellular signalling via the T cell receptor complex. The interaction  
 CC of a lipid kinase, such as PI 3-kinase or PI 4- kinase, with CD4-p56lck,  
 CC may be blocked by administering a peptide. This peptide may be a fragment  
 CC of the cytoplasmic domain of CD4 (eg AAR60987-R60991), a fragment of  
 CC p56lck (eg AAR60992, AAR60993), a fragment of PI 3-kinase (eg AAR60994,  
 CC AAR60995), or a fragment of PI 4-kinase. Other proline-rich peptides that  
 CC bind to SH3 binding sequences can also be used, such as the fragment of  
 CC 3BP1 protein that binds to the SH3 of the Ab1 kinase (AAR60997), or a  
 CC sequence found in the SOS protein (AAR60999). (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 7 AA;  
 Query Match 76.2%; Score 32; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 PPPLP 7  
 Db 1 PPPLP 5  
 .  
 RESULT 28  
 AAR91752  
 ID AAR91752 standard; peptide; 7 AA.  
 XX  
 AC AAR91752;  
 XX  
 DT 14-AUG-1996 (first entry)  
 XX  
 DE Prolyl endopeptidase inhibitor peptide #7.  
 XX  
 KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;  
 KW prevention; dementia; human.  
 XX  
 XX Synthetic.  
 OS  
 XX JP08059697-A.  
 XX  
 XX 05-MAR-1996.  
 PD  
 XX 09-MAR-1995; 95JP-00079661.  
 PF  
 XX 15-JUN-1994; 94JP-00158031.  
 PR  
 XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 XX (NIHA-) NIPPON HAM KK.  
 PA  
 XX WPI; 1996-184809/19.  
 DR  
 XX Prolyl-endo:peptidase inhibitory peptide(s) - useful as additives for  
 PT food and animal feed and to treat and prevent dementia.  
 PT  
 XX Claim 1; Page 11; 11pp; Japanese.  
 PS  
 XX AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.  
 CC These peptides are useful as PEP inhibitors in functional foods and in  
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical  
 CC preparations for the treatment and prevention of dementia of animals,  
 CC including humans. The advantage with using these peptides, is that they  
 CC are safe and easily absorbed  
 XX  
 SQ Sequence 7 AA;  
 Query Match 76.2%; Score 32; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query Match 76.2%; Score 32; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 2 PPPLP 6

## RESULT 29

AAM46827  
 ID AAM46827 standard; peptide; 7 AA.

XX AC AAM46827;  
 XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #308.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependynoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.  
 OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-02290722.

XX 08-DEC-1999; 99CA-02290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.

XX Example 4; Page 112; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependynoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention

XX Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

## RESULT 31

AAM46876  
 ID AAM46876 standard; peptide; 7 AA.

XX AC AAM46876;

## RESULT 30

AAM46861  
 ID AAM46861 standard; peptide; 7 AA.

XX AC AAM46861;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #3132.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependynoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.  
 OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-02290722.

XX 08-DEC-1999; 99CA-02290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.

XX Example 4; Page 112; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependynoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention

XX Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

Db 3 PPPLP 7

XX 25-OCT-2001 (first entry)  
 XX H11 binding site consensus conforming peptide (CCP) #3147.  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-Al.  
 XX 08-JUN-2001.  
 XX 08-DEC-1999; 99CA-02290722.  
 XX 08-DEC-1999; 99CA-02290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 XX Kaplan HA, Maiti PK, Past DG, Herman W, Dan MD, Lewis KB;  
 PI Entwistle JM, Macdonald GC;  
 XX WPI; 2001-425937/46.  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX Example 4; Page 112; 154pp; English.  
 XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX Sequence 7 AA;  
 SQ  
 Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPLP 7  
 Db |||||  
 3 PPPLP 7  
 RESULT 32  
 AAM47027  
 ID AAM47027 standard; peptide; 7 AA.  
 XX AC AAM47027;  
 XX 25-OCT-2001 (first entry)  
 XX H11 binding site consensus conforming peptide (CCP) #3298.

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-Al.  
 XX 08-JUN-2001.  
 XX 08-DEC-1999; 99CA-02290722.  
 XX 08-DEC-1999; 99CA-02290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 XX Kaplan HA, Maiti PK, Past DG, Herman W, Dan MD, Lewis KB;  
 PI Entwistle JM, Macdonald GC;  
 XX WPI; 2001-425937/46.  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX Example 4; Page 112; 154pp; English.  
 XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX Sequence 7 AA;  
 SQ  
 Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPLP 7  
 Db |||||  
 3 PPPLP 7  
 RESULT 33  
 AAM46856  
 ID AAM46856 standard; peptide; 7 AA.  
 XX AC AAM46856;  
 XX 25-OCT-2001 (first entry)  
 XX H11 binding site consensus conforming peptide (CCP) #3127.  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

```
XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-02290722.
XX PR 08-DEC-1999; 99CA-02290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX PI Entwistle JM, Macdonald GC;
XX DR WPI; 2001-425937/46.
XX PS Composition useful for treating and diagnosing cancer, comprises stress
XX PT protein-peptide complexes associated with tumor, and isolated antigen-
XX PT binding fragments of an antibody that binds specifically to the complex.
XX PS Example 4; Page 112; 154pp; English.
XX CC The present invention describes a composition (I) comprising stress
XX CC protein-peptide complexes (SPPC) associated with tumours that is
XX CC specifically immunogenically cross-reactive with cell surface-associated
XX CC SPPCs specific to target cancer (TC). Also described is an isolated
XX CC antigen-binding fragment of an antibody that binds specifically to SPPCs
XX CC or a population of different SPPCs consisting of immunogenic cancer cell
XX CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX CC used in vaccine production and as a tumour-specific immunogenic response
XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX CC or imaging cancer cells, and to monitor the course of amelioration of
XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 3 PPPLP 7

RESULT 34
AAM46871
ID AAM46871 standard; peptide; 7 AA.
AC AAM46871;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3142.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
```

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XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-02290722.
XX PR 08-DEC-1999; 99CA-02290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX PI Entwistle JM, Macdonald GC;
XX DR WPI; 2001-425937/46.
XX PS Composition useful for treating and diagnosing cancer, comprises stress
XX PT protein-peptide complexes associated with tumor, and isolated antigen-
XX PT binding fragments of an antibody that binds specifically to the complex.
XX PS Example 4; Page 112; 154pp; English.
XX CC The present invention describes a composition (I) comprising stress
XX CC protein-peptide complexes (SPPC) associated with tumours that is
XX CC specifically immunogenically cross-reactive with cell surface-associated
XX CC SPPCs specific to target cancer (TC). Also described is an isolated
XX CC antigen-binding fragment of an antibody that binds specifically to SPPCs
XX CC or a population of different SPPCs consisting of immunogenic cancer cell
XX CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX CC used in vaccine production and as a tumour-specific immunogenic response
XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX CC or imaging cancer cells, and to monitor the course of amelioration of
XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 3 PPPLP 7

RESULT 35
AAM46851
ID AAM46851 standard; peptide; 7 AA.
AC AAM46851;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3122.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-02290722.
```

```

PR 08-DEC-1999; 99CA-02290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, Macdonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated antigen-
XX binding fragments of an antibody that binds specifically to the complex.
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention
XX
XX Sequence 7 AA;
XX
XX Query Match 76.2%; Score 32; DB 4; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 3 PPPLP 7
XX DB 3 PPPLP 7
XX
XX RESULT 36
XX AAM46866
XX ID AAM46866 standard; peptide; 7 AA.
XX AC AAM46866;
XX XX
XX DT 25-OCT-2001 (first entry)
XX DE H11 binding site consensus conforming peptide (CCP) #3137.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytosstatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX OS Synthetic.
XX XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-02290722.
XX 08-DEC-1999; 99CA-02290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX

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PI Entwistle JM, Macdonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated antigen-
XX binding fragments of an antibody that binds specifically to the complex.
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention
XX
XX Sequence 7 AA;
XX
XX Query Match 76.2%; Score 32; DB 4; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 3 PPPLP 7
XX DB 3 PPPLP 7
XX
XX RESULT 37
XX AAR71945
XX ID AAR71945 standard; peptide; 8 AA.
XX AC AAR71945;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 17-OCT-1995 (first entry)
XX XX
XX DE Human 3BP1 peptide.
XX
XX Grb3-3; cancer; apoptosis; AIDS; gene therapy; 3BP1; SH3 domain.
XX
XX Synthetic.
XX
XX WO9507981-A1.
XX
XX 23-MAR-1995.
XX
XX 09-MAY-1994; 94WO-FR000542.
XX
XX 15-SEP-1993; 93FR-00010971.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Schweighoffer F, Tocque B;
XX
XX WPI; 1995-131349/17.
XX
XX New human Grb3-3 gene and vectors contg. it - useful in control of cell
XX death etc. partic. for treating cancer and AIDS.
XX
XX Example 2; Page 11; 31pp; French.
XX
XX The hSOS1 and 3BP1 peptides given in AAR71944-45 were used to demonstrate
XX

```

CC that the newly isolated human Grb3-3 protein was able to bind hSOS1, but  
 CC not to the 3BP1 peptide, which corresponds to the SH3 domain of Abl and  
 CC Src. A Grb3-3G162R mutant was unable to bind the hSOS1 peptide. (Updated  
 CC on 25-MAR-2003 to correct PN field.)  
 XX  
 XX

SO Sequence 8 AA;

Query Match 76.2%; Score 32; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 1 PPPLP 5

RESULT 38  
 ABW01573  
 ID ABW01573 standard; peptide; 9 AA.

XX  
 XX ABW01573;  
 AC  
 DT 12-FEB-2004 (first entry)  
 DE Mouse Fmn-2 FH1 domain proline repeat motif #4.  
 XX  
 XX Recurrent pregnancy loss; RPL; formin-2; Fmn-2; diagnosis; therapy;  
 KW mouse.  
 XX  
 XX Mus musculus.  
 OS  
 XX US2003170683-A1.  
 PN  
 XX 11-SEP-2003.  
 PD  
 XX 03-DEC-2002; 2002US-00308485.  
 PF  
 XX 13-APR-2000; 2000US-0196811P.  
 PR  
 XX 12-APR-2001; 2001US-00835232.  
 ,XX  
 PA (LEDE/) LEADER P.  
 PA (LEAD/) LEADER B.  
 XX  
 XX Leder P, Leader B;  
 PI  
 XX WPI; 2003-830607/77.  
 DR  
 XX

Diagnosing recurrent pregnancy loss comprises examining formin-2 gene for  
 a mutation and measuring biological activity and expression of formin-2  
 identified to play a role in oocyte development.

Example 1; Page 7; Opp; English.

The invention relates to a method of diagnosing recurrent pregnancy loss  
 (RPL). The method involves examining formin (Fmn)-2 gene for a mutation  
 and measuring biological activity and expression of Fmn-2, in which  
 decreased levels indicates an increased risk for RPL; or examining the  
 person's formin-2 gene for polymorphisms, in which the presence of a  
 polymorphism indicates an altered risk for RPL. The method is used for  
 diagnosing and treating RPL e.g. in humans. The present sequence is mouse  
 Fmn-2 FH1 domain proline repeat motif

Sequence 9 AA;

Query Match 76.2%; Score 32; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 4 PPPLP 8

RESULT 39

AAR77371  
 ID AAR77371 standard; peptide; 10 AA.  
 XX  
 AC AAR77371;  
 XX  
 DT 17-JAN-1996 (first entry)  
 DE SH3 binding domain 3BP-1.  
 XX  
 KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;  
 XX Src homology 3; SH3 binding domain; 3BP-1.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9525125-A1.  
 PN  
 XX 21-SEP-1995.  
 PD  
 XX 14-MAR-1995; 95WO-US003610.  
 PF  
 XX 14-MAR-1994; 94US-00212190.  
 PR  
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Kohn EC, Liotta LA, Kim YS;  
 PI  
 XX WPI; 1995-336944/43.  
 DR  
 XX DNA encoding CAI resistance proteins - used in gene therapy, and for  
 XX detecting CAI resistance in biological samples.  
 PT  
 XX Example 4; Page 40; 56pp; English.  
 PS  
 XX CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human  
 CC melanoma cells, contains a unique proline-rich sequence which fulfills  
 CC the consensus definition for Src homology 3 (SH3) binding proteins  
 CC (AAR77366). 4 Unique versions (AAR77367-70) are present that show  
 CC homology to the known SH3 binding domains: 3BP-1, and the p85-alpha-1 and  
 CC -2 subunits of phosphatidylinositol 3' kinase (AAR77371-73)  
 XX  
 XX Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 5 PPPLP 9

RESULT 40

AAW06861  
 ID AAW06861 standard; peptide; 10 AA.

XX  
 AC AAW06861;  
 XX  
 DT 16-FEB-1997 (first entry)  
 DE Peptide binding the Crk-SH3 domain, used to treat cancer.  
 XX  
 XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;  
 KW diagnosis; antibody; signal transduction; disease; disorder;  
 KW intracellular signalling protein.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9621011-A2.  
 PN  
 XX 11-JUL-1996.  
 PD  
 XX 28-DEC-1995; 95WO-US016979.  
 PF



XX 30-DEC-1994; 94US-00367070.  
PR (UVRQ ) UNIV ROCKEFELLER.  
XX  
XX Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;  
PI Cowburn D;  
XX  
XX WPI; 1996-333986/33.  
XX  
XX New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for  
PT the diagnosis and treatment of defects in intracellular signal  
PT transduction, partic. in cancer.  
XX  
XX Claim 3; Page 93; 120pp; English.  
XX  
XX New peptides or proteins which comprise these peptides, bind to the Crk-  
CC SH3 domain and competitively inhibit the binding of intracellular  
CC signalling proteins. They can be used in the treatment of a disease or  
CC disorder associated with a defect in intracellular signal transduction,  
CC particularly cancer. They can also be used to diagnose such diseases and  
CC disorders. Antibodies raised against these proteins can be used for the  
CC same purposes. The peptides are derived from the Crk-SH3 binding domains  
CC of intracellular signalling proteins. Peptides related to the invention  
CC are described in AAW03149-63 and AAW06842-W06866  
XX  
SQ Sequence 10 AA;  
Query Match 76.2%; Score 32; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred.No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 PPPLP 7  
Db 2 PPPLP 6  
Search completed: June 7, 2005, 23:10:38  
Job time : 42.6727 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 9.54545 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	33	78.6	10	3	US-08-602-999A-278
3	33	78.6	10	4	US-09-500-124-278
4	32	76.2	7	1	US-08-230-047-40
5	32	76.2	7	5	PCT-US94-01840-11
6	32	76.2	8	1	US-09-641-640-8
7	32	76.2	8	2	US-08-612-857-8
8	32	76.2	10	1	US-08-230-047-12
9	32	76.2	10	1	US-08-230-047-14
10	32	76.2	10	1	US-08-212-190A-8
11	32	76.2	10	2	US-08-900-321-8
12	32	76.2	10	3	US-08-899-595-8
13	32	76.2	10	4	US-09-436-469-8
14	32	76.2	10	5	PCT-US95-03610-8
15	32	76.2	11	1	US-08-336-343A-25
16	32	76.2	11	3	US-08-652-877-22
17	32	76.2	11	3	US-08-652-877-32
18	32	76.2	11	3	US-08-476-515A-22
19	32	76.2	11	3	US-08-476-515A-32
20	32	76.2	12	1	US-08-230-047-17
21	32	76.2	12	3	US-08-602-999A-251
22	32	76.2	12	3	US-08-602-999A-267
23	32	76.2	12	4	US-09-500-124-251
24	32	76.2	12	4	US-09-500-124-267
25	32	76.2	13	4	US-09-485-529-103
26	32	76.2	14	1	US-08-185-432-12
27	32	76.2	14	3	US-08-630-916A-63
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## ALIGNMENTS

RESULT 1  
US-09-641-803-1  
; Sequence 1, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-1

Query Match 100.0%; Score 42; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
: |||||  
DB 1 MQPPPLP 7

RESULT 2  
US-08-602-999A-278  
; Sequence 278, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 278:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-278  
Query Match 78.6%; Score 33; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 38;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QPPPLP 7  
: |||||  
DB 1 KPPPLP 6  
; RESULT 3  
US-09-500-124-278  
; Sequence 278, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 278:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-278

Query Match 78.6%; Score 33; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 38;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPLP 7  
:|||||  
Db 1 KPPLP 6

RESULT 4  
US-08-230-047-40  
; Sequence 40, Application US/08230047  
; Patent No. 554109  
; GENERAL INFORMATION:  
; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3043  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-40

Query Match 76.2%; Score 32; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
:|||||  
Db 1 PPPLP 5

RESULT 5  
PCT-US94-01840-11  
; Sequence 11, Application PC/TUS9401840  
; GENERAL INFORMATION:  
; APPLICANT: Christopher E. Rudd  
; APPLICANT: Prasad Kanteti  
; APPLICANT: Lewis Cantley  
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF  
; TITLE OF INVENTION: LIPID KINASES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street

CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01840  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/023,915  
; FILING DATE: February 26, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janis K. Fraser  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/063001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: Linear  
PCT-US94-01840-11

Query Match 76.2%; Score 32; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
:|||||  
Db 1 PPPLP 5

RESULT 6  
US-09-641-640-8  
; Sequence 8, Application US/09641640  
; Patent No. RE37952  
; GENERAL INFORMATION:  
; APPLICANT: SCHWEIGHOFFER, Fabien  
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Rd. 3043  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/641,640  
; FILING DATE: 15-Aug-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,857  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: WO PCT/FR94/00542  
; FILING DATE: 09-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: 38,619  
REFERENCE/DOCKET NUMBER: ST93044-US  
TELEPHONE: (610)454-3839  
TELEFAX: (610)454-3808  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..8  
OTHER INFORMATION: /note= "3BPl peptide"  
US-09-641-640-8

Query Match 76.2%; Score 32; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 1 PPPLP 5

RESULT 7  
US-08-612-857-8  
Sequence 8, Application US/08612857  
Patent No. 5831048  
GENERAL INFORMATION:  
APPLICANT: SCHWEIGHOFFER, Fabien  
APPLICANT: TOCQUE, Bruno  
TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd. 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,857  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93-10971  
FILING DATE: 15-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR94/00542  
FILING DATE: 09-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: 38,619  
REFERENCE/DOCKET NUMBER: ST93044-US  
TELEPHONE: (610)454-3839  
TELEFAX: (610)454-3808  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..8  
OTHER INFORMATION: /note= "3BPl peptide"  
US-08-612-857-8

Query Match 76.2%; Score 32; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 1 PPPLP 5

RESULT 8  
US-08-230-047-12  
Sequence 12, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:  
APPLICANT: Searfoss III, George H.  
APPLICANT: Ivashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-12

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 9  
US-08-230-047-14  
Sequence 14, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:

APPLICANT: Searfoss III, George H.  
APPLICANT: Ivashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (Patentin)  
CURRENT APPLICATION DATA:  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-14

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 6 PPPLP 10

RESULT 10  
US-08-212-190A-8  
Sequence 8, Application US/08212190A  
Patent No. 5652223  
GENERAL INFORMATION:  
APPLICANT: KOHN, Elise C.  
APPLICANT: LIOTTA, Lance A.  
APPLICANT: KIM, Young Sook  
TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/212,190A  
FILING DATE: 14-MAR-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 15280-204US  
REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-212-190A-8

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 11  
US-08-900-321-8  
Sequence 8, Application US/08900321  
Patent No. 5981712  
GENERAL INFORMATION:  
APPLICANT: Kohn, Elise C.  
APPLICANT: Liotta, Lance A.  
APPLICANT: Kim, Young S.  
TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,321  
FILING DATE: 25-JUL-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,190  
FILING DATE: 14-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-204100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-900-321-8

Query Match 76.2%; Score 32; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 5 PPPLP 9

RESULT 12  
US-08-899-595-8  
; Sequence 8, Application US/08899595  
; Patent No. 6111072  
; GENERAL INFORMATION:  
; APPLICANT: Narumiya, Shuh  
; APPLICANT: Takahashi, No. 6111072uaki  
; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,595  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-242701  
; FILING DATE: 26-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 9-90170  
; FILING DATE: 25-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stephen A. Bent  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 049441/0112  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 10  
; OTHER INFORMATION: /product= "G/S/A/V"  
US-08-899-595-8

Query Match 76.2%; Score 32; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 4 PPPLP 8

RESULT 13  
US-09-436-469-8  
; Sequence 8, Application US/09436469

; Patent No. 6790936  
; GENERAL INFORMATION:  
; APPLICANT: Kohn, Elise C.  
; Liotta, Lance A.  
; Kim, Young S.  
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and  
; Uses Thereof  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/436,469  
; FILING DATE: 08-NO. 6790936-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/900,321  
; FILING DATE: 25-JUL-1997  
; APPLICATION NUMBER: US 08/212,190  
; FILING DATE: 14-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-204100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-436-469-8

Query Match 76.2%; Score 32; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 5 PPPLP 9

RESULT 14  
PCT-US95-03610-8  
; Sequence 8, Application PC/TUS9503610  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
; USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03610  
; FILING DATE: 14-MAR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 08/212,190  
FILING DATE: 14-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-204000PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-03610-8

Query Match 76.2%; Score 32; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 15  
US-08-336-343A-25  
Sequence 25, Application US/08336343A  
Patent No. 5677144  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
APPLICANT: Alves, Frauke  
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,343A  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742.  
REFERENCE/DOCKET NUMBER: 7683-065  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-336-343A-25

Query Match 76.2%; Score 32; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 4 PPPLP 8

RESULT 16  
US-08-652-877-22  
Sequence 22, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjaln, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15203  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355E-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-652-877-22

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 4 PPPLP 8

RESULT 17

US-08-652-877-32  
; Sequence 32, Application US/08652877  
; Patent No. 6187548

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjaln, Goran

TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
THEREOF AND DNA ENCODING SAME

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd., 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426-0107

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.5.1

SOFTWARE: Word 6.0 (Patentin)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,877

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15203

FILING DATE: 22-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/344,836

FILING DATE: 23-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,314

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: A1355E-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-454-3816

TELEFAX: 610-454-3808

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

US-08-652-877-32

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

Db 4 PPPLP 8

RESULT 18

US-08-476-515A-22

; Sequence 22, Application US/08476515A

; Patent No. 6239270

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran

APPLICANT: Juhlin, Claes

APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjaln, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
THEREOF AND DNA ENCODING SAME  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Martin Savitzky  
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
STREET: 3C43,  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Compaq PC  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Word 7.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,515A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/SE94/00483  
FILING DATE: 24-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9301764-8  
FILING DATE: 24-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-476-515A-22

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

Db 4 PPPLP 8

RESULT 19

US-08-476-515A-32

; Sequence 32, Application US/08476515A

; Patent No. 6239270

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran

APPLICANT: Juhlin, Claes

APPLICANT: Rask, Lars

APPLICANT: Crumley, Gregg R.

APPLICANT: Morse, Clarence C.

APPLICANT: Murray, Edward M.

APPLICANT: Hjaln, Goran

;; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
;; TITLE OF INVENTION: Thereof and DNA Encoding Same  
;; NUMBER OF SEQUENCES: 84  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Martin Savitzky  
;; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
;; STREET: 3C43,  
;; CITY: Collegeville  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19426-0107  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Compaq PC  
;; OPERATING SYSTEM: Windows 95  
;; SOFTWARE: Word 7.0 (Patentin)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/476.515A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/344.836  
;; FILING DATE: 23-NOV-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/SE94/00483  
;; FILING DATE: 24-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: SE 9301764-8  
;; FILING DATE: 24-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Savitzky, Martin  
;; REGISTRATION NUMBER: 29,699  
;; REFERENCE/DOCKET NUMBER: A1355D  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610-454-3816  
;; TELEFAX: 610-454-3808  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 11 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; FRAGMENT TYPE: internal  
;; US-08-476-515A-32  
  
Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PPPLP 7  
Db 4 PPPLP 8  
  
RESULT 20  
US-08-230-047-17  
; Sequence 17, Application US/08230047  
; Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA

;; ZIP: 19426  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Macintosh  
;; OPERATING SYSTEM: System 7.1  
;; SOFTWARE: Word 5.0 (Patentin)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/230.047  
;; FILING DATE: 19-APR-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goodman, Rosanne  
;; REGISTRATION NUMBER: 32,534  
;; REFERENCE/DOCKET NUMBER: A1465-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (610) 454-3817  
;; TELEFAX: (610) 454-3808  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-230-047-17  
  
Query Match 76.2%; Score 32; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PPPLP 7  
Db 4 PPPLP 8  
  
RESULT 21  
US-08-602-999A-251  
; Sequence 251, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602.999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-251

Query Match 76.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 6 PPPLP 10

RESULT 22  
US-08-602-999A-267  
Sequence 267, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 267:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-267

Query Match 76.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 6 PPPLP 10

RESULT 23  
US-09-500-124-251  
Sequence 251, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-251

Query Match 76.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 6 PPPLP 10

RESULT 24  
US-09-500-124-267  
Sequence 267, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 267:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-267

Query Match 76.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 6 PPPLP 10

NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500.124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602.999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 267:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-267

Query Match 76.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 6 PPPLP 10

RESULT 25  
US-09-485-529-103  
Sequence 103, Application US/09485529  
Patent No. 6762348  
GENERAL INFORMATION:  
APPLICANT: Harberd, Nicholas P  
APPLICANT: Richards, Donald E  
APPLICANT: Peng, Jinrong  
TITLE OF INVENTION: Genetic Control of Plant Growth and Development  
FILE REFERENCE: 620-91  
CURRENT APPLICATION NUMBER: US/09/485.529  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/GB98/02383  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: GB 9717192.0  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 103  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Triticum aestivum  
US-09-485-529-103

Query Match 76.2%; Score 32; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 26  
US-08-185-432-12  
Sequence 12, Application US/08185432  
Patent No. 5750652  
GENERAL INFORMATION:  
APPLICANT: Artavanis-Tsakonas, Spyridon  
APPLICANT: Busseau, Isabelle  
APPLICANT: Diederich, Robert J.  
APPLICANT: Xu, Tian  
APPLICANT: Matsuno, Kenji  
TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND  
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/185.432  
FILING DATE: 21-JAN-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-006  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-185-432-12

Query Match 76.2%; Score 32; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 4 PPPLP 8

RESULT 27  
US-08-630-916A-63  
Sequence 63, Application US/08630916A  
Patent No. 6011137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas

;; CITY: New York  
;; STATE: New York  
;; COUNTRY: United States  
;; ZIP: 10036-2711  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/630,916A  
;; FILING DATE: 03-APR-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MISROCK, S. LESLIE  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-203  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 896-8864/9741  
;;  
;; INFORMATION FOR SEQ ID NO: 63:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;;  
;; US-08-630-916A-63

Query Match 76.2%; Score 32; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 28  
US-08-630-915A-186  
; Sequence 186, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-8864/9741  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 186:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;;  
;; US-08-630-915A-186

Query Match 76.2%; Score 32; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 29  
US-09-879-957-186  
; Sequence 186, Application US/09879957  
; Patent No. 6709821  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6709821h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,957  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,915  
; FILING DATE: 03-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 186:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:  
; US-09-879-957-186

Query Match

76.2%; Score 32; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

## RESULT 30

US-08-185-432-10  
; Sequence 10, Application US/08185432  
; Patent No. 5750652  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Busseau, Isabelle  
; APPLICANT: Diederich, Robert J.  
; APPLICANT: Xu, Tian  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185,432  
; FILING DATE: 21-JAN-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-185-432-10

Query Match 76.2%; Score 32; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

## RESULT 31

US-08-769-745-31  
; Sequence 31, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02

Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 7 PPPLP 11

; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-08-769-745-31

Query Match 76.2%; Score 32; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 4 PPPLP 8

## RESULT 32

US-08-602-999A-356  
; Sequence 356, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEX: (212) 869-9741/8864  
; INFORMATION FOR SEQ ID NO: 356:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-356

Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33  
US-08-602-999A-385  
; Sequence 385, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 385:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-385  
Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;  
QY 3 PPPLP 7  
Db 7 PPPLP 11

RESULT 34  
US-08-602-999A-404  
; Sequence 404, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 404:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-404  
Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;  
QY 3 PPPLP 7  
Db 4 PPPLP 8

RESULT 35  
US-08-602-999A-414  
; Sequence 414, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:



```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-414

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 36
US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 37
US-08-602-999A-436
; Sequence 436, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-436

Query Match 76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 2 LSPPPIP 8

RESULT 38
US-08-602-999A-441
; Sequence 441, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
```

APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 441:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-441

Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

OY 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 39  
US-08-602-999A-452  
Sequence 452, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 452:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-452

Query Match 76.2%; Score 32; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

OY 3 PPPLP 7  
Db 7 PPPLP 11

RESULT 40  
US-09-500-124-356  
Sequence 356, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 356:  
SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-356

Query Match 76.2%; Score 32; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||  
Db 7 PPPLP 11

Search completed: June 7, 2005, 23:23:09  
Job time : 11.5455 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 31.5 Seconds  
(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPLP 7

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Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	14	US-10-281-652-1
2	42	100.0	7	16	US-10-691-157-1
3	42	100.0	7	17	US-10-691-330-1
4	36	85.7	12	16	US-10-649-873-112
5	34	81.0	12	16	US-10-704-363-53
6	33	78.6	10	14	US-10-161-791-278
7	33	78.6	13	14	US-10-185-050-139
8	32	76.2	9	9	US-09-835-232-11
9	32	76.2	9	14	US-10-308-485-11
10	32	76.2	10	14	US-10-185-050-141
11	32	76.2	10	14	US-10-185-050-178
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 11, Appl
					Sequence 112, App
					Sequence 53, Appl
					Sequence 278, App
					Sequence 139, App
					Sequence 11, Appl
					Sequence 11, Appl
					Sequence 141, App
					Sequence 178, App

11	76.2	32	12	9	US-09-835-232-8	Sequence 8, Appli
11	76.2	32	13	9	US-09-835-232-9	Sequence 9, Appli
11	76.2	32	14	14	US-10-308-485-8	Sequence 8, Appli
11	76.2	32	15	14	US-10-308-485-9	Sequence 9, Appli
12	76.2	32	16	10	US-09-845-612B-9	Sequence 9, Appli
12	76.2	32	17	14	US-10-161-791-251	Sequence 251, App
12	76.2	32	18	14	US-10-161-791-267	Sequence 267, App
13	76.2	32	19	14	US-09-945-917-13	Sequence 13, Appl
13	76.2	32	20	10	US-09-945-917-14	Sequence 14, Appl
13	76.2	32	21	10	US-09-945-917-19	Sequence 19, Appl
13	76.2	32	22	10	US-09-945-917-21	Sequence 21, Appl
13	76.2	32	23	14	US-10-067-668-11	Sequence 11, Appl
13	76.2	32	24	14	US-10-175-696-11	Sequence 11, Appl
13	76.2	32	25	16	US-10-776-871-11	Sequence 11, Appl
13	76.2	32	26	17	US-10-809-945-103	Sequence 103, App
14	76.2	32	27	9	US-09-879-957-186	Sequence 186, App
14	76.2	32	28	14	US-10-185-050-63	Sequence 63, Appl
14	76.2	32	29	14	US-10-148-936-3	Sequence 3, Appli
14	76.2	32	30	16	US-10-807-856-186	Sequence 186, App
15	76.2	32	31	15	US-10-161-791-356	Sequence 356, App
15	76.2	32	32	15	US-10-161-791-385	Sequence 385, App
15	76.2	32	33	14	US-10-161-791-404	Sequence 404, App
15	76.2	32	34	14	US-10-161-791-414	Sequence 414, App
15	76.2	32	35	14	US-10-161-791-435	Sequence 435, App
15	76.2	32	36	14	US-10-161-791-436	Sequence 436, App
15	76.2	32	37	14	US-10-161-791-441	Sequence 441, App
15	76.2	32	38	15	US-10-161-791-452	Sequence 452, App
15	76.2	32	39	17	US-10-794-514A-80	Sequence 80, Appl
15	76.2	32	40	17	US-10-794-514A-81	Sequence 81, Appl
15	76.2	32	41	17	US-10-794-514A-82	Sequence 82, Appl
16	76.2	32	42	16	US-10-161-791-197	Sequence 197, App
16	76.2	32	43	14	US-10-161-791-360	Sequence 360, App
17	76.2	32	44	14	US-10-161-791-374	Sequence 374, App
18	76.2	32	45	14	US-10-161-791-320	Sequence 320, App
18	76.2	32	46	14	US-10-161-791-409	Sequence 409, App
18	76.2	32	47	14	US-10-235-175-16	Sequence 16, Appl
13	73.8	31	48	9	US-09-879-957-143	Sequence 143, App
13	73.8	31	49	14	US-10-185-050-8	Sequence 8, Appli
13	73.8	31	50	14	US-10-185-050-87	Sequence 87, Appl
13	73.8	31	51	16	US-10-807-856-143	Sequence 143, App
13	73.8	31	52	15	US-10-393-815-235	Sequence 235, App
15	73.8	31	53	14	US-10-161-791-301	Sequence 301, App
16	73.8	31	54	14	US-10-161-791-344	Sequence 344, App
17	73.8	31	55	14	US-10-185-050-10	Sequence 10, Appl
10	71.4	30	56	10	US-10-062-710-77	Sequence 77, Appl
10	71.4	30	57	15	US-10-285-394-212	Sequence 212, App
12	71.4	30	58	14	US-10-158-596A-25	Sequence 25, Appl
12	71.4	30	59	14	US-10-157-775B-25	Sequence 25, Appl
12	71.4	30	60	14	US-10-185-050-135	Sequence 135, App
12	71.4	30	61	14	US-10-254-446A-25	Sequence 25, Appl
12	71.4	30	62	14	US-10-155-883B-25	Sequence 25, Appl
12	71.4	30	63	14	US-10-161-791-266	Sequence 266, App
12	71.4	30	64	15	US-10-609-217-312	Sequence 312, App
12	71.4	30	65	15	US-10-632-388-312	Sequence 312, App
12	71.4	30	66	15	US-10-651-723-312	Sequence 312, App
12	71.4	30	67	15	US-10-645-761-312	Sequence 312, App
12	71.4	30	68	15	US-10-666-696-312	Sequence 312, App
12	71.4	30	69	15	US-10-653-048-312	Sequence 312, App
12	71.4	30	70	16	US-10-668-600-25	Sequence 25, Appl
13	71.4	30	71	14	US-10-156-932-75	Sequence 75, Appl
15	71.4	30	72	14	US-10-161-791-373	Sequence 373, App
15	71.4	30	73	15	US-10-161-791-382	Sequence 382, App
15	71.4	30	74	14	US-10-161-791-415	Sequence 415, App
15	71.4	30	75	14	US-10-161-791-430	Sequence 430, App
15	71.4	30	76	14	US-10-161-791-431	Sequence 431, App
15	71.4	30	77	15	US-10-328-916-58	Sequence 58, Appl
16	71.4	30	78	14	US-10-161-791-179	Sequence 179, App
16	71.4	30	79	14	US-10-161-791-199	Sequence 199, App
17	71.4	30	80	14	US-10-161-791-413	Sequence 413, App
9	69.0	29	81	14	US-10-193-709-8	Sequence 8, Appli
9	69.0	29	82	10	US-09-932-165-51	Sequence 51, Appl
9	69.0	29	83	10	US-10-185-050-1050	Sequence 1050, App
10	69.0	29	84	9	US-09-938-315-5	Sequence 5, Appli

85 29 69.0 10 10 US-09-932-165-152 Sequence 152, App  
86 29 69.0 10 10 US-09-932-165-568 Sequence 568, App  
87 29 69.0 10 14 US-10-161-791-5 Sequence 5, Appli  
88 29 69.0 11 9 US-09-904-117-6 Sequence 6, Appli  
89 29 69.0 11 14 US-10-161-791-261 Sequence 261, App  
90 29 69.0 11 14 US-10-161-791-262 Sequence 262, App  
91 29 69.0 11 14 US-10-161-791-290 Sequence 290, App  
92 29 69.0 12 10 US-09-945-917-10 Sequence 10, Appl  
93 29 69.0 12 10 US-09-945-917-22 Sequence 22, Appl  
94 29 69.0 12 10 US-09-990-832C-84 Sequence 84, Appl  
95 29 69.0 12 10 US-09-990-832C-96 Sequence 96, Appl  
96 29 69.0 12 14 US-10-185-050-154 Sequence 154, App  
97 29 69.0 12 14 US-10-161-791-268 Sequence 268, App  
98 29 69.0 12 14 US-10-161-791-269 Sequence 269, App  
99 29 69.0 12 15 US-10-418-751-47 Sequence 47, Appl  
100 29 69.0 12 15 US-10-418-752-47 Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-1  
; Sequence 1, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-1  
Query Match 100.0%; Score 42; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQPPPLP 7  
Db 1 MQPPPLP 7  
RESULT 2  
US-10-691-157-1  
; Sequence 1, Application US/10691157  
; Publication No. US20040266681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265.00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-1

Query Match 100.0%; Score 42; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
Db 1 MQPPPLP 7

RESULT 3  
US-10-691-330-1  
; Sequence 1, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Kruzel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265.00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-1

Query Match 100.0%; Score 42; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
Db 1 MQPPPLP 7

RESULT 4  
US-10-649-873-112  
; Sequence 112, Application US/10649873  
; Publication No. US20040171552A1  
; GENERAL INFORMATION:  
; APPLICANT: Biokine Therapeutics Ltd.  
; APPLICANT: Peled, Amnon  
; APPLICANT: Eizenberg, Orly  
; APPLICANT: Vaisel-Ohayon, Dalit  
; TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE

;; TITLE OF INVENTION: BIOLOGICAL ACTIVITY OF CHEMOKINES  
;; FILE REFERENCE: 26732  
;; CURRENT APPLICATION NUMBER: US/10/649,873  
;; CURRENT FILING DATE: 2003-08-28  
;; NUMBER OF SEQ ID NOS: 157  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 112  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide  
US-10-649-873-112

Query Match 85.7%; Score 36; DB 16; Length 12;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
Db 5 MQPPRP 11

RESULT 5  
US-10-704-363-53  
;; Sequence 53, Application US/10704363  
;; Publication No. US20040249145A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Stark, Karen A.  
;; APPLICANT: Weaver, Alix  
;; APPLICANT: Hoffmann, Heidi M.  
;; APPLICANT: Krauss, Raul  
;; APPLICANT: Saini, Kulvinder S.  
;; APPLICANT: Valenzuela, Dario B.  
;; TITLE OF INVENTION: Cell Adhesion-Mediating Proteins and  
;; FILE REFERENCE: 1966.1014003  
;; CURRENT APPLICATION NUMBER: US/10/704,363  
;; CURRENT FILING DATE: 2003-11-07  
;; PRIOR APPLICATION NUMBER: PCT/US02/14457  
;; PRIOR FILING DATE: 2002-05-07  
;; PRIOR APPLICATION NUMBER: 60/289,179  
;; PRIOR FILING DATE: 2001-05-07  
;; PRIOR APPLICATION NUMBER: 60/315,736  
;; PRIOR FILING DATE: 2001-08-29  
;; NUMBER OF SEQ ID NOS: 88  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 53  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: Homo Sapiens  
US-10-704-363-53

Query Match 81.0%; Score 34; DB 16; Length 12;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
Db 1 MQPPDLP 7

RESULT 6  
US-10-161-791-278  
;; Sequence 278, Application US/10161791  
;; Publication No. US20030186863A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SPARKS, Andrew B.  
;; APPLICANT: KAY, Brian K.  
;; APPLICANT: THORN, Judith M.  
;; APPLICANT: QUILLIAM, Lawrence A.  
;; APPLICANT: DER, Channing J.  
;; APPLICANT: FOWLKES, Dana M.

;; APPLICANT: RIDER, James E.  
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
;; TITLE OF INVENTION: ISOLATING AND USING SAME  
;; NUMBER OF SEQUENCES: 467  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/161,791  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/602,999  
;; FILING DATE: 16-FEB-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Misrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 278:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-10-161-791-278

Query Match 78.6%; Score 33; DB 14; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
Db 1 KPPPLP 6

RESULT 7  
US-10-185-050-139  
;; Sequence 139, Application US/10185050  
;; Publication No. US20030077577A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Pirozzi, Gregorio  
;; Kay, Brian K.  
;; Fowlkes, Dana M.  
;; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
;; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
;; NUMBER OF SEQUENCES: 233  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: PENNIE & EDMONDS LLP  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10036-2711  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 139:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 139:  
US-10-185-050-139

Query Match 78.6%; Score 33; DB 14; Length 13;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
Db 2 VQPPAP 8

## RESULT 8

US-09-835-232-11  
; Sequence 11, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-835-232-11

Query Match 76.2%; Score 32; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 4 PPPLP 8

## RESULT 9

US-10-308-485-11  
; Sequence 11, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 00383/052002

; CURRENT APPLICATION NUMBER: US/10/308,485  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US/09/835,232  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-308-485-11

Query Match 76.2%; Score 32; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 4 PPPLP 8

## RESULT 10

US-10-185-050-141  
; Sequence 141, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 141:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 141:  
US-10-185-050-141

Query Match 76.2%; Score 32; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;



Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 11  
US-10-185-050-178  
; Sequence 178, Application US/10185050  
; Publication No. US2003007577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/POCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 178:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:  
US-10-185-050-178

Query Match 76.2%; Score 32; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 12  
US-09-835-232-8  
; Sequence 8, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=Met or Val  
US-09-835-232-8

Query Match 76.2%; Score 32; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 6 PPPLP 10

RESULT 13  
US-09-835-232-9  
; Sequence 9, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-835-232-9

Query Match 76.2%; Score 32; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 7 PPPLP 11

RESULT 14  
US-10-308-485-8  
; Sequence 8, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/10/308,485  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US/09/835,232  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=Met or Val  
US-10-308-485-8

Query Match 76.2%; Score 32; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 6 PPPLP 10

RESULT 15  
US-10-308-485-9  
; Sequence 9, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/10/308,485  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US/09/835,232  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-308-485-9

Query Match 76.2%; Score 32; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 7 PPPLP 11

RESULT 16  
US-09-845-612B-9  
; Sequence 9, Application US/09845612B  
; Publication No. US20030083261A1  
; GENERAL INFORMATION:  
; APPLICANT: YU, HONGTAO  
; APPLICANT: TANG, ZHANYUN  
; APPLICANT: LUO, XUELIAN  
; APPLICANT: RIZO-REY, JOSE  
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOTIN  
; FILE REFERENCE: UTSID:795  
; CURRENT APPLICATION NUMBER: US/09/845,612B  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 12  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(12)  
; OTHER INFORMATION: synthetic peptide  
US-09-845-612B-9

Query Match 76.2%; Score 32; DB 10; Length 12;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPL 6  
Db 5 LQPPPL 10

RESULT 17  
US-10-161-791-251  
; Sequence 251, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 251:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-251

Query Match 76.2%; Score 32; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 6 PPPLP 10

RESULT 18  
US-10-161-791-267  
; Sequence 267, Application US/10161791  
; Publication No. US2003018683A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: O'QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 267:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-267

Query Match 76.2%; Score 32; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 6 PPPLP 10

RESULT 19  
US-09-945-917-13  
; Sequence 13, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1

; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-13

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 20  
US-09-945-917-14  
; Sequence 14, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-14

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 57.1%; Pred. No. 4.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
Db 3 LSPPPIP 9

RESULT 21  
US-09-945-917-19  
; Sequence 19, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-19

Query Match 76.2%; Score 32; DB 10; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
      |||||  
Db 6 PPPLP 10

## RESULT 22

US-09-945-917-21  
; Sequence 21, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-21

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
      |||||  
Db 5 PPPLP 9

## RESULT 23

US-10-067-668-11  
; Sequence 11, Application US/10067668  
; Publication No. US20030022334A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN  
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-136001  
; CURRENT APPLICATION NUMBER: US/10/067,668  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-067-668-11

Query Match 76.2%; Score 32; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
      |||||  
Db 4 PPPLP 8

## RESULT 24

US-10-175-696-11

; Sequence 11, Application US/10175696  
; Publication No. US20030092658A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10/175,696  
; CURRENT FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 10/067,668  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/823,901  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US01/10720  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/193,920  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/862,658  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US01/16380  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/205,675  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/882,837  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: PCT/US01/19319  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/211,727  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence  
US-10-175-696-11

Query Match 76.2%; Score 32; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
      |||||  
Db 4 PPPLP 8

## RESULT 25

US-10-776-871-11  
; Sequence 11, Application US/10776871  
; Publication No. US20040132087A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10/776,871  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/10/175,696  
; PRIOR FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 10/067,668  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/823,901  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US01/10720  
; PRIOR FILING DATE: 2001-04-02

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; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-776-871-11

Query Match          76.2%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 26
US-10-809-945-103
; Sequence 103, Application US/10809945
; Publication No. US20050060773A1
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinrong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/10/809,945
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/485,529
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-809-945-103

Query Match          76.2%; Score 32; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 27
US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. US20020034755A1h
; APPLICANT: KAY, Brian K.

; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-776-871-11

Query Match          76.2%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 26
US-10-809-945-103
; Sequence 103, Application US/10809945
; Publication No. US20050060773A1
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinrong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/10/809,945
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/485,529
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-809-945-103

Query Match          76.2%; Score 32; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 27
US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. US20020034755A1h
; APPLICANT: KAY, Brian K.

; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-879-957-186

Query Match          76.2%; Score 32; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 28
US-10-185-050-63
; Sequence 63, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; FOWLKES, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-185-050-63

Query Match 76.2%; Score 32; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 29
US-10-148-936-3
; Sequence 3, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA3963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-3

Query Match 76.2%; Score 32; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 30
US-10-807-856-186
; Sequence 186, Application US/10807856
; Publication No. US20040157216A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Noah
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/807,856
; FILING DATE: 23-Mar-2004
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-10-807-856-186

Query Match 76.2%; Score 32; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 31
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
```

;; TITLE OF INVENTION: ISOLATING AND USING SAME  
;; NUMBER OF SEQUENCES: 467  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/161,791  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/602,999  
;; FILING DATE: 16-FEB-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 356:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-10-161-791-356

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 7 PPPLP 11

RESULT 32  
US-10-161-791-385  
; Sequence 385, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 356:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-356

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/161,791  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/602,999  
;; FILING DATE: 16-FEB-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 385:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-10-161-791-385

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 7 PPPLP 11

RESULT 33  
US-10-161-791-404  
; Sequence 404, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 385:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-385

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 404:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-404

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 4 PPPLP 8

RESULT 34  
US-10-161-791-414  
; Sequence 414, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 414:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-414

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

DB 4 PPPLP 8

RESULT 35  
US-10-161-791-435  
; Sequence 435, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 435:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-435

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
DB 4 PPPLP 8

RESULT 36  
US-10-161-791-436  
; Sequence 436, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.



APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 436:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-436

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MOPPPPLP 7  
Db 2 LSPPPIP 8

RESULT 37  
US-10-161-791-441  
Sequence 441, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 441:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-441

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PPPLP 7  
Db 5 PPPLP 9

RESULT 38  
US-10-161-791-452  
Sequence 452, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 452:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-452

Query Match 76.2%; Score 32; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 7 PPPLP 11

## RESULT 39

US-10-794-514A-80  
; Sequence 80, Application US/10794514A  
; Publication No. US20050112134A1  
; GENERAL INFORMATION:  
; APPLICANT: Graddis, Thomas  
; APPLICANT: Laus, Reiner  
; APPLICANT: Diegel, Michael  
; APPLICANT: Vidovic, Damir  
; TITLE OF INVENTION: Compositions and Methods Employing Alternative  
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of  
; TITLE OF INVENTION: Cancer and Infectious Disease  
; FILE REFERENCE: 11311.1003U  
; CURRENT APPLICATION NUMBER: US/10/794,514A  
; CURRENT FILING DATE: 2004-03-05  
; NUMBER OF SEQ ID NOS: 733  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab from synthetic material  
US-10-794-514A-80

Query Match 76.2%; Score 32; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 10 PPPLP 14

## RESULT 40

US-10-794-514A-81  
; Sequence 81, Application US/10794514A  
; Publication No. US20050112134A1  
; GENERAL INFORMATION:  
; APPLICANT: Graddis, Thomas  
; APPLICANT: Laus, Reiner  
; APPLICANT: Diegel, Michael  
; APPLICANT: Vidovic, Damir  
; TITLE OF INVENTION: Compositions and Methods Employing Alternative  
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of  
; TITLE OF INVENTION: Cancer and Infectious Disease  
; FILE REFERENCE: 11311.1003U  
; CURRENT APPLICATION NUMBER: US/10/794,514A  
; CURRENT FILING DATE: 2004-03-05  
; NUMBER OF SEQ ID NOS: 733  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab from synthetic material  
US-10-794-514A-81

Query Match 76.2%; Score 32; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
Db 6 PPPLP 10

Search completed: June 7, 2005, 23:31:30  
Job time : 33.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 6.49091 Seconds

(without alignments)

103.763 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	76.2	18	2	PC2280
2	27	64.3	15	2	hypothenical 1.5K
3	26	61.9	7	2	ICL2 protein - Par
4	25	59.5	10	2	trypsin-modulating
5	25	59.5	13	2	inhibin alpha chain
6	25	59.5	13	2	2S albumin large c
7	25	59.5	14	2	phosphoprotein, bo
8	25	59.5	15	2	light harvesting c
9	25	59.5	16	2	superoxide dismuta
10	25	59.5	17	2	hydroxyproline-ric
11	24	57.1	11	2	173K exoantigen -
12	23	54.8	11	1	bradykinin-potenti
13	23	54.8	13	2	tryptophyllin-rela
14	23	54.8	13	2	tryptophyllin-13 -
15	23	54.8	17	2	hydroxyproline-ric
16	22	52.4	12	2	ribosomal protein
17	22	52.4	15	2	urease (EC 3.5.1.5
18	22	52.4	17	2	45/47K antigen - M
19	22	52.4	18	2	u-plasminogen acti
20	22	52.4	18	2	Na+/K+-exchanging
21	21	50.0	11	2	complement C3b rec
22	21	50.0	12	2	cytrophin-associa
23	21	50.0	12	2	neural cell adhesi
24	21	50.0	13	2	neural cell adhesi
25	21	50.0	14	2	protein kinase (EC
26	21	50.0	15	2	capsid protein VP1
27	21	50.0	16	2	insulin-like growt
28	20	47.6	10	2	protein Fil - curl
29	20	47.6	13	2	cell surface glyco

30	20	47.6	15	2	PA0002	photosystem II oxy
31	20	47.6	15	2	S67918	serine proteinase
32	19.5	46.4	14	2	H64008	hypothetical prote
33	19	45.2	7	2	PT0283	Ig heavy chain CRD
34	19	45.2	10	2	B59272	peptide-M4-(N-acet
35	19	45.2	11	1	XASNEA	bradykinin-potenti
36	19	45.2	11	2	C37196	bradykinin-potenti
37	19	45.2	11	2	D37196	bradykinin-potenti
38	19	45.2	11	2	YHHU	morphogenetic neur
39	19	45.2	11	2	YHBO	morphogenetic neur
40	19	45.2	11	2	YHJFHY	morphogenetic neur
41	19	45.2	11	2	YHXAE	morphogenetic neur
42	19	45.2	11	2	YHRT	Ig lambda chain V-
43	19	45.2	13	2	G61458	Ig lambda chain V-
44	19	45.2	13	2	A86126	hypothetical prote
45	19	45.2	15	2	PA0088	protein QP200051 -
46	19	45.2	15	2	A60221	apolipoprotein A-I
47	19	45.2	16	2	C49048	T-cell receptor be
48	19	45.2	17	2	I49593	cystic fibrosis tr
49	19	45.2	17	2	I84733	gene CFTR protein
50	19	45.2	17	2	PT0235	Ig heavy chain CRD
51	19	45.2	17	2	S05033	photosystem II pro
52	19	45.2	17	2	S10786	enamelin, 26K - bo
53	19	45.2	17	2	B25348	glycogen(starch) s
54	18	42.9	8	2	B39745	endoglycosylcerami
55	18	42.9	8	2	S10783	enamelin f - bovin
56	18	42.9	9	2	B41983	orf downstream to b
57	18	42.9	10	2	PC2171	triacylglycerol li
58	18	42.9	10	2	C39745	sphingomyelinase -
59	18	42.9	11	2	S07203	uperolein - frog (
60	18	42.9	13	2	I84603	deoxynucleotidyltr
61	18	42.9	14	2	B60683	malate dehydrogena
62	18	42.9	15	2	A32322	gentisate 1,2-diox
63	18	42.9	15	2	S27248	pseudogerm - whe
64	18	42.9	15	2	PA0060	protein QP200037 -
65	18	42.9	15	2	B61457	alpha-glucosidase
66	18	42.9	16	2	I57530	gene c-fms protein
67	18	42.9	16	2	PH1302	Ig heavy chain DJ
68	18	42.9	16	2	S57517	T cell receptor be
69	18	42.9	16	2	JT0609	leukocyte chemotatt
70	18	42.9	17	2	S33609	extensin - maize (
71	18	42.9	17	2	A42920	fatty acid ethyl e
72	18	42.9	18	2	S04229	N4-(beta-N-acetyl
73	17	40.5	9	2	S26508	collagen alpha 2(V
74	17	40.5	10	2	H37196	bradykinin-potenti
75	17	40.5	11	2	D56979	collagen alpha 1(I
76	17	40.5	11	2	C60409	kassinin-like pept
77	17	40.5	11	2	B60409	substance P-like p
78	17	40.5	11	2	B60409	substance P-like p
79	17	40.5	11	2	D60409	kassinin-like pept
80	17	40.5	11	2	D60409	napiin small chain
81	17	40.5	12	2	S70337	tachykinin - Afric
82	17	40.5	12	2	S07436	seed storage prote
83	17	40.5	15	2	PA0014	seed storage prote
84	17	40.5	15	2	PN0173	seed storage prote
85	17	40.5	15	2	A60929	dichloromethane de
86	17	40.5	15	2	B60929	dichloromethane de
87	17	40.5	15	2	PA0071	superoxide dismuta
88	17	40.5	18	2	C56211	progesterone recep
89	17	40.5	18	2	A40760	basic fibroblast g
90	16	38.1	5	2	B37988	acid proteinase 11
91	16	38.1	8	2	PT0559	T-cell receptor be
92	16	38.1	10	1	XAVI6B	angiotensin-conver
93	16	38.1	10	2	B37196	bradykinin-potenti
94	16	38.1	11	2	PH1583	Ig H chain V-D-J r
95	16	38.1	11	2	I52304	gene rSSTR4 protei
96	16	38.1	11	2	C61497	seed protein ws-18
97	16	38.1	11	2	PN0042	statthmin - mouse (
98	16	38.1	12	2	E45691	probable minor cap
99	16	38.1	12	2	JU0356	cycloleumunirin -
100	16	38.1	12	2	PQ0786	NADH2 dehydrogenas

## ALIGNMENTS

## RESULT 1

PC3280  
 prollydopeptidase-inhibiting peptide - bovine (fragment)  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997  
 C/Accession: PC2280  
 R/Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.  
 Biochem. Biophys. Res. Commun. 202, 809-815, 1994  
 A>Title: Isolation of prollydopeptidase-inhibiting peptides from bovine brain.  
 A/Reference number: PC3280; MUID:94324971; PMID:8048952

A;Accession: P02200  
A;Molecule type: protein  
A;Residues: 1-18 <OH>  
A;Experimental source: brain  
C;Superfamily: cytoskeletal keratin

```

Query Match          76.2%; Score 32; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPLP 7
        |||||
Db      2 PPPLP 6

RESULT 2
B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; J01585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: A39109; MUID:91156678; PMID:1705704

```

A/Accession: B3103  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-15 <HAN>  
A/Cross-references: GB:M58406  
R: Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol 73, 1521-1525, 1992  
A/Title: Cloning and sequencing of the structural region and expression of putative core  
A/Reference number: JQ1584; MUID:92300349; PMID:1318944  
A/Accession: JQ1585  
A/Molecule type: genomic RNA  
A/Residues: 1-15 <KUM>  
A/Experimental source: strain U. K.

```

Query Match      64.3%; Score 27; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy      1 MQP--PPLP 7
        :||| ||||
Db      4 VQPPGPPLP 12

RESULT 3
S71299
ICL2 protein - Paramecium tetraurelia (fragment)
C;Species: Paramecium tetraurelia
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C;Accession: S71299
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A;Title: Characterization of centrin genes in Paramecium.
A;Reference number: S71298; MUID:96248429; PMID:8665928
A;Accession: S71299

```

A;Molecule type: protein  
A;Residues: 1-7 <MAD>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGC5

```

Query Match      61.9%; Score 26; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 QPPP 5
Db      2 Oppp 5

```

RESULT 4  
A36454  
trypsin-modulating oostatic factor - yellow fever mosquito  
C:Species: Aedes aegypti (yellow fever mosquito)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004  
C:Accession: A36454; A61630  
R:Barovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
FASEB J. 4, 3015-3020, 1990  
A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-L  
A:Reference number: A36454; MUID:90367888; PMID:2394318  
A:Accession: A36454  
A:Molecule type: protein  
A:Residues: 1-10 <BOR>  
A:Cross-references: UNIPROT:Pl9425  
R:Barovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
Insect Biochem. Mol. Biol. 23, 703-712, 1993  
A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin mol  
A:Reference number: A61630; MUID:993557794; PMID:8353526  
A:Accession: A61630  
A:Molecule type: protein  
A:Residues: 1-10 <B02>  
C:Function:  
A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes  
C:Keywords: hormone

Query Match	59.5%	Score 25;	DB 2;	Length 10;
Best Local Similarity	80.0%;	Pred. No. 1.8e+02;		
Matches 4;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
Qy	3	pppLf	7	
Db	5	ppppp	9	

```

RESULT 5
A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60856
E:Leverisha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W
J. Endocrinol. 113, 213-221, 1987
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; MUID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match      59.5%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps

```

Db 3 PPLP 6

#### RESULT 6

S09716  
2S albumin large chain (1 and 2) nII - rape (fragments)  
N:Alternate names: 2S albumin large chain nIII  
C:Species: Brassica napus (rape)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998  
C:Accession: S09716; S09718; S09717  
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263: 209-212, 1990  
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins  
A:Reference number: S09720; PMID:90242974; PMID:2185951  
A:Accession: S09716  
A:Molecule type: protein  
A:Residues: 1-9;10-13 <MON>  
A:Experimental source: seed  
A:Note: 3-Ser was also found  
A:Accession: S09718  
A:Molecule type: protein  
A:Residues: 1-9;10-13 <MO2>  
A:Experimental source: seed  
A:Accession: S09717  
A:Molecule type: protein  
A:Residues: 1-9;10-13 <MO3>  
A:Experimental source: seed

Query Match 59.5%; Score 25; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 2.4e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PPLP 7

Db 7 RPPCP 12

#### RESULT 7

S11129  
phosphoprotein, bone - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996  
C:Accession: S11129  
R:Mikuni-Takagaki, Y.; Glimcher, M.J.  
Biochem. J. 268, 585-591, 1990  
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification of  
A:Reference number: S11127; PMID:90303246; PMID:2363696  
A:Accession: S11129  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <MIK>  
C:Keywords: phosphoprotein

Query Match 59.5%; Score 25; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPLP 6

Db 5 PPLP 8

#### RESULT 8

PT0037  
light harvesting complex chain III/b, photosystem I - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: PT0037; PS0205  
R:Uchiyama, Y.; Tsugita, A.  
submitted to JIPID, June 1991  
A:Reference number: PS0189  
A:Accession: PT0037  
A:Molecule type: protein

A:Residues: 1-15 <UCH>

A:Cross-references: UNIPROT:Q7M1V1

Query Match 59.5%; Score 25; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPLP 7

Db 8 PPLP 12

#### RESULT 9

E58503  
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)  
N:Alternate names: 21.3K bladder and kidney stone protein  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: E58503  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: E58503  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <BIN>  
A:Cross-references: UNIPROT:Q7M137  
A:Experimental source: human bladder and kidney stones  
C:Function:  
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C:Keywords: metalloprotein; oxidoreductase

Query Match 59.5%; Score 25; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7

Db 6 PPLP 9

#### RESULT 10

S57991  
hydroxyproline-rich protein - Sesbania rostrata (fragment)  
C:Species: Sesbania rostrata  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S57991  
R:Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.  
submitted to the EMBL Data Library, March 1995  
A:Description: Use of differential display to identify novel Sesbania rostrata genes en  
A:Reference number: S57991  
A:Accession: S57991  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-17 <GOO>  
A:Cross-references: UNIPROT:Q41400; EMBL:248673; NID:g899484; PID:g899485  
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 59.5%; Score 25; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPLP 7

Db 10 PPLP 14

#### RESULT 11

I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: I33098  
 R;Nichols, J.H.; Hager, L.P.  
 Submitted to the Protein Sequence Database, May 1990  
 A;Reference number: A33098  
 A;Accession: I33098  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <NIC>

Query Match 57.1%; Score 24; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

RESULT 12  
 XAVIBH  
 bradykinin-potentiating peptide - halys viper  
 N;Alternate names: BPP  
 C;Species: Agkistrodon halys (halys viper)  
 C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
 C;Accession: JCO002  
 R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.  
 Peptides 6, 339-342, 1985  
 A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese  
 A;Reference number: JCO002; MUID:86177022; PMID:3008123  
 A;Accession: JCO002  
 A;Molecule type: protein  
 A;Residues: 1-11 <CHI>  
 A;Cross-references: UNIPROT:P04562  
 C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7  
 |||||  
 Db 7 PPIP 10

RESULT 13  
 S21152  
 tryptophyllin-related peptide - two-colored leaf frog  
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004  
 C;Accession: S21152  
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
 FEBS Lett. 302, 151-154, 1992  
 A;Title: Identification and characterization of two dermorphins from skin extracts of th  
 A;Reference number: S21152; MUID:92339502; PMID:1633946  
 A;Accession: S21152  
 A;Molecule type: protein  
 A;Residues: 1-13 <MIG>  
 A;Cross-references: UNIPROT:Q7LZ51  
 A;Experimental source: skin

Query Match 54.8%; Score 23; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 4.8e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6  
 |||||  
 Db 7 PPPI 10

RESULT 14

A05174  
 tryptophyllin-13 - Rohde's leaf frog  
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
 C;Accession: A05174  
 R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.  
 Int. J. Pept. Protein Res. 27, 175-182, 1986  
 A;Reference number: A05174  
 A;Accession: A05174  
 A;Molecule type: protein  
 A;Residues: 1-13 <MON>  
 A;Cross-references: UNIPROT:P04096  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: pyroglutamic acid; skin  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 4.8e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6  
 |||||  
 Db 7 PPPI 10

RESULT 15  
 S59481  
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
 C;Species: Phaseolus vulgaris (kidney bean)  
 C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: S59481  
 R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A;Title: Specificity in the immobilisation of cell wall proteins in response to differer  
 A;Reference number: S59481; MUID:96011753; PMID:7548825  
 A;Accession: S59481  
 A;Molecule type: protein  
 A;Residues: 1-17 <WOJ>  
 A;Cross-references: UNIPROT:Q7MLI3  
 C;Keywords: glycoprotein; hydroxyproline  
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
 |||||  
 Db 2 MYLPVP 8

RESULT 16  
 PA0098  
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
 C;Species: Fusarium sporotrichioides  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: PA0098  
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A;Reference number: PA0051  
 A;Accession: PA0098  
 A;Molecule type: protein  
 A;Residues: 1-12 <CHO>  
 A;Cross-references: UNIPROT:Q7MAX9

Query Match 52.4%; Score 22; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 6.3e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7  
 |||||  
 Db 4 PPVP 7

RESULT 17  
B35389  
urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)  
C:Species: Morganella morganii  
C>Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004  
C:Accession: B35389  
R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
J. Bacteriol. 172, 3073-3080, 1990  
A:Title: Morganella morganii urease: purification, characterization, and isolation of gene  
A:Reference number: A35389; MUID:90264298; PMID:2345135  
A:Accession: B35389  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <HUA>  
A:Cross-references: UNIPROT:P17338  
C:Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPL 6  
|||  
DB 5 QPTPL 9

RESULT 18  
A49237  
45/47K antigen - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C>Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A49237  
R:Romain, F.; Laquerriere, A.; Millitzer, P.; Pescher, P.; Chavarot, P.; Lagranderie, M.;  
Infect. Immun. 61, 742-750, 1993  
A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a  
A:Reference number: A49237; MUID:93138802; PMID:8423100  
A:Contents: BCG  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <ROM>  
A:Cross-references: UNIPROT:P80069  
A:Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 52.4%; Score 22; DB 2; Length 17;  
Best Local Similarity 75.0%; Pred. No. 8.9e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7  
|||  
DB 6 PPVP 9

RESULT 19  
I52614  
u-plasminogen activator receptor precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: I52614  
R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.  
Blood 86, 624-635, 1995  
A:Title: A conserved TATA-less proximal promoter drives basal transcription from the urc  
A:Reference number: I52614; MUID:95329719; PMID:7605992  
A:Accession: I52614  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-18 <RES>  
A:Cross-references: UNIPROT:Q03405; GB:S78532; NID:999307; PIDN:AA014289.1; PID:g426198  
C:Genetics:  
A:Gene: uPAR  
C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 52.4%; Score 22; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7  
|||  
DB 4 PPLLP 8

RESULT 20  
A54195  
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)  
C:Species: Squalus acanthias (spiny dogfish)  
C>Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A54195  
R:Esmann, M.; Karlish, S.J.; Sottrup-Jensen, L.; Marsh, D.  
Biochemistry 33, 8044-8050, 1994  
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATP  
A:Reference number: A54195; MUID:94297020; PMID:8025109  
A:Accession: A54195  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <ESM>  
A:Cross-references: UNIPROT:Q9PSP6  
A:Experimental source: rectal gland  
A:Note: sequence extracted from NCBI backbone (NCBIP:149363)  
C:Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 9.5e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQPPP 5  
|||  
DB 6 LTPPP 10

RESULT 21  
D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: D45900  
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.  
J. Immunol. 144, 3581-3591, 1990  
A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gen  
A:Reference number: A45900; MUID:90229754; PMID:2139460  
A:Accession: D45900  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-11 <KUR>

Query Match 50.0%; Score 21; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 9 PPP 11

RESULT 22  
PN0663  
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C:Accession: PN0663  
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993  
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A:Reference number: PN0662; MUID:94156881; PMID:8113213  
A:Accession: PN0663

A:Molecule type: protein  
A:Residues: 1-12 <YOS>  
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C:Keywords: glycoprotein; skeletal muscle

Query Match 50.0%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 5 PPP 7

## RESULT 23

B39690  
neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C:Accession: B39690  
R:Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
A:Reference number: A39690; MUID:91141516; PMID:1996115  
C:Accession: B39690  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-12 <REY>  
A:Cross-references: GB:M63970  
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 6 PPP 8

## RESULT 24

B39690  
neural cell adhesion molecule, cardiac splice form +,-,-,- - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C:Accession: B39690  
R:Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
A:Reference number: A39690; MUID:91141516; PMID:1996115  
C:Accession: B39690  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-13 <REY>  
A:Cross-references: GB:M63970  
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like growth factor-binding protein  
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 21; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 6 PPP 8

## RESULT 25

S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C:Species: Pisaster ochraceus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S12904

R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C  
A:Reference number: S12904; MUID:91032186; PMID:1699809  
C:Accession: S12904  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SAN>  
A:Cross-references: UNIPROT:Q7M3M4  
C:Keywords: phosphotransferase

Query Match 50.0%; Score 21; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 8 PPP 10

## RESULT 26

PQ0545  
capsid protein VP19C - human herpesvirus 1 (fragment)  
C:Species: human herpesvirus 1  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: PQ0545  
R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.  
J. Gen. Virol. 73, 2709-2713, 1992  
A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpesvirus 1  
A:Reference number: PQ0544; MUID:93019027; PMID:1328483  
C:Accession: PQ0545  
A:Molecule type: protein  
A:Residues: 1-15 <DAV>  
A:Cross-references: UNIPROT:Q7LZW6  
A:Experimental source: strain 17  
C:Genetics:  
A:Gene: UL38  
C:Keywords: capsid protein

Query Match 50.0%; Score 21; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
|:|:|  
DB 1 MKTNPLP 7

## RESULT 27

JH0517  
insulin-like growth factor-binding protein 4 - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JH0517  
R:Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.  
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991  
A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins from pig  
A:Reference number: JH0515; MUID:92109718; PMID:1722398  
C:Accession: JH0517  
A:Molecule type: protein  
A:Residues: 1-16 <COL>  
A:Cross-references: UNIPROT:P24854  
A:Experimental source: serum  
C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat homology

Query Match 50.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 7 PPP 9



## RESULT 28

H28027  
protein P11 - curled-leaved tobacco (fragment)  
C:Species: Nicotiana glauca (curled-leaved tobacco)  
C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993  
C:Accession: H28027  
R:Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-  
A:Reference number: A34167  
A:Accession: H28027  
A:Molecule type: protein  
A:Residues: 1-10 <BAU>  
A>Note: 4-Val was also found

Query Match 47.6%; Score 20; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 7 PPXP 10

## RESULT 29

A40207  
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)  
C:Species: Dictyostelium discoideum  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: A40207  
R:Gao, E.N.; Shier, P.; Siu, C.H.  
J. Biol. Chem. 267, 9409-9415, 1992  
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150) i  
A:Reference number: A40207; MUID:92250549; PMID:1577768  
A:Accession: A40207  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <GAO>  
A:Cross-references: UNIPROT:Q7M3T0  
C:Keywords: glycoprotein

Query Match 47.6%; Score 20; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 3 PPTP 6

## RESULT 30

PA0002  
photosystem II oxygen-evolving complex protein 3 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Nov-1994 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C:Accession: PA0002  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsegata, A.  
submitted to JPIID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
A:Reference number: PA0001  
A:Accession: PA0002  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Experimental source: stem  
C:Keywords: photosynthesis; photosystem II

Query Match 47.6%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||

Db 10 PPXP 13

## RESULT 31

S67918  
serine proteinase laeD (EC 3.4.21.-), staphylytic - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S67918  
R:Park, S.; Galloway, D.R.  
Mol. Microbiol. 16, 263-270, 1995  
A:Title: Purification and characterization of laeD: a second staphylytic proteinase p  
A:Reference number: S67918; MUID:96015439; PMID:7565088  
A:Accession: S67918  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <PAR>  
A:Cross-references: UNIPROT:Q9RMI4; UNIPROT:Q9I589  
C:Genetics:  
A:Gene: laeD  
C:Keywords: hydrolase; serine proteinase

Query Match 47.6%; Score 20; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5  
|||  
Db 4 METPP 8

## RESULT 32

H64008  
hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
C:Accession: H64008  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.  
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: H64008  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-14 <TIGR>  
A:Cross-references: GB:U32731; GB:L42023; NID:G1573465; PID:G1573478; TIGR:HI0492

Query Match 46.4%; Score 19.5; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 1.7e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 1 MQP-----PPLP 7  
|||  
Db 1 MKPKYKMPKP 12

## RESULT 33

PT0283  
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0283  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0283  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte

Query Match 46.4%; Score 19.5; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 1.7e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 1 MQP-----PPLP 7  
|||  
Db 1 MKPKYKMPKP 12

C;Keywords: heterotetramer; immunoglobulin

Query Match 45.2%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;  
QY 2 QPP 4  
DB 5 QPP 7  
RESULT 34  
B59272  
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain  
N;Alternate names: peptide N-glycosidase  
C;Species: Prunus dulcis var. saciva (sweet almond)  
C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
C;Accession: B59272  
R;Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.  
Eur. J. Biochem. 252, 118-123, 1998  
A;Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A  
A;Reference number: A59272; PMID:98181894; PMID:9523720  
A;Accession: B59272  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <ALT>  
A;Cross-references: UNIPROT:P81898  
C;Keywords: hydrolase

Query Match 45.2%; Score 19; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

QY 2 QPPPL 6  
DB 1 EPTPL 5

RESULT 35  
XASNBA  
bradykinin-potentiating peptide B - mamushi  
C;Species: Agkistrodon blomhoffi (mamushi)  
C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004  
C;Accession: A01254  
R;Kato, H.; Suzuki, T.  
Proc. Jpn. Acad. 46, 176-181, 1970  
A;Reference number: A01254  
A;Accession: A01254  
A;Molecule type: protein  
A;Residues: 1-11 <KAT>  
A;Cross-references: UNIPROT:P01021  
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; vena  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPLP 7  
DB 4 PPPP 7

RESULT 36  
B37196  
bradykinin-potentiating peptide 3 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: C37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; PMID:90351557; PMID:2386615  
A;Accession: C37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <CIN>  
A;Cross-references: UNIPROT:P30423  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPLP 7  
DB 4 PPPP 7

RESULT 37  
D37196  
bradykinin-potentiating peptide 4 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: D37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; PMID:90351557; PMID:2386615  
A;Accession: D37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <CIN>  
A;Cross-references: UNIPROT:P30424  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPLP 7  
DB 4 PPPP 7

RESULT 38  
YHHU  
morphogenetic neuropeptide - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
C;Accession: B01427; A01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele  
A;Reference number: A93266; PMID:82035850; PMID:7290191  
A;Accession: B01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
A;Cross-references: UNIPROT:P01163  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; PMID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structu  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head  
malian intestine and hypothalamus.  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropep  
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 QPP 3

Qy 2 QPP 4

Db 1 QPP 3

Search completed: June 7, 2005, 23:20:34  
Job time : 9.49091 secs

#### RESULT 39

YHBO

morphogenetic neuropeptide - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
C:Accession: C01427; A01427  
R:Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis  
A:Reference number: A93266; MUID:82035850; PMID:7290191  
A:Accession: C01427  
A:Molecule type: protein  
A:Residues: 1-11 <BOD>  
A:Cross-references: UNIPROT:P01163  
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
PEBS Lett. 131, 317-321, 1981  
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A:Reference number: A91296; MUID:82050803; PMID:7297679  
A:Contents: annotation; synthesis  
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
F:/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status

Query Match 45.2%; Score 19; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

Db 1 QPP 3

#### RESULT 40

YHFBHY

morphogenetic neuropeptide - Hydra attenuata  
N:Alternate names: head activator  
C:Species: Hydra attenuata  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
C:Accession: B93900; A01427  
R:Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A:Reference number: A93900  
A:Accession: B93900  
A:Molecule type: protein  
A:Residues: 1-11 <SCH>  
A:Cross-references: UNIPROT:P01163  
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
PEBS Lett. 131, 317-321, 1981  
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A:Reference number: A91296; MUID:82050803; PMID:7297679  
A:Contents: annotation; synthesis  
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

Db 1 QPP 3

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 30.8 Seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-1

Perfect score: 42

Sequence: 1 MQPPPLP 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	26	61.9	17 1 APID_BOMPA	P81464 bombus pasc
2	26	61.9	18 2 Q9UCT9	Q9uct9 homo sapien
3	25	59.5	10 1 TMOF_AEDAE	P19425 aedes aegypt
4	25	59.5	15 2 P82439	P82439 nicotiana t
5	25	59.5	15 2 Q7M1V1	Q7mlv1 oryza sativ
6	25	59.5	16 2 Q7M137	Q7ml37 unidentified
7	25	59.5	17 2 Q41400	Q41400 sesbania ro
8	25	59.5	18 2 Q84129	Q84129 influenza a
9	24	57.1	9 2 Q9TWV0	Q9twv0 anthopleura
10	24	57.1	16 2 Q6W631	Q6w631 sphagnum cu
11	24	57.1	18 2 Q6W322	Q6w322 andreaea ro
12	24	57.1	18 2 Q8W619	Q8w619 sphagnum wu
13	24	57.1	18 2 Q6W622	Q6w622 sphagnum sq
14	24	57.1	18 2 Q6W628	Q6w628 sphagnum la
15	24	57.1	18 2 Q6W634	Q6w634 sphagnum se
16	24	57.1	18 2 Q6W637	Q6w637 sphagnum af
17	23	54.8	11 1 BPP_ACKHP	P04562 agkistrodon
18	23	54.8	13 1 TV13_PHYRO	P04096 phyllomedus
19	23	54.8	13 2 Q7LZ51	Q7lzs1 phyllomedus
20	23	54.8	14 1 TV13_BOMVA	P84215 bombina var
21	23	54.8	17 2 Q9NQY8	Q9nqy8 homo sapien
22	23	54.8	17 2 Q7M1I3	Q7ml13 phaseolus v
23	22	52.4	12 2 Q7M4X9	Q7m4x9 fusarium sp
24	22	52.4	15 1 URE2_MORMO	P17338 morganella
25	22	52.4	16 2 Q9TRR1	Q9trr1 oryctolagus
26	22	52.4	17 1 A45K_MYCBO	P80069 mycobacteri
27	22	52.4	17 2 Q90XE2	Q90xe2 gallus gall
28	22	52.4	18 2 Q6DNI9	Q6dni9 oncorhynch
29	22	52.4	18 2 Q6WTX0	Q6wtx0 eleutheroda
30	22	52.4	18 2 Q6WTZ8	Q6wtz8 eleutheroda
31	22	52.4	18 2 Q6WU54	Q6wu54 eleutheroda

32	22	52.4	18	2	Q6WU67	Q6wu67 eleutheroda
33	21	50.0	10	2	Q8JV66	Q8jv66 polyomaviru
34	21	50.0	10	2	Q8JV68	Q8jv68 polyomaviru
35	21	50.0	10	2	Q8JV70	Q8jv70 polyomaviru
36	21	50.0	10	2	Q8JV72	Q8jv72 polyomaviru
37	21	50.0	10	2	Q8JV74	Q8jv74 polyomaviru
38	21	50.0	10	2	Q8JV76	Q8jv76 polyomaviru
39	21	50.0	10	2	Q8JV80	Q8jv80 polyomaviru
40	21	50.0	10	2	Q8JV82	Q8jv82 polyomaviru
41	21	50.0	10	2	Q9Q0V7	Q9q0v7 polyomaviru
42	21	50.0	10	2	Q9Q0V9	Q9q0v9 polyomaviru
43	21	50.0	10	2	Q9Q0W1	Q9q0w1 polyomaviru
44	21	50.0	10	2	Q9Q0W3	Q9q0w3 polyomaviru
45	21	50.0	10	2	Q9Q0W5	Q9q0w5 polyomaviru
46	21	50.0	10	2	Q9Q0W7	Q9q0w7 polyomaviru
47	21	50.0	10	2	Q9Q0W9	Q9q0w9 polyomaviru
48	21	50.0	10	2	Q9Q0X1	Q9q0x1 polyomaviru
49	21	50.0	10	2	Q9Q0X3	Q9q0x3 polyomaviru
50	21	50.0	10	2	Q9Q0X5	Q9q0x5 polyomaviru
51	21	50.0	10	2	Q9Q0X9	Q9q0x9 polyomaviru
52	21	50.0	11	2	P82436	P82436 nicotiana t
53	21	50.0	11	2	Q8UUP1	Q8uup1 xenopus lae
54	21	50.0	12	2	Q9BZ49	Q9bz49 homo sapien
55	21	50.0	12	2	Q6X7V1	Q6x7v1 canis famil
56	21	50.0	12	2	Q93X21	Q93x21 zea mays (m
57	21	50.0	13	2	Q6LBR0	Q6lbr0 pseudomonas
58	21	50.0	14	2	Q7M3M4	Q7m3m4 pisaster oc
59	21	50.0	15	1	PRP_MYCBO	P80149 mycobacteri
60	21	50.0	15	1	UC29_MAIZE	P80635 zea mays (m
61	21	50.0	15	2	Q9UC22	Q9ucc2 homo sapien
62	21	50.0	15	2	Q9TR14	Q9tr14 bos taurus
63	21	50.0	15	2	Q9S8N8	Q9s8n8 hordeum vul
64	21	50.0	15	2	Q7LZM6	Q7lzm6 human herpe
65	21	50.0	15	2	Q6WFA4	Q6wfa4 sturnus vul
66	21	50.0	15	2	Q6WFA5	Q6wfa5 anas platyr
67	21	50.0	15	2	Q6WFA6	Q6wfa6 podager nac
68	21	50.0	15	2	Q6WFA7	Q6wfa7 falco pereg
69	21	50.0	15	2	Q6WFA8	Q6wfa8 strix urale
70	21	50.0	15	2	Q6WFA9	Q6wfa9 surria ulul
71	21	50.0	15	2	Q6WFB0	Q6wfb0 tyto alba (
72	21	50.0	16	1	IBP4_PIG	P24854 sus scrofa
73	21	50.0	17	2	Q14001	Q14001 homo sapien
74	21	50.0	17	2	Q9TR22	Q9tr22 bos taurus
75	21	50.0	17	2	O49225	O49225 glycine max
76	21	50.0	18	2	Q8NFB4	Q8nfb4 homo sapien
77	21	50.0	18	2	Q9H1I3	Q9h1i3 homo sapien
78	21	50.0	18	2	Q9JIE9	Q9jie9 mus musculu
79	21	50.0	18	2	Q8QFT3	Q8qft3 gallus gall
80	20	47.6	9	2	Q9UCS8	Q9ucs8 homo sapien
81	20	47.6	11	2	Q8IVG8	Q8ivg8 homo sapien
82	20	47.6	12	2	P82441	P82441 nicotiana t
83	20	47.6	13	2	Q7M3T0	Q7m3t0 dictyosteli
84	20	47.6	13	2	Q67604	Q67604 squash leaf
85	20	47.6	16	1	FOR2_MYRGU	P81437 myrmecia gu
86	20	47.6	16	2	Q8RVF4	Q8rvf4 zea mays (m
87	20	47.6	17	2	Q96P96	Q96p96 homo sapien
88	19.5	46.4	17	2	Q9TR78	Q9tr78 didelphis m
89	19	45.2	9	2	Q9UMF3	Q9umf3 homo sapien
90	19	45.2	9	2	P82429	P82429 nicotiana t
91	19	45.2	9	2	Q6QVK7	Q6qvk7 phaseolus v
92	19	45.2	10	1	PNAS_PRUDU	P81898 prunus dulc
93	19	45.2	10	2	Q6QVG6	Q6qvg6 phaseolus v
94	19	45.2	11	1	BPP3_BOTIN	P30423 bothrops in
95	19	45.2	11	1	BPP4_BOTIN	P30424 bothrops in
96	19	45.2	11	1	BPPB_AGKHA	P01021 agkistrodon
97	19	45.2	11	1	MORN_HUMAN	P01163 homo sapien
98	19	45.2	11	2	Q80W11	Q80w11 mus sp. nt-
99	19	45.2	12	1	F1F1_SARBU	P83349 sarcophaga
100	19	45.2	12	2	P82328	P82328 pisum sativ

ALIGNMENTS

```

RESULT 1
APID_BOMPA STANDARD; PRT; 17 AA.
ID P81464;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN [1]_TaxID=65598;
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=97362903; PubMed=9219367; DOI=10.1016/S0965-1748(97)00013-1;
RA Rees J.A., Moniatte M., Bulet P.;
RT "Novel antibacterial peptides isolated from a European bumblebee,
RT Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By bacterial infection.
CC -!- SIMILARITY: Belongs to the apidaecin family.
DR InterPro; IPR004828; Apidaecin.
DR Pfam; PF00807; Apidaecin; 1.
KW Antibiotic; Direct protein sequencing; Hemolymph; Insect immunity.
SQ SEQUENCE 17 AA; 1963 MW; CD1DD02C8BC23D1 CRC64;

Query Match 61.9%; Score 26; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

QY 3 PPPLP 7
DB 8 PPRP 12

RESULT 2
Q9UCT9 PRELIMINARY; PRT; 18 AA.
AC Q9UCT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PRG=PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.
DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6FBOA83D2E40 CRC64;

Query Match 61.9%; Score 26; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

QY 3 PPPLP 7
DB 8 PPRP 12

```

```

Db 4 PPRP 8

RESULT 3
TMOF_AEDAE STANDARD; PRT; 10 AA.
ID P19425;
AC 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]_TaxID=7159;
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
RT enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]_TaxID=7159;
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
CC and stops at 56 hrs.
DR PIR; A36454; A36454.
KW Direct protein sequencing; Hormone.
FT DOMAIN 3 10 Poly-Pro.
FT VARIANT 1 2 YD -> DY (in TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 59.5%; Score 25; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

QY 3 PPPLP 7
DB 5 PPRP 9

RESULT 4
P82439 PRELIMINARY; PRT; 15 AA.
ID P82439;
AC P82439;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ~200 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed

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RT tobacco culture.;  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall; Hydroxylation.  
 FT MOD\_RES 6  
 FT NON\_TER 15 15 HYDROXYLATION.  
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;  
  
 Query Match 59.5%; Score 25; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 3 PPPLP 7  
 Db 6 PPPPP 10  
  
 RESULT 5  
 Q7M1V1 PRELIMINARY; PRT; 15 AA.  
 AC Q7M1V1;  
 DT 01-MAR-2004 (TReMBLrel. 26, Created)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Light harvesting complex chain III/b, photosystem I (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriaraloideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.  
 RA Uchiyama Y., Teugita A.;  
 RL Submitted (JUN-1991) to the PIR data bank.  
 DR PIR; P70037; P70037.  
 DR Gramene; Q7M1V1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1441 MW; 3D92222733333672 CRC64;  
  
 Query Match 59.5%; Score 25; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 3 PPPLP 7  
 Db 8 PPPPP 12  
  
 RESULT 6  
 Q7M137 PRELIMINARY; PRT; 16 AA.  
 AC Q7M137;  
 DT 01-MAR-2004 (TReMBLrel. 26, Created)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Superoxide dismutase (EC 1.15.1.1) (Fragment).  
 OS unidentified bacterium.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=2338;  
 RN [1]  
 RP SEQUENCE.  
 RA Binette J.P., Binette M.B.;  
 RL Submitted (OCT-1996) to the PIR data bank.  
 CC -!- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
 CC family.  
 DR PIR; E58503; E58503.  
 DR GO; GO:0046872; P:metal ion binding; IEA.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.  
 DR GO; GO:0004784; P:superoxide dismutase activity; IEA.  
 DR GO; GO:0006801; P:superoxide metabolism; IEA.  
 DR InterPro; IPR001189; SODismutase.  
 DR Pfam; PF00081; Sod\_Fe\_N; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 16  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1828 MW; 12DE78949AC43609 CRC64;  
  
 Query Match 59.5%; Score 25; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 4 PPPLP 7  
 Db 6 PPPLP 9  
  
 RESULT 7  
 Q41400 PRELIMINARY; PRT; 17 AA.  
 AC Q41400;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Hydroxyproline-rich protein (Fragment).  
 OS Sesbania rostrata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
 OX NCBI\_TaxID=3895;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bacterial infected stem located root primordia;  
 EX MEDLINE=96112737; PubMed=8664492;  
 RA Coormachig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M.,  
 RA Holsters M., De Bruijn F.;  
 RT "Use of differential display to identify novel Sesbania rostrata genes  
 enhanced by Azorhizobium caulinodans infection.";  
 RL Mol. Plant Microbe Interact. 8:816-824(1995).  
 DR EMBL; Z48673; CAA88592.1; -.  
 DR PIR; S57991; S57991.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;  
  
 Query Match 59.5%; Score 25; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 3 PPPLP 7  
 Db 10 PPPPP 14  
  
 RESULT 8  
 Q84129 PRELIMINARY; PRT; 18 AA.  
 AC Q84129;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (seg  
 8), COOH terminus of NS1. (Fragment).  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=83303830; PubMed=6612993;  
 RA Parvin J.D., Young J.P., Palese P.;  
 RT "Nonsense mutations affecting the lengths of the NS1 nonstructural  
 proteins of influenza A virus isolates.";

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RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FEBEF CRC64;

Query Match 59.5%; Score 25; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
DB 11 PPLP 14

RESULT 9
Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Antho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actinilidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510; DOI=10.1016/0196-9781(92)90040-A;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 290817637686777 CRC64;

Query Match 57.1%; Score 24; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
DB 1 LPPGFLP 7

RESULT 10
Q6W631 PRELIMINARY; PRT; 16 AA.
AC Q6W631;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Sphagnum cuspidatum (Bog moss).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=41840;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309629; AAP70619.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1843 MW; 56167D25E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
DB 6 EPPKIP 11

RESULT 11
Q6W322 PRELIMINARY; PRT; 18 AA.
AC Q6W322;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Andraea rothii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Andraeopsida; Andraeales; Andraeaceae; Andraea.
OX NCBI_TaxID=50745;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY312864; AAQ8205.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4E675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
DB 8 EPPKIP 13

RESULT 12
Q6W619 PRELIMINARY; PRT; 18 AA.
AC Q6W619;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Photosystem II subunit T (Fragment).
GN Name=psbt;
OS Sphagnum wulfianum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
OX NCBI_TaxID=128256;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaw A.J., Cox C.J., Boles S.B.;
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have
RT no roots?";
RL Am. J. Bot. 90:1777-1787(2003).
DR EMBL; AY309633; AAP70629.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2143 MW; 2FA4E675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7
DB 8 EPPKIP 13

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Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
: || : |  
Db 8 EPPKIP 13

## RESULT 13

Q6W622 PRELIMINARY; PRT; 18 AA.  
AC Q6W622; (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Photosystem II subunit T (Fragment).  
GN Name=psbt;  
OS Sphagnum squarrosum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.  
OX NCBI\_TaxID=128240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shaw A.J., Cox C.J., Boles S.B.;  
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have  
no roots?";  
RL Am. J. Bot. 90:1777-1787(2003).  
DR EMBL; AY309632; AAP70626.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
: || : |  
Db 8 EPPKIP 13

## RESULT 14

Q6W628 PRELIMINARY; PRT; 18 AA.  
AC Q6W628; (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Photosystem II subunit T (Fragment).  
GN Name=psbt;  
OS Sphagnum lapazense.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.  
OX NCBI\_TaxID=231110;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shaw A.J., Cox C.J., Boles S.B.;  
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have  
no roots?";  
RL Am. J. Bot. 90:1777-1787(2003).  
DR EMBL; AY309630; AAP70621.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7

Db 8 EPPKIP 13

## RESULT 15

Q6W634 PRELIMINARY; PRT; 18 AA.  
AC Q6W634; (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Photosystem II subunit T (Fragment).  
GN Name=psbt;  
OS Sphagnum sericeum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.  
OX NCBI\_TaxID=128237;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shaw A.J., Cox C.J., Boles S.B.;  
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have  
no roots?";  
RL Am. J. Bot. 90:1777-1787(2003).  
DR EMBL; AY309628; AAP70616.1; -.  
DR EMBL; AY309631; AAP70623.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
: || : |  
Db 8 EPPKIP 13

## RESULT 16

Q6W637 PRELIMINARY; PRT; 18 AA.  
AC Q6W637; (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Photosystem II subunit T (Fragment).  
GN Name=psbt;  
OS Sphagnum affine.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.  
OX NCBI\_TaxID=128174;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shaw A.J., Cox C.J., Boles S.B.;  
RT "Polarity of peatmoss (Sphagnum) evolution: who says bryophytes have  
no roots?";  
RL Am. J. Bot. 90:1777-1787(2003).  
DR EMBL; AY309627; AAP70611.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 2143 MW; 2FA4B675E92FE42E CRC64;

Query Match 57.1%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
: || : |  
Db 8 EPPKIP 13

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RESULT 17
BPP_AGRHP STANDARD; PRT; 11 AA.
ID P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme
DE inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it. It acts
CC as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Direct protein sequencing; Hypotensive agent;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1112 MW; 30B8F1277686777 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
DB 7 PPPI 10

RESULT 18
TY13_PHYRO STANDARD; PRT; 13 AA.
ID P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucci P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Direct protein sequencing;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
DB 7 PPPI 10

RESULT 19
Q7LZ51 PRELIMINARY; PRT; 13 AA.
ID Q7LZ51;
AC Q7LZ51;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tryptophyllin-related peptide.
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE.
RX MEDLINE=92339502; PubMed=1633846; DOI=10.1016/0014-5793(92)80427-I;
RA Mignogna G., Severini C., Simmaco M., Negri L.,
RA Falconieri Erspamer G., Kreil G., Barra D.;
RT "Identification and characterization of two dermorphins from skin
RT extracts of the Amazonian frog Phyllomedusa bicolor.";
RL FEBS Lett. 302:151-154(1992).
DR PIR; S21152; S21152.
SQ SEQUENCE 13 AA; 1575 MW; 094C33A21BC5777B CRC64;

Query Match 54.8%; Score 23; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
DB 7 PPPI 10

RESULT 20
TY13_BOMVA STANDARD; PRT; 14 AA.
ID TY13_BOMVA;
AC P84215;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tryptophyllin-13.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Skin secretion;
RX PubMed=15134346;
RA Marenah L., Flatt P.R., Orr D.F., McClean S., Shaw C.,
RA Abdel-Wahab Y.H.;
RT "Skin secretion of the toad Bombina variegata contains multiple
RT insulin-releasing peptides including bombesin and entirely novel
RT insulinotropic structures.";
RL Biol. Chem. 385:315-321(2004).
CC -|- FUNCTION: Possesses insulin-releasing activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=1650.5; METHOD=Electrospray; RANGE=1-14;
CC NOTE=Ref.1.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 14 AA; 1651 MW; 23C4809C33A0DC77 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.1e+03;
```

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 6  
Db 6 PPPI 9

## RESULT 21

Q9NQY8 ID Q9NQY8 PRELIMINARY; PRT; 17 AA.  
AC Q9NQY8; DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Transcription factor 12 (Fragment).  
GN Name=TCF12;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gan T.-I., O'Sickey T., Zhang Y., Kim U.-J., Bina M.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF271610; AAF82574.1;  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1802 MW; E26E7FB1D7903679 CRC64;

Query Match 54.8%; Score 23; DB 2; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
Db 11 PPGLP 15

## RESULT 22

Q7M113 ID Q7M113 PRELIMINARY; PRT; 17 AA.  
AC Q7M113; DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96011753; PubMed=7548825;  
RA Wojtaszek P., Trethowan J., Bolwell G.P.;  
RT "Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.).";  
RL Plant Mol. Biol. 28:1075-1087(1995).  
DR PIR; S59481; S59481.  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE555 CRC64;

Query Match 54.8%; Score 23; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 3.8e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
Db 2 MYLPVP 8

## RESULT 23

Q7M4X9 ID Q7M4X9 PRELIMINARY; PRT; 12 AA.  
AC Q7M4X9; DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Ribosomal protein S3 (Fragment).  
OS Fusarium sporotrichioides.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
OX NCBI\_TaxID=5514;  
RN [1]  
RP SEQUENCE.

RA Chow L.P., Fukaya N., Sugiyama Y., Ueno Y., Tabuchi K., Taugita A.;  
RL Submitted (OCT-1994) to the PIR data bank.

DR PIR; PA0098; PA0098. 1  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1242 MW; 227EFCBA7C727D7 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
Db 4 PPVP 7

## RESULT 24

URE2 MORMO ID URE2 MORMO STANDARD; PRT; 15 AA.  
AC P17338; DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea amidohydrolase) (Fragment).  
GN Name=ureB;  
OS Morganella morganii (Proteus morganii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Morganella.  
OX NCBI\_TaxID=582;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90264298; PubMed=2345135;  
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
RT "Morganella morganii urease: purification, characterization, and isolation of gene sequences.";  
RL J. Bacteriol. 172:3073-3080(1990).  
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
CC -1- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).  
CC -1- SIMILARITY: Belongs to the urease beta subunit family.  
DR PIR; B35389; B35389.  
KW Direct protein sequencing; Hydrolase.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPLP 6  
Db 5 QPTPL 9

## RESULT 25

Q9TRR1 ID Q9TRR1 PRELIMINARY; PRT; 16 AA.  
AC Q9TRR1; DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 OS Fibronectin 47 kDa fragment (Fragment).  
 OC Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92283375; PubMed=1597256;  
 RA Lesot H., Fausser J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,  
 RA Ruch J.V.;  
 RT "The carboxy-terminal extension of the collagen binding domain of  
 RT fibronectin mediates interaction with a 165 kDa membrane protein  
 RT involved in osteoclast differentiation.";  
 RL Differentiation 49:109-118 (1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1764 MW; B196CAAC53F5739 CRC64;  
  
 Query Match 52.4%; Score 22; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 5e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 2 QPPPLP 7  
 | | | | |  
 Db 1 QPQHP 6  
  
 RESULT 26  
 A45K MYCBO STANDARD; PRT; 17 AA.  
 AC P80069;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE 45/47 kDa antigen (Fragment).  
 OS Mycobacterium bovis.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=BCG / Paris 1173 P2;  
 RX MEDLINE=93138802; PubMed=8423100;  
 RA Romain F., Laqueyrie A., Miltzer P., Pescher P., Chavarot P.,  
 RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
 RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen  
 RT complex, an immunodominant target for antibody response after  
 RT immunization with living bacteria.";  
 RL Infect. Immun. 61:742-750 (1993).  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: To M.leprae NL43, and M.tuberculosis MPT32.  
 DR PIR; A49237; A49237.  
 KW Antigen; Direct protein sequencing.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;  
  
 Query Match 52.4%; Score 22; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 PPLP 7  
 | | | | |  
 Db 6 PPVP 9  
  
 RESULT 27  
 Q90XE2 PRELIMINARY; PRT; 17 AA.  
 AC Q90XE2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Transforming growth factor beta 4 (Fragment).  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22533207; PubMed=12646161; DOI=10.1016/S0006-291X(03)00300-0;  
 RA Pan H.J., Halper J.;  
 RT "Cloning, expression, and characterization of chicken transforming  
 RT growth factor beta 4.";  
 RL Biochem. Biophys. Res. Commun. 303:24-30 (2003).  
 DR EMBL; AF395834; AAL05481.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;  
  
 Query Match 52.4%; Score 22; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 5.4e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1 MQPPPL 6  
 | | | | |  
 Db 1 MDPSPL 6  
  
 RESULT 28  
 Q6DNI9 PRELIMINARY; PRT; 18 AA.  
 AC Q6DNI9;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Urotensin I (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bernier N.J., Craig P.M.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY651778; AAT70095.1; -.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1945 MW; ABC326A1540B8366 CRC64;  
  
 Query Match 52.4%; Score 22; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 5.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 MQPPPL 6  
 | | | | |  
 Db 1 MKPVPL 6  
  
 RESULT 29  
 Q6WTX0 PRELIMINARY; PRT; 18 AA.  
 AC Q6WTX0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cellular myelocytomatosis (fragment).  
 GN Name=c-myc;  
 OS Eutherodactylus persimilis.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
 CC Telmatobatinae; Eleutherodactylus.  
 OX NCBI\_TaxID=228453;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RX MEDLINE=22850980; PubMed=12969459;
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269379; AAQ01124.1; -
DR EMBL; AY269380; AAQ01125.1; -
DR EMBL; AY269381; AAQ01126.1; -
DR EMBL; AY269382; AAQ01127.1; -
DR EMBL; AY269383; AAQ01128.1; -
DR EMBL; AY269384; AAQ01129.1; -
DR EMBL; AY269385; AAQ01130.1; -
DR EMBL; AY269386; AAQ01131.1; -
DR EMBL; AY269387; AAQ01132.1; -
DR EMBL; AY269388; AAQ01133.1; -
DR EMBL; AY269389; AAQ01134.1; -
DR EMBL; AY269390; AAQ01135.1; -
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db |:|:
4 METPPI 9

RESULT 30
Q6WTZ8
ID Q6WTZ8 PRELIMINARY; PRT; 18 AA.
AC Q6WTZ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular myelocytomatosis (Fragment).
GN Name=c-myc;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobinae; Eleutherodactylus.
OX NCBI_TaxID=228451;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269351; AAQ01096.1; -
DR EMBL; AY269352; AAQ01097.1; -
DR EMBL; AY269353; AAQ01098.1; -
DR EMBL; AY269354; AAQ01099.1; -
DR EMBL; AY269355; AAQ01100.1; -
DR EMBL; AY269356; AAQ01101.1; -
DR EMBL; AY269357; AAQ01102.1; -
DR EMBL; AY269358; AAQ01103.1; -
DR EMBL; AY269359; AAQ01104.1; -
DR EMBL; AY269360; AAQ01105.1; -
DR EMBL; AY269361; AAQ01106.1; -
DR EMBL; AY269362; AAQ01107.1; -
DR EMBL; AY269363; AAQ01108.1; -
DR EMBL; AY269364; AAQ01109.1; -
DR EMBL; AY269365; AAQ01110.1; -
DR EMBL; AY269366; AAQ01111.1; -
DR EMBL; AY269367; AAQ01112.1; -
DR EMBL; AY269368; AAQ01113.1; -
DR EMBL; AY269369; AAQ01114.1; -
DR EMBL; AY269370; AAQ01115.1; -
DR EMBL; AY269371; AAQ01116.1; -
DR EMBL; AY269372; AAQ01117.1; -

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DR EMBL; AY269373; AAQ01118.1; -
DR EMBL; AY269374; AAQ01119.1; -
DR EMBL; AY269375; AAQ01120.1; -
DR EMBL; AY269377; AAQ01122.1; -
DR EMBL; AY269378; AAQ01123.1; -
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPL 6
Db |:|:
4 METPPI 9

RESULT 31
Q6WU54
ID Q6WU54 PRELIMINARY; PRT; 18 AA.
AC Q6WU54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular myelocytomatosis (Fragment).
GN Name=c-myc;
OS Eleutherodactylus stejnegerianus (Stejneger's rainfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobinae; Eleutherodactylus.
OX NCBI_TaxID=228449;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford A.J.;
RT "Huge populations and old species of Costa Rican and Panamanian dirt
RT frogs inferred from mitochondrial and nuclear gene sequences.";
RL Mol. Ecol. 12:2525-2540(2003).
DR EMBL; AY269295; AAQ01040.1; -
DR EMBL; AY269296; AAQ01041.1; -
DR EMBL; AY269297; AAQ01042.1; -
DR EMBL; AY269298; AAQ01043.1; -
DR EMBL; AY269299; AAQ01044.1; -
DR EMBL; AY269300; AAQ01045.1; -
DR EMBL; AY269301; AAQ01046.1; -
DR EMBL; AY269302; AAQ01047.1; -
DR EMBL; AY269303; AAQ01048.1; -
DR EMBL; AY269304; AAQ01049.1; -
DR EMBL; AY269305; AAQ01050.1; -
DR EMBL; AY269306; AAQ01051.1; -
DR EMBL; AY269307; AAQ01052.1; -
DR EMBL; AY269308; AAQ01053.1; -
DR EMBL; AY269309; AAQ01054.1; -
DR EMBL; AY269310; AAQ01055.1; -
DR EMBL; AY269311; AAQ01056.1; -
DR EMBL; AY269312; AAQ01057.1; -
DR EMBL; AY269313; AAQ01058.1; -
DR EMBL; AY269314; AAQ01059.1; -
DR EMBL; AY269315; AAQ01060.1; -
DR EMBL; AY269316; AAQ01061.1; -
DR EMBL; AY269317; AAQ01062.1; -
DR EMBL; AY269318; AAQ01063.1; -
DR EMBL; AY269319; AAQ01064.1; -
DR EMBL; AY269320; AAQ01065.1; -
DR EMBL; AY269321; AAQ01066.1; -
DR EMBL; AY269322; AAQ01067.1; -
DR EMBL; AY269323; AAQ01068.1; -
DR EMBL; AY269324; AAQ01069.1; -
DR EMBL; AY269325; AAQ01070.1; -
DR EMBL; AY269326; AAQ01071.1; -
DR EMBL; AY269327; AAQ01072.1; -
DR EMBL; AY269328; AAQ01073.1; -

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DR EMBL; AY269329; AAQ01074.1; -  
 DR EMBL; AY269330; AAQ01075.1; -  
 DR EMBL; AY269331; AAQ01076.1; -  
 DR EMBL; AY269332; AAQ01077.1; -  
 DR EMBL; AY269333; AAQ01078.1; -  
 DR EMBL; AY269334; AAQ01079.1; -  
 DR EMBL; AY269335; AAQ01080.1; -  
 DR EMBL; AY269336; AAQ01081.1; -  
 DR EMBL; AY269337; AAQ01082.1; -  
 DR EMBL; AY269338; AAQ01083.1; -  
 DR EMBL; AY269339; AAQ01084.1; -  
 DR EMBL; AY269340; AAQ01085.1; -  
 DR EMBL; AY269341; AAQ01086.1; -  
 DR EMBL; AY269342; AAQ01087.1; -  
 DR EMBL; AY269343; AAQ01088.1; -  
 DR EMBL; AY269344; AAQ01089.1; -  
 DR EMBL; AY269345; AAQ01090.1; -  
 DR EMBL; AY269346; AAQ01091.1; -  
 DR EMBL; AY269347; AAQ01092.1; -  
 DR EMBL; AY269348; AAQ01093.1; -  
 DR EMBL; AY269349; AAQ01094.1; -  
 DR EMBL; AY269350; AAQ01095.1; -  
 FT NON\_TER 1  
 FT NON\_TER 18  
 SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPPL 6  
 | : |||  
 Db 4 METPPI 9

RESULT 32  
 Q6WU67 PRELIMINARY; PRT; 18 AA.  
 ID Q6WU67;  
 AC Q6WU67;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Cellular myelocytomatosis (Fragment).  
 GN Name=c-myc;  
 OS Eleutherodactylus bransfordii (Bransford's litter frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
 OC Telmatobiinae; Eleutherodactylus.  
 OC NCBI\_TaxID=228452;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22850980; PubMed=12969459;  
 RA Crawford A.J.;  
 RT "Huge populations and old species of Costa Rican and Panamanian dirt  
 frogs inferred from mitochondrial and nuclear gene sequences.";  
 RL Mol. Ecol. 12:2525-2540(2003).  
 DR EMBL; AY269282; AAQ01027.1; -  
 DR EMBL; AY269283; AAQ01028.1; -  
 DR EMBL; AY269284; AAQ01029.1; -  
 DR EMBL; AY269285; AAQ01030.1; -  
 DR EMBL; AY269286; AAQ01031.1; -  
 DR EMBL; AY269287; AAQ01032.1; -  
 DR EMBL; AY269288; AAQ01033.1; -  
 DR EMBL; AY269289; AAQ01034.1; -  
 DR EMBL; AY269290; AAQ01035.1; -  
 DR EMBL; AY269292; AAQ01037.1; -  
 DR EMBL; AY269293; AAQ01038.1; -  
 DR EMBL; AY269294; AAQ01039.1; -  
 DR EMBL; AY269281; AAQ01026.1; -  
 FT NON\_TER 1  
 FT NON\_TER 18  
 SQ SEQUENCE 18 AA; 1882 MW; 7F844740EE93A30 CRC64;

Query Match 52.4%; Score 22; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MOPPL 6  
 | : |||  
 Db 4 METPPI 9

RESULT 33  
 Q8JUV66 PRELIMINARY; PRT; 10 AA.  
 ID Q8JUV66;  
 AC Q8JUV66;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OC NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21465052; PubMed=11581397;  
 RX DOI=10.1128/JVI.75.21.10290-10299.2001;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304389; AAM97808.1; -  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
 |||  
 Db 7 PPP 9

RESULT 34  
 Q8JUV68 PRELIMINARY; PRT; 10 AA.  
 ID Q8JUV68;  
 AC Q8JUV68;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OC NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21465052; PubMed=11581397;  
 RX DOI=10.1128/JVI.75.21.10290-10299.2001;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304388; AAM97806.1; -  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
 |||  
 Db 7 PPP 9

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 35
Q8JV70 PRELIMINARY; PRT; 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 36
Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304386; AAM97802.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 37
Q8JV74 PRELIMINARY; PRT; 10 AA.
ID Q8JV74
AC Q8JV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303948; AAM97800.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 38
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID Q8JV76
AC Q8JV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303947; AAM97798.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 39
Q8JV80 PRELIMINARY; PRT; 10 AA.
ID Q8JV80
AC Q8JV80;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RA DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAM97794.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 40
Q8JV82
ID Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
RA DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303944; AAM97792.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

Search completed: June 7, 2005, 23:18:47
Job time : 34.8 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 91.4909 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89  
Sequence: 1 LQTFQPLLQVMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	17	4	AAB72501 Colostrin
2	89	100.0	17	4	AAB59310 Ewe colos
3	89	100.0	17	4	AAB72247 Colostrin
4	89	100.0	17	4	AAB72533 Colostrin
5	89	100.0	17	5	AAO14578 Neural ce
6	89	100.0	17	5	AAW51037 Colostrin
7	89	100.0	17	5	AAE20229 Colostrin
8	89	100.0	17	8	ADN60296 Constitue
9	89	100.0	17	8	ADS74386 Ovine col
10	89	100.0	18	4	AAB59341 Ewe colos
11	56	62.9	11	4	AAE07185 Colostrin
12	56	62.9	12	4	AAE07195 Modified
13	39	43.8	13	7	ADG73339 Enterococ
14	34.5	38.8	15	8	ADN17037 Gi-alpha
15	34	38.2	15	5	ABN99038 Carbamyla
16	33	37.1	12	7	ADC44467 Endotheli
17	33	37.1	15	4	AAB72531 Colostrin
18	33	37.1	15	4	AAB59334 Ewe colos
19	33	37.1	15	4	AAB72279 Colostrin
20	33	37.1	15	4	AAB72563 Colostrin
21	33	37.1	15	5	AAO14610 Neural ce
22	33	37.1	15	5	AAW51066 Colostrin
23	33	37.1	15	5	AAE20261 Colostrin
24	33	37.1	15	8	ADN60328 Constitue
25	33	37.1	15	8	ADS74410 Ovine col

26	32	36.0	8	2	AAR21055	Gamma-car
27	32	36.0	15	6	ABR31148	Human can
28	32	36.0	15	6	ABR31149	Human can
29	32	36.0	15	6	ABR30440	Human can
30	32	36.0	15	6	ABR31517	Human can
31	32	36.0	15	6	ABR30536	Human can
32	32	36.0	15	6	ABR30847	Human can
33	32	36.0	18	8	ADH14837	Gliadin r
34	31	34.8	12	3	AAB23189	Hsp47-bin
35	31	34.8	14	4	AAW97279	Human pep
36	31	34.8	14	7	ADP71116	Saccharom
37	31	34.8	15	2	AAW56352	LO-CD2a 1
38	31	34.8	15	2	AAW56352	LO-CD2a 1
39	31	34.8	15	5	AAU74511	Human ATP
40	31	34.8	15	6	ABR38577	Human can
41	31	34.8	15	6	ABR38568	Human can
42	31	34.8	15	6	ABR38729	Human can
43	30	33.7	10	7	ADD15523	Predicted
44	30	33.7	12	8	ADJ57286	Provasopr
45	30	33.7	14	4	AAW96749	Human pep
46	30	33.7	15	5	AAW47320	Human zin
47	30	33.7	15	6	ABR30169	Human can
48	30	33.7	15	6	ABR30262	Human can
49	30	33.7	15	6	ABR30274	Human can
50	30	33.7	15	6	ABR30229	Human can
51	30	33.7	15	6	ABR30154	Human can
52	30	33.7	15	6	ABR31758	Human can
53	30	33.7	15	6	ABR30297	Human can
54	30	33.7	16	3	AAV65560	Oestrogen
55	30	33.7	16	5	AAU86297	Oestrogen
56	30	33.7	16	8	ADM79008	Oestrogen
57	30	33.7	17	4	AAU01845	Wheat pep
58	30	33.7	17	4	AAU01825	Wheat Gli
59	30	33.7	17	8	ADH16206	Gliadin r
60	30	33.7	17	8	ADH14681	Gliadin r
61	30	33.7	17	8	ADH14675	Gliadin r
62	30	33.7	17	8	ADH14695	Gliadin r
63	30	33.7	17	8	ADH14685	Gliadin r
64	30	33.7	17	8	ADH14646	Gliadin r
65	30	33.7	17	8	ADH14602	Gliadin r
66	29	32.6	8	6	ABP73085	Amino aci
67	29	32.6	9	5	ABB08361	Synthetic
68	29	32.6	9	7	ABR82213	Human ant
69	29	32.6	10	2	RAY05729	Human G p
70	29	32.6	10	6	ABR05972	Human can
71	29	32.6	10	6	ABR05795	Human can
72	29	32.6	10	6	ABR05791	Human can
73	29	32.6	10	6	ADA14236	Human GPR
74	29	32.6	12	3	AAW92994	Transform
75	29	32.6	12	6	ABU07930	Neisseria
76	29	32.6	13	6	ABP81099	Human TPO
77	29	32.6	15	3	AAV93031	Transform
78	29	32.6	15	3	AAV93032	Transform
79	29	32.6	15	5	ABB09888	N-termina
80	29	32.6	15	6	ABR31395	Human can
81	29	32.6	15	6	ABR30682	Human can
82	29	32.6	15	6	ABR31783	Human can
83	29	32.6	15	6	ABR31394	Human can
84	29	32.6	18	2	AAW66658	HSV-2 gly
85	29	32.6	18	4	AAW20225	Peptide #
86	29	32.6	18	4	ABB40529	Peptide #
87	29	32.6	18	4	AAW34255	Peptide #
88	29	32.6	18	4	ABB24849	Protein #
89	29	32.6	18	4	AAW74093	Human bon
90	29	32.6	18	4	AAW61355	Human bra
91	29	32.6	18	4	ABG55849	Human liv
92	29	32.6	18	5	ABG43991	Human pep
93	29	32.6	18	8	ADH14842	Gliadin r
94	28	31.5	7	2	AAW17515	Protein k
95	28	31.5	9	7	ADD99989	Human 193
96	28	31.5	9	7	ADD99556	Human 193
97	28	31.5	9	7	ADD99875	Human 193
98	28	31.5	9	7	ADD99363	Human 193



DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator.

XX

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The peptides

CC have immune response modulatory activity, and are capable of inducing

CC cytokines. Colostrinin and its derived peptides are useful for inducing

CC cytokine production, for modulating an immunological response and for

CC inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLQLQVMMPEQGD 17

Db 1 LQTPQPLQLQVMMPEQGD 17

RESULT 4

AAB72533

ID AAB72533 standard; peptide; 17 AA.

XX

AC AAB72533;

XX

XX 09-MAY-2001 (first entry)

XX

XX Colostrinin peptide #2.

XX

XX Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

OS Unidentified.

XX

XX WO200112651-A2.

XX

XX 22-FEB-2001.

XX

XX 17-AUG-2000; 2000WO-US022774.

XX

XX 17-AUG-1999; 99US-0149633P.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

XX

XX Boldogh I;

XX

XX WPI; 2001-226545/23.

XX

XX Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

XX

XX Claim 6; Page 21; 35pp; English.

XX

CC The present invention relates to a method for promoting neural cell

CC differentiation and treating damaged neural cells, using colostrinin and

CC colostrinin constituent peptides (e.g. the present peptide) as a neural

CC cell regulator. Colostrinin is a polypeptide complex found in colostrum

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLQLQVMMPEQGD 17

Db 1 LQTPQPLQLQVMMPEQGD 17

RESULT 5

AAO14578

ID AAO14578 standard; peptide; 17 AA.

XX

XX AAO14578;

XX

XX 27-MAY-2002 (first entry)

XX

XX Neural cell regulatory colostrinin peptide 2.

XX

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX neural cell treatment.

XX

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

FT Modified-site 17

FT /note= "Optional C-terminal amide"

XX

XX WO200213851-A1.

XX

XX 21-FEB-2002.

XX

XX 17-AUG-2000; 2000WO-US022777.

XX

XX 17-AUG-2000; 2000WO-US022777.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

XX

XX Boldogh I, Stanton JG, Hughes TK;

XX

XX WPI; 2002-269152/31.

XX

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog.

XX

XX Claim 7; Page 21; 37pp; English.

XX

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLQLQVMMPEQGD 17

Db 1 LQTPQPLQLQVMMPEQGD 17

RESULT 6

AAMS1037

```

ID XX AAM51037 standard; peptide; 17 AA.
AC XX AAM51037;
DT XX 30-MAY-2002 (first entry)
DE XX Colostrinin constituent peptide.
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.
OS XX Homo sapiens.
XX Key Location/Qualifiers
XX Modified-site 17 /note= "optional C-terminal amidation"
FT FT
XX WO200213849-A1.
XX 21-FEB-2002.
XX 17-AUG-2000; 2000WO-US022775.
XX 17-AUG-2000; 2000WO-US022775.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX (REGE-) REGEN THERAPEUTICS PLC.
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2002-269150/31.
XX Modulation of blood cell proliferation in a patient involves use of blood
XX cell regulator selected from colostrinin, its constituent peptide and/or
XX analog.
XX Claim 1; Page 34; 54pp; English.
XX The present sequence is that of a colostrinin constituent peptide that is
XX preferred for use as an immunological regulator and as a blood cell
XX regulator in claimed methods of the invention. Methods are claimed for:
XX inducing a cytokine in a cell by contact with an immunological regulator,
XX where the cell is present in a cell culture, a tissue, an organ or an
XX organism, and the cell is mammalian, including human; modulating an
XX immune response in a cell by contact with the immunological regulator
XX under conditions effective to induce a cytokine; modulating an immune
XX response in a patient by administering an immunological regulator under
XX conditions effective to induce a cytokine, where the immunological
XX regulator is administered topically or as part of a dietary supplement,
XX and where the immune response is specific or non specific, an interferon
XX response or an antibody response; modulating blood cell proliferation by
XX contacting blood cells with a blood cell regulator, where the blood cells
XX are present in a cell culture or an organism, are mammalian or human, and
XX where the blood cells are increased in number or differentiated; and a
XX method for modulating blood cell proliferation in a patient. A claimed
XX cytokine-inducing composition comprises a pharmaceutical carrier and an
XX active agent such as the present peptide. Cytokines induced by this
XX peptide in human leucocyte cultures include interferon-gamma, tumour
XX necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
XX interleukin-12. It was one of the best overall inducers in almost all
XX cytokine and blood cell proliferation experiments conducted
XX
XX Sequence 17 AA;
XX Query Match 100.0%; Score 89; DB 5; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-07;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LQTPQLQVNMPEQGD 17
XX |||||
XX DB 1 LQTPQLQVNMPEQGD 17
XX |||||
XX
XX RESULT 8
XX ADN60296

```

RESULT 7  
AAE20229 standard; peptide; 17 AA.  
AC AAE20229;  
DT 18-JUN-2002 (first entry)  
DE Colostrinin constituent peptide #2.  
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.  
XX Unidentified.  
XX Key Location/Qualifiers  
XX Modified-site 17 /note= "Optionally C-terminal amide"  
XX WO200213850-A1.  
XX 21-FEB-2002.  
XX 17-AUG-2000; 2000WO-US022776.  
XX 17-AUG-2000; 2000WO-US022776.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX Composition useful for the modulation of blood cell proliferation in a  
XX patient comprises a blood cell regulator selected from colostrinin, its  
XX constituent peptide and/or analog.  
XX Claim 6; Page 25; 51pp; English.  
XX The invention relates to a composition which comprises a blood cell  
XX regulator selected from colostrinin, its constituent peptide and/or  
XX analogue. The invention is used for modulating the oxidative stress level  
XX in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
XX organ, or organism; or for treating oxidative damage to the skin of a  
XX patient e.g. animal or human; to modulate oxidative stress during/ after  
XX a premature birth or normal birth, preventing/delaying aging in a  
XX patient, enhancing wound healing, and the reduction of side effects of  
XX cosmetic procedures. The method changes the level of an oxidising species  
XX in the cell, such as decreases or prevents increase in the level of  
XX damage to a biomolecule of the patient selected from DNA, protein and/or  
XX lipid, compared to the same conditions when the oxidative stress  
XX regulator is not present. The modulation of oxidative stress results in  
XX enhanced repair, regeneration, and replacement of cells, tissues and  
XX organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
XX external organs), as well as enhanced preservation of such organs for  
XX transplantation, implantation, or scientific research. The present  
XX sequence is a colostrinin constituent peptide  
XX  
XX Sequence 17 AA;  
XX Query Match 100.0%; Score 89; DB 5; Length 17;  
XX Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 LQTPQLQVNMPEQGD 17  
XX |||||  
XX DB 1 LQTPQLQVNMPEQGD 17  
XX |||||  
XX  
XX RESULT 8  
XX ADN60296

ID ADN60296 standard; peptide; 17 AA.  
XX AC ADN60296;  
XX DT 29-JUL-2004 (first entry)  
XX DE Constituent peptide of colostrinin SEQ ID NO:2.  
XX KW modulator; colostrinin; intracellular signaling molecule modulator;  
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
KW DNA damage; beta-amyloid; retinoic acid; cytosolic; 4HNE inhibitor;  
KW 4HNE-protein adduct formation reduction;  
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
KW c-Jun NH2-terminal kinase inhibition.  
XX OS Synthetic.  
XX PN WO2004037851-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033423.  
XX PR 22-OCT-2002; 2002US-0420369P.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (BOLD/) BOLDOGH I.  
PA (STAN/) STANTON J G.  
PA (GEOR/) GEORGIADIS J A.  
PA (HUGH/) HUGHES T K.  
PA (KRUZ/) KRUZEL M.  
XX PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
XX WPI; 2004-365494/34.  
XX DR Use of colostrinin for e.g. modulating an intracellular signaling  
XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
XX PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
XX PT a cell.  
XX PS Claim 6; SEQ ID NO 2; 46pp; English.  
XX CC The present invention describes the use of a modulator selected from  
XX CC colostrinin, its constituent peptide, its active analogue, and a  
XX CC combination of these, for modulating an intracellular signaling molecule  
XX CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
XX CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
XX CC The modulator has cytostatic activity, and can be used as a 4HNE  
XX CC inhibitor. The modulator is useful in the manufacture of a medicament for  
XX CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
XX CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
XX CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
XX CC Colostrinin, or its constituent peptide or active analogue is useful for  
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
XX CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
XX CC The present sequence represents a synthetic constituent peptide of  
XX CC colostrinin, which can be used as a modulator in the present invention.  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 89; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LQTPQLLQVNMPEQGD 17  
Db 1 LQTPQLLQVNMPEQGD 17  
RESULT 9  
ADN60296

ID ADS74386 standard; peptide; 17 AA.  
XX AC ADS74386;  
XX DT 16-DEC-2004 (first entry)  
XX DE Ovine colostrinin peptide.  
XX KW Colostrum; colostrinin; sheep; peptide purification.  
XX OS Ovis aries.  
XX PN WO2004081038-A1.  
XX PD 23-SEP-2004.  
XX PF 10-MAR-2004; 2004WO-GB001014.  
XX PR 11-MAR-2003; 2003GB-00005552.  
XX PR 08-MAR-2004; 2004GB-00005190.  
XX PA (REGB-) REGEN THERAPEUTICS PLC.  
XX PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
XX WPI; 2004-677519/66.  
XX DR Recovering peptides such as colostrinin from mammalian colostrum, by  
XX PT mixing colostrum with alcohol to form alcohol phase containing peptides  
XX PT and precipitate, separating alcohol phase from precipitate, and  
XX PT recovering alcohol phase.  
XX PS Example; SEQ ID NO 1; 41pp; English.  
XX CC The present sequence is that of a peptide that can be recovered from  
XX CC ovine colostrinin using the method of the invention. The invention  
XX CC provides a method for the recovery of peptides (especially colostrinin)  
XX CC from colostrum in substantially pure, biologically active form and in  
XX CC high yield. The method involves mixing the colostrum with an alcohol to  
XX CC form an alcohol phase containing the colostrinin and a precipitate  
XX CC containing higher molecular weight caseins and other proteins. Best  
XX CC results are obtained using methanol or ethanol of at least 80%, and  
XX CC preferably up to 100%, purity. The alcohol phase is then separated from  
XX CC the precipitate, and the colostrinin is separated from the alcohol,  
XX CC preferably by evaporation, to form a colostrinin-rich phase, which is  
XX CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
XX CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
XX CC to induce precipitation of the colostrinin peptides. The method is  
XX CC generally applicable to the separation of peptides from fluids containing  
XX CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
XX CC acids. In an example from the invention, the antigenic profile of  
XX CC peptides recovered from sheep colostrum using the alcohol precipitation  
XX CC methods was determined by ELISA using antibodies prepared against 9  
XX CC synthetic peptides, including a peptide having the present sequence  
XX CC (denoted antigen class A-1).  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 89; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LQTPQLLQVNMPEQGD 17  
Db 1 LQTPQLLQVNMPEQGD 17  
RESULT 10  
AAB59341  
ID AAB59341 standard; peptide; 18 AA.  
XX AC AAB59341;  
XX AC AAB59341;

DT 21-MAR-2001 (first entry)  
 XX Ewe colostrinin peptide fragment derived sequence #1.  
 DE  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB002128.  
 XX  
 PR 02-JUN-1999; 99GB-00012852.  
 XX  
 PA (REGGE-) REGEN THERAPEUTICS PLC.  
 PI Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 XX  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 PS Claim 8; Page 27; 63pp; English.  
 XX  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX  
 XX Sequence 18 AA;  
 SQ  
 Query Match 100.0%; Score 89; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQLQVMPEQGD 17  
 DB 2 LQTPQPLQLQVMPEQGD 18  
 RESULT 11  
 AAE07185  
 ID AAE07185 standard; peptide; 11 AA.  
 XX  
 AC AAE07185;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DE  
 XX  
 DE Colostrinin peptide 1.  
 KW  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200155199-A1.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX

PF 26-JAN-2001; 2001WO-GB000329.  
 XX  
 PR 26-JAN-2000; 2000GB-00001825.  
 XX  
 PA (REGGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 PI  
 XX WPI; 2001-488775/53.  
 XX  
 XX Peptide useful as an interalia in the treatment of e.g. disorders of the  
 PT immune system and the central nervous system comprises ten amino-terminal  
 PT amino acid sequence derived from peptides present in colostrinin.  
 XX  
 PS Claim 1; Page 15; 40pp; English.  
 XX  
 XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is colostrinin peptide 1 related to the invention  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 62.9%; Score 56; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLLQVMPEQ 15  
 DB 1 QPLLQVMPEQ 11  
 RESULT 12  
 AAE07195  
 ID AAE07195 standard; peptide; 12 AA.  
 XX  
 AC AAE07195;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DE  
 XX  
 DE Modified colostrinin cyclic peptide #1.  
 KW  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Gln found at the C-terminal end"  
 XX  
 XX WO200155199-A1.  
 PN  
 XX

PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-GB0003329.  
 XX  
 PR 26-JAN-2000; 2000GB-00001825.  
 XX  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Georgiades JA;  
 XX  
 DR WPI; 2001-488775/53.  
 XX  
 XX Peptide useful as an interalia in the treatment of e.g. disorders of the  
 PT immune system and the central nervous system comprises ten amino-terminal  
 PT amino acid sequence derived from peptides present in colostrinin.  
 XX  
 PS Example 2; Page 8; 40pp; English.  
 XX  
 XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is modified colostrinin cyclic peptide #1 related to the  
 XX invention  
 XX  
 SQ Sequence 12 AA;  
 Query Match 62.9%; Score 56; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 QPLLQVWMEPQ 15  
 |||||  
 Db 2 QPLLQVWMEPQ 12  
 |||||  
 RESULT 13  
 ADG73339  
 ID ADG73339 standard; peptide; 13 AA.  
 XX  
 AC ADG73339;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 XX Enterococcus faecalis EFG (fusa) epitopic region peptide - SEQ ID 47.  
 XX (5-methylaminomethyl-2-thiouridylylate)-methyltransferase; antibacterial;  
 KW bacterial infection; antimicrobial; disinfectant; soap; additive;  
 KW culture media; enzyme; epitopic region; translation elongation factor G;  
 KW EFG; fusa.  
 XX  
 XX Enterococcus faecalis.  
 OS  
 XX WO2003083099-A2.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 02-APR-2003; 2003WO-CA000462.  
 PF  
 XX

PR 02-APR-2002; 2002US-0369511P.  
 PR 31-MAY-2002; 2002US-0385089P.  
 PR 04-JUN-2002; 2002US-0385751P.  
 PR 05-JUN-2002; 2002US-0386367P.  
 PR 05-JUN-2002; 2002US-0386553P.  
 PR 05-JUN-2002; 2002US-0386566P.  
 PR 06-JUN-2002; 2002US-0386577P.  
 PR 06-JUN-2002; 2002US-0386390P.  
 PR 31-JUL-2002; 2002US-0399972P.  
 PR 05-NOV-2002; 2002US-0424053P.  
 PR 27-DEC-2002; 2002US-0436804P.  
 PR 27-DEC-2002; 2002US-0436834P.  
 PR 27-DEC-2002; 2002US-0436861P.  
 PR 31-DEC-2002; 2002US-0437281P.  
 PR 31-DEC-2002; 2002US-0437527P.  
 XX  
 PA (AFFI-) AFFINIUM PHARM INC.  
 XX  
 XX Edwards, A, Dharamsi A, Vedadi M, Alam MZ, Arrowsmith C, Awrey D;  
 PI Beattie B, Richards D, Canadien V, Domagala M, Houston S;  
 PI Mansoury K, Li Q, Nethery K, Virag C, Ng I, Ouyang H, Tai M;  
 PI Thalakada R, Kanagarajah D;  
 XX WPI; 2003-812543/76.  
 XX  
 XX New isolated recombinant bacterial peptides, useful as targets for  
 PT antibacterial agents, also screening methods and host cells that express  
 PT them.  
 XX  
 XX Disclosure; SEQ ID NO 47; 369pp; English.  
 PS  
 XX The invention relates to a novel isolated recombinant polypeptide that  
 CC has at least one of the biological activities of (5-methylaminomethyl-2-  
 CC thiouridylylate)-methyltransferase of Staphylococcus aureus. The  
 CC polypeptide of the invention demonstrates antibacterial activity and may  
 CC be useful for rational design of agents that may be utilised for treating  
 CC bacterial infections or as general antimicrobials, for example, as  
 CC disinfectants, soaps or additives for culture media. The current sequence  
 CC is that of the (5-methylaminomethyl-2-thiouridylylate)-methyltransferase-  
 CC related protein epitopic region peptide of the invention.  
 XX  
 XX Sequence 13 AA;  
 Query Match 43.8%; Score 39; DB 7; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 24;  
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 QPLLQVWMEPQ 15  
 |||||  
 Db 2 PDPVIQVAEPK 13  
 |||||  
 RESULT 14  
 ADNI7037  
 ID ADNI7037 standard; peptide; 15 AA.  
 XX  
 AC ADNI7037;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 XX Gi-alpha 1 GDP-specific phase D peptide motif, SEQ ID 46.  
 DE  
 XX G alpha subunit; G protein; G protein coupled receptor; GPCR;  
 KW allosteric modulator; Gi-alpha 1; GDP-specific phase; D peptide.  
 KW Unidentified.  
 OS  
 XX WO2004035614-A1.  
 PN  
 XX 29-APR-2004.  
 PD  
 XX 15-JAN-2003; 2003WO-EP000352.  
 PF





CC endothelial cells, by treating the cells with an ECBP agonist, which is  
 CC preferably the peptide, to promote proliferation and/or migration of the  
 CC treated cells, and for reducing or promoting angiogenesis, by treating  
 CC the cells with an ECBP antagonist, which is preferably the peptide of the  
 CC invention. A peptide of the invention is also useful for manufacturing a  
 CC medicament for promoting angiogenesis, by admixing an ECBP agonist or  
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in  
 CC a treated mammal. The medicament is useful for promoting or reducing  
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum  
 CC of a viral particle. The present sequence represents an ECBP of the  
 CC invention.

XX SQ Sequence 12 AA;

Query Match 37.1%; Score 33; DB 7; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQP 6  
 |||||  
 DB 2 LQTPQP 7

RESULT 17  
 AAB72531  
 ID AAB72531 standard; peptide; 15 AA.

XX AC AAB72531;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US022665.

XX PR 17-AUG-1999; 99US-0149310P.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the cell  
 with an oxidative stress regulator selected from colostrinin, its  
 constituent peptide, analog or their combinations.

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
 stress level in a cell or a patient, comprising contacting the cell with,  
 or administering to the patient, an oxidative stress regulator selected  
 from colostrinin, or its constituent peptide (e.g. the present peptide),  
 to change the level of an oxidising species in the cell. The method can  
 be used to treat oxidative damage to skin, by decreasing or preventing an  
 increase in the level of damage to a biomolecule of the patient

XX SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14  
 |||||:|

DB 3 QPPQPLPPTVMFP 15

RESULT 18

AAB59334

ID AAB59334 standard; peptide; 15 AA.

XX AC AAB59334;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-9.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB002128.

XX PR 02-JUN-1999; 99GB-00012852.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from  
 colostrinin for treating e.g. disorders of the central nervous system and  
 immune system, viral and bacterial infections, and diseases characterized  
 by amyloid plaques.

XX PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides  
 found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 fragment of colostrum. These peptides can be used in the treatment of  
 central nervous system disorders such as senile dementia, Parkinson's  
 disease, Alzheimer's disease, psychosis and neurosis, immune system  
 disorders such as bacterial and viral infections, to improve the  
 development of a child's immune system, as a dietary supplement, and to  
 promote the dissolution of beta-amyloid plaques

XX SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;

Best Local Similarity 53.8%; Pred. No. 2.6e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMMEP 14

|||||:|  
 DB 3 QPPQPLPPTVMFP 15

RESULT 19

AAB72279

ID AAB72279 standard; peptide; 15 AA.

XX AC AAB72279;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 34.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 central nervous system disorder; neurological disorder; mental disorder;  
 dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 neurosis; infection.

XX OS Synthetic.  
XX PN WO200111937-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US022818.  
XX PR 17-AUG-1999; 99US-0149311P.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PA (REGE-) REGEN THERAPEUTICS PLC.  
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2001-202804/20.  
XX DR Inducing a cytokine and modulating an immune response, useful for  
XX PT treating central nervous system diseases and bacterial and viral  
XX PT infections, comprises administering colostrinin as an immunological  
XX PT regulator.  
XX PS Claim 1; Page 34; 50pp; English.  
XX SS Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
XX CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
XX CC have immune response modulatory activity, and are capable of inducing  
XX CC cytokines. Colostrinin and its derived peptides are useful for inducing  
XX CC cytokine production, for modulating an immunological response and for  
XX CC inducing blood cell proliferation. The peptides are useful in the  
XX CC treatment of disorders of the central nervous system, neurological  
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,  
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
XX CC disorders of the immune system, bacterial and viral infections and  
XX CC acquired immunological deficiencies  
XX SQ Sequence 15 AA;  
Query Match 37.1%; Score 33; DB 4; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 QTPQPLQVMMEP 14  
Db | | | | | : | |  
3 QPPQPLPPTVMFP 15  
RESULT 20  
AAB72563  
ID AAB72563 standard; peptide; 15 AA.  
XX AC AAB72563;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #32.  
XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
XX KW colostrum.  
XX OS Unidentified.  
XX PN WO200112651-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US022774.  
XX PR 17-AUG-1999; 99US-0149633P.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX

PI Boldogh I;  
XX WPI; 2001-226545/23.  
XX Use of colostrinin, its constituent peptide or analog as a neural cell  
XX PT regulator, for promoting neural cell differentiation and treating damaged  
XX PT neural cells in a patient.  
XX PS Claim 6; Page 22; 35pp; English.  
XX CC The present invention relates to a method for promoting neural cell  
XX CC differentiation and treating damaged neural cells, using colostrinin and  
XX CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
XX CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
XX SQ Sequence 15 AA;  
Query Match 37.1%; Score 33; DB 4; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 QTPQPLQVMMEP 14  
Db | | | | | : | |  
3 QPPQPLPPTVMFP 15  
RESULT 21  
AAO14610  
ID AAO14610 standard; peptide; 15 AA.  
XX AC AAO14610;  
XX DT 27-MAY-2002 (first entry)  
XX DE Neural cell regulatory colostrinin peptide 32.  
XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
XX KW neural cell treatment.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 15  
XX FT /note= "Optional C-terminal amide"  
XX PN WO200213851-A1.  
XX PD 21-FEB-2002.  
XX PF 17-AUG-2000; 2000WO-US022777.  
XX PR 17-AUG-2000; 2000WO-US022777.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Boldogh I, Stanton JG, Hughes TK;  
XX WPI; 2002-269152/31.  
XX Promoting cell differentiation in a patient involves use of blood cell  
XX PT regulator selected from colostrinin, its constituent peptide and/or  
XX PT analog.  
XX PS Claim 7; Page 22; 37pp; English.  
XX CC The invention comprises a method for promoting cell differentiation (e.g.  
XX CC neural cell differentiation). The method involves contacting cells with a  
XX CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
XX CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
XX CC polypeptide aggregate that is present in colostrum. The method of the  
XX CC invention is useful for promoting the differentiation of cells and for  
XX CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention  
XX  
SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQLQVMMEP 14  
| | | | | : | |  
Db 3 QPPQPLPTVMFP 15

RESULT 22  
AAM51066  
ID AAM51066 standard; peptide; 15 AA.  
XX  
AC AAM51066;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Colostrinin constituent peptide (casein amino acids 159-173).  
XX  
KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; beta-casein; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 15 /note= "optional C-terminal amidation"  
XX  
PW WO200213849-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022775.  
XX  
PR 17-AUG-2000; 2000WO-US022775.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REG-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
PI WPI; 2002-269150/31.  
XX  
DR Modulation of blood cell proliferation in a patient involves use of blood  
XX cell regulator selected from colostrinin, its constituent peptide and/or  
XX analog.  
XX  
PS Claim 1; Page 34; 54pp; English.

The present sequence is that of a colostrinin constituent peptide that is  
used as an immunological regulator and as a blood cell regulator in  
claimed methods of the invention. It is classified as having a beta-  
casein homologue precursor, and corresponds to casein amino acids 159-  
173. Methods are claimed for: inducing a cytokine in a cell by contact  
with an immunological regulator, where the cell is present in a cell  
culture, a tissue, an organ or an organism, and the cell is mammalian,  
including human; modulating an immune response in a cell by contact with  
the immunological regulator under conditions effective to induce a  
cytokine; modulating an immune response in a patient by administering an  
immunological regulator under conditions effective to induce a cytokine,  
where the immunological regulator is administered topically or as part of  
a dietary supplement, and where the immune response is specific or non  
specific, an interferon response or an antibody response; modulating  
blood cell proliferation by contacting blood cells with a blood cell  
regulator, where the blood cells are present in a cell culture or an  
organism, are mammalian or human, and where the blood cells are increased  
in number or differentiated; and a method for modulating blood cell  
proliferation in a patient. A claimed cytokine-inducing composition

CC comprises a pharmaceutical carrier and an active agent such as the  
CC present peptide  
XX  
SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQLQVMMEP 14  
| | | | | : | |  
Db 3 QPPQPLPTVMFP 15

RESULT 23  
AAE20261  
ID AAE20261 standard; peptide; 15 AA.  
XX  
AC AAE20261;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Colostrinin constituent peptide #32.  
XX  
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 15 /note= "Optionally C-terminal amide"  
XX  
PW WO200213850-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022776.  
XX  
PR 17-AUG-2000; 2000WO-US022776.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA Stanton GJ, Hughes TK, Boldogh I;  
PI WPI; 2002-269151/31.  
XX  
DR Composition useful for the modulation of blood cell proliferation in a  
XX patient comprises a blood cell regulator selected from colostrinin, its  
XX constituent peptide and/or analog.  
XX  
PS Claim 6; Page 26; 51pp; English.

The invention relates to a composition which comprises a blood cell  
regulator selected from colostrinin, its constituent peptide and/or  
analog. The invention is used for modulating the oxidative stress level  
in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
organ, or organism; or for treating oxidative damage to the skin of a  
patient e.g. animal or human; to modulate oxidative stress during/ after  
a premature birth or normal birth, preventing/delaying aging in a  
patient, enhancing wound healing, and the reduction of side effects of  
cosmetic procedures. The method changes the level of an oxidising species  
in the cell, such as decreases or prevents increase in the level of  
damage to a biomolecule of the patient selected from DNA, protein and/or  
lipid, compared to the same conditions when the oxidative stress  
regulator is not present. The modulation of oxidative stress results in  
enhanced repair, regeneration, and replacement of cells, tissues and  
organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
external organs), as well as enhanced preservation of such organs for  
transplantation, implantation, or scientific research. The present  
sequence is a colostrinin constituent peptide

XX SQ Sequence 15 AA;  
Query Match 37.1%; Score 33; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 QTPQPLQVMMEP 14  
DB 3 QPPQPLPTVMFP 15

RESULT 24  
ADN60328  
ID ADN60328 standard; peptide; 15 AA.  
XX  
AC ADN60328;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Constituent peptide of colostrinin SEQ ID NO:34.  
XX  
KW modulator; colostrinin; intracellular signaling molecule modulator;  
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
KW DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;  
KW 4HNE-protein adduct formation reduction;  
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
KW c-Jun NH2-terminal kinase inhibition.  
XX  
OS Synthetic.  
XX  
FN WO2004037851-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033423.  
XX  
PR 22-OCT-2002; 2002US-0420369P.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (BOLD/) BOLDGOH I.  
PA (STAN/) STANTON J G.  
PA (GEOR/) GEORGIADIS J A.  
PA (HUGH/) HUGHES T K.  
PA (KRUZ/) KRUEL M.  
XX  
PI Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
XX  
DR WPI; 2004-365494/34.  
XX  
PT Use of colostrinin for e.g. modulating an intracellular signaling  
PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
PT a cell.  
XX  
PS Claim 6; SEQ ID NO 34; 46pp; English.  
XX  
CC The present invention describes the use of a modulator selected from  
CC colostrinin, its constituent peptide, its active analogue, and a  
CC combination of these, for modulating an intracellular signaling molecule  
CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
CC The modulator has cytostatic activity, and can be used as a 4HNE  
CC inhibitor. The modulator is useful in the manufacture of a medicament for  
CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
CC Colostrinin, or its constituent peptide or active analogue is useful for  
CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
CC The present sequence represents a synthetic constituent peptide of  
CC colostrinin, which can be used as a modulator in the present invention.

XX SQ Sequence 15 AA;  
Query Match 37.1%; Score 33; DB 8; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 QTPQPLQVMMEP 14  
DB 3 QPPQPLPTVMFP 15

RESULT 25  
ADS74410  
ID ADS74410 standard; peptide; 15 AA.  
XX  
AC ADS74410;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Ovine colostrinin peptide.  
XX  
KW Colostrum; colostrinin; sheep; peptide purification.  
XX  
OS Ovis aries.  
XX  
FN WO2004081038-A1.  
XX  
PD 23-SEP-2004.  
XX  
PF 10-MAR-2004; 2004WO-GB001014.  
XX  
PR 11-MAR-2003; 2003GB-00005552.  
PR 08-MAR-2004; 2004GB-00005190.  
XX  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
XX  
DR WPI; 2004-677519/66.  
XX  
PT Recovering peptides such as colostrinin from mammalian colostrum, by  
PT mixing colostrum with alcohol to form alcohol phase containing peptides  
PT and precipitate, separating alcohol phase from precipitate, and  
PT recovering alcohol phase.  
XX  
PS Disclosure; SEQ ID NO 27; 41pp; English.  
XX  
CC The present sequence is that of a peptide that can be recovered from  
CC ovine colostrinin using the method of the invention. The invention  
CC provides a method for the recovery of peptides (especially colostrinin)  
CC from colostrum in substantially pure, biologically active form and in  
CC high yield. The method involves mixing the colostrum with an alcohol to  
CC form an alcohol phase containing the colostrinin and a precipitate  
CC containing higher molecular weight caseins and other proteins. Best  
CC results are obtained using methanol or ethanol of at least 80%, and  
CC preferably up to 100%, purity. The alcohol phase is then separated from  
CC the precipitate, and the colostrinin is separated from the alcohol,  
CC preferably by evaporation, to form a colostrinin-rich phase, which is  
CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
CC to induce precipitation of the colostrinin peptides. The method is  
CC generally applicable to the separation of peptides from fluids containing  
CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
CC acids.  
XX  
SQ Sequence 15 AA;  
Query Match 37.1%; Score 33; DB 8; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 QTPQPLQVMMEP 14

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Db      3 QPPQPLPPTVMPF 15
      ||||| :||
      |
RESULT 26
AAR21055
ID AAR21055 standard; peptide; 8 AA.
XX
AC AAR21055;
XX
XX 25-MAR-2003 (revised)
DT 01-JUN-1992 (first entry)
XX
XX Gamma-carboxylase, N-terminus.
DE
XX Degenerate; Vitamin K dependent proteins; PCR.
KW
XX Homo sapiens.
OS
XX WO9201795-A.
PN
XX 06-FEB-1992.
PD
XX 23-JUL-1990; 90US-00557220.
PF
XX 23-JUL-1990; 90US-00557220.
PR 14-MAR-1991; 91US-00669735.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX Berkner KL;
PI
XX WPI; 1992-064951/08.
XX
XX Gamma-carboxylase protein compans. - used in recombinant prodn. of active
PT vitamin-K dependent proteins.
XX
XX Claim 6; Table 9; 91pp; English.
PS
XX Nucleotide sequences encoding gamma-carboxylase were obtd. using PCR, and
CC oligonucleotides designed from amino acid sequences determined by
CC microsequencing of partially purified material. SEQ ID No 19 (peptide 5)
CC is one of seven alternative sequences for the N-terminus of gamma
CC carboxylase, due to the degeneracy of the genetic code. Obtaining the
CC full DNA and protein sequence of gamma-carboxylase will allow proteins
CC such as Factor VII, Factor IX, prothrombin, (activated) protein C,
CC protein S, protein Z, or osteocalcin to be easily produced by recombinant
CC techniques. See also AAR21049-56, AAR23010. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX Sequence 8 AA;
SQ
      Query Match      36.0%; Score 32; DB 2; Length 8;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TPQPLL 8
      |||||
Db      1 TPQPLL 6

RESULT 27
ABR31148
ID ABR31148 standard; peptide; 15 AA.
XX
AC ABR31148;
XX
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 83P4B8 HLA peptide #2210.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX

Db      3 QPPQPLPPTVMPF 15
      ||||| :||
      |
RESULT 26
AAR21055
ID AAR21055 standard; peptide; 8 AA.
XX
AC AAR21055;
XX
XX 25-MAR-2003 (revised)
DT 01-JUN-1992 (first entry)
XX
XX Gamma-carboxylase, N-terminus.
DE
XX Degenerate; Vitamin K dependent proteins; PCR.
KW
XX Homo sapiens.
OS
XX WO9201795-A.
PN
XX 06-FEB-1992.
PD
XX 23-JUL-1990; 90US-00557220.
PF
XX 23-JUL-1990; 90US-00557220.
PR 14-MAR-1991; 91US-00669735.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX Berkner KL;
PI
XX WPI; 1992-064951/08.
XX
XX Gamma-carboxylase protein compans. - used in recombinant prodn. of active
PT vitamin-K dependent proteins.
XX
XX Claim 6; Table 9; 91pp; English.
PS
XX Nucleotide sequences encoding gamma-carboxylase were obtd. using PCR, and
CC oligonucleotides designed from amino acid sequences determined by
CC microsequencing of partially purified material. SEQ ID No 19 (peptide 5)
CC is one of seven alternative sequences for the N-terminus of gamma
CC carboxylase, due to the degeneracy of the genetic code. Obtaining the
CC full DNA and protein sequence of gamma-carboxylase will allow proteins
CC such as Factor VII, Factor IX, prothrombin, (activated) protein C,
CC protein S, protein Z, or osteocalcin to be easily produced by recombinant
CC techniques. See also AAR21049-56, AAR23010. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX Sequence 8 AA;
SQ
      Query Match      36.0%; Score 32; DB 2; Length 8;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TPQPLL 8
      |||||
Db      1 TPQPLL 6

RESULT 27
ABR31148
ID ABR31148 standard; peptide; 15 AA.
XX
AC ABR31148;
XX
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 83P4B8 HLA peptide #2210.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX

XX Homo sapiens.
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
XX 10-APR-2001; 2001US-0283112P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB,
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX Claim 13; Page 487; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX SQ Sequence 15 AA;
      Query Match      36.0%; Score 32; DB 6; Length 15;
      Best Local Similarity 58.3%; Pred. No. 3.8e+02;
      Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 LQTPQPLIQVNM 12
      | : ||||| :|
Db      4 LKAVQPLLKVSM 15

RESULT 28
ABR31149
ID ABR31149 standard; peptide; 15 AA.
XX
AC ABR31149;
XX
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 83P4B8 HLA peptide #2211.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US011654.
PF
XX 10-APR-2001; 2001US-0282739P.
XX

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PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 487; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 15 AA;
SQ
Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LQTPQPLQVMM 12
DB 1 LKAVQPLLVSM 12
|: ||||:|
1 LKAVQPLLVSM 12
RESULT 29
ABR30440
ID ABR30440 standard; peptide; 15 AA.
XX
XX ABR30440;
AC
XX
XX 19-MAY-2003 (first entry)
DT
XX
XX Human cancer-related protein 83P4B8 HLA peptide #1502.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX
XX WO200283921-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US011654.
PF
XX
XX 10-APR-2001; 2001US-0282739P.
PR
XX 10-APR-2001; 2001US-0283112P.
PR
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 494; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 15 AA;
SQ
Query Match 36.0%; Score 32; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LQTPQPLQVMM 12
DB 1 LKAVQPLLVSM 12
|: ||||:|
1 LKAVQPLLVSM 12
RESULT 30
ABR31517
ID ABR31517 standard; peptide; 15 AA.
XX
XX ABR31517;
AC
XX
XX 19-MAY-2003 (first entry)
DT
XX
XX Human cancer-related protein 83P4B8 HLA peptide #2579.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX
XX WO200283921-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US011654.
PF
XX
XX 10-APR-2001; 2001US-0282739P.
PR
XX 10-APR-2001; 2001US-0283112P.
PR
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 494; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.

```

CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 3.8e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12  
|: ||||:|  
Db 1 LKAVQLLKVSM 12

RESULT 31  
ABR30536  
ID ABR30536 standard; peptide; 15 AA.

XX ABR30536;  
XX  
XX  
XX 19-MAY-2003 (first entry)  
XX Human cancer-related protein 83P4B8 HLA peptide #1598.  
XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
XX Homo sapiens.  
XX WO200283921-A2.  
XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US011654.  
XX 10-APR-2001; 2001US-0282739P.  
XX 10-APR-2001; 2001US-0283112P.  
XX 25-APR-2001; 2001US-0286630P.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response in  
XX cancer patients.  
XX Claim 13; Page 476; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention

SQ Sequence 15 AA;  
Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 3.8e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12  
|: ||||:|  
Db 4 LKAVQLLKVSM 15

RESULT 32  
ABR30847  
ID ABR30847 standard; peptide; 15 AA.

XX ABR30847;  
XX  
XX 19-MAY-2003 (first entry)  
XX Human cancer-related protein 83P4B8 HLA peptide #1909.  
XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
XX Homo sapiens.  
XX WO200283921-A2.  
XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US011654.  
XX 10-APR-2001; 2001US-0282739P.  
XX 10-APR-2001; 2001US-0283112P.  
XX 25-APR-2001; 2001US-0286630P.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response in  
XX cancer patients.  
XX Claim 13; Page 482; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 3.8e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMM 12  
|: ||||:|  
Db 1 LKAVQLLKVSM 12









PT Human ATP dependent serien proteinase 21 and encoding polynucleotide,  
 PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.

XX  
 XX  
 PS: Example 5; Page 18; 32pp; Chinese.

CC The invention relates to an isolated polypeptide of human ATP dependent  
 CC serine proteinase 21. The protein of the invention and its associated  
 CC cDNA sequence are used in the treatment of various diseases including  
 CC malignant tumors, haemopathy, human immunodeficiency virus (HIV)  
 CC infection, immunological diseases and various inflammations. This  
 CC sequence represents the N-terminal peptide of ATP dependent serine  
 CC proteinase 21, used in ELISA

XX  
 XX  
 SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 5; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 5.4e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 5 QPLIQVMMEPOGD 17  
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 Db 3 QLESTVIQPOGD 15

# RESULT 40

ABR38577  
 ID ABR38577 standard; peptide; 15 AA.

XX  
 AC ABR38577;

XX  
 DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 192P2G7 HLA peptide #1437.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX  
 OS Homo sapiens.

XX WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX FI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.

XX PS Claim 13; Page 622; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention

XX  
 SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 6; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 5.4e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LQTPQPLIQVMME 13  
 | : | | | : : |  
 Db 2 LEYFPQGLDIKE 14

Search completed: June 7, 2005, 23:10:42  
 Job time : 95.4909 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 23.1818 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMEPQGD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	17	4	US-09-641-803-2
2	33	37.1	15	4	US-09-641-803-34
3	32	36.0	8	5	PCT-US91-05177-19
4	31	34.8	13	2	US-08-162-081B-5
5	31	34.8	13	2	US-08-780-872-5
6	31	34.8	13	3	US-09-085-957-5
7	31	34.8	15	1	US-08-477-877B-30
8	31	34.8	15	2	US-08-472-281A-30
9	31	34.8	15	2	US-08-477-989B-30
10	29	32.6	18	2	US-09-017-205-35
11	28	31.5	7	1	US-08-594-447-74
12	28	31.5	7	1	US-08-541-964-73
13	28	31.5	7	2	US-08-665-647-88
14	28	31.5	10	3	US-08-981-392-53
15	28	31.5	10	4	US-09-908-322-53
16	28	31.5	15	2	US-08-553-257A-21
17	28	31.5	15	4	US-09-441-992-21
18	28	31.5	16	3	US-08-602-999A-195
19	28	31.5	16	4	US-09-500-124-195
20	27	30.3	15	3	US-08-646-865A-125
21	27	30.3	15	4	US-09-947-372A-27
22	27	30.3	16	3	US-08-837-226-2
23	27	30.3	16	4	US-09-537-226-2
24	26.5	29.8	18	4	US-09-829-855-240
25	26	29.2	8	4	US-08-475-955-182
26	26	29.2	8	4	US-08-475-955-185
27	26	29.2	9	3	US-08-159-339A-1062

28	26	29.2	9	4	US-08-737-109-5	Sequence 5, Appli
29	26	29.2	9	6	5204326-100	Patent No. 5204326
30	26	29.2	9	6	5204326-100	Patent No. 5204326
31	26	29.2	10	3	US-08-159-339A-971	Sequence 971, App
32	26	29.2	10	3	US-08-159-339A-1070	Sequence 1070, App
33	26	29.2	13	3	US-09-023-173-9	Sequence 9, Appli
34	26	29.2	13	3	US-09-023-339-7	Sequence 7, Appli
35	26	29.2	14	4	US-08-855-744-2	Sequence 2, Appli
36	26	29.2	14	6	5204326-36	Patent No. 5204326
37	26	29.2	14	6	5204326-95	Patent No. 5204326
38	26	29.2	14	6	5204326-36	Patent No. 5204326
39	26	29.2	14	6	5204326-95	Patent No. 5204326
40	26	29.2	15	3	US-08-096-044C-14	Sequence 14, Appli
41	26	29.2	15	4	US-09-514-245-121	Sequence 121, App
42	26	29.2	15	6	5204326-37	Patent No. 5204326
43	26	29.2	15	6	5204326-40	Patent No. 5204326
44	26	29.2	15	6	5204326-71	Patent No. 5204326
45	26	29.2	15	6	5204326-74	Patent No. 5204326
46	26	29.2	15	6	5204326-37	Patent No. 5204326
47	26	29.2	15	6	5204326-40	Patent No. 5204326
48	26	29.2	15	6	5204326-71	Patent No. 5204326
49	26	29.2	15	6	5204326-74	Patent No. 5204326
50	26	29.2	16	1	US-07-700-526-8	Sequence 8, Appli
51	26	29.2	16	3	US-08-096-044C-13	Sequence 13, Appli
52	26	29.2	16	3	US-08-096-044C-15	Sequence 15, Appli
53	26	29.2	16	5	PCT-US92-03132-8	Sequence 8, Appli
54	26	29.2	16	6	5204326-96	Patent No. 5204326
55	26	29.2	16	6	5204326-96	Patent No. 5204326
56	26	29.2	17	2	US-08-675-921B-7	Sequence 7, Appli
57	26	29.2	17	6	5204326-97	Patent No. 5204326
58	26	29.2	17	6	5204326-97	Patent No. 5204326
59	26	29.2	18	4	US-08-945-038-12	Sequence 12, Appli
60	26	29.2	18	6	5204326-38	Patent No. 5204326
61	26	29.2	18	6	5204326-41	Patent No. 5204326
62	26	29.2	18	6	5204326-98	Patent No. 5204326
63	26	29.2	18	6	5204326-101	Patent No. 5204326
64	26	29.2	18	6	5204326-38	Patent No. 5204326
65	26	29.2	18	6	5204326-41	Patent No. 5204326
66	26	29.2	18	6	5204326-98	Patent No. 5204326
67	26	29.2	18	6	5204326-101	Patent No. 5204326
68	25	28.1	6	3	US-09-467-423-1	Sequence 1, Appli
69	25	28.1	6	3	US-09-467-423-5	Sequence 5, Appli
70	25	28.1	7	1	US-08-594-447-75	Sequence 75, Appli
71	25	28.1	7	1	US-08-541-964-74	Sequence 74, Appli
72	25	28.1	7	2	US-08-665-647-89	Sequence 89, Appli
73	25	28.1	7	3	US-09-467-423-80	Sequence 80, Appli
74	25	28.1	7	3	US-09-467-423-94	Sequence 94, Appli
75	25	28.1	7	3	US-09-467-423-166	Sequence 166, App
76	25	28.1	7	3	US-09-467-423-180	Sequence 180, App
77	25	28.1	8	3	US-09-467-423-65	Sequence 65, Appli
78	25	28.1	8	3	US-09-467-423-79	Sequence 79, Appli
79	25	28.1	8	3	US-09-467-423-93	Sequence 93, Appli
80	25	28.1	8	3	US-09-467-423-151	Sequence 151, App
81	25	28.1	8	3	US-09-467-423-165	Sequence 165, App
82	25	28.1	8	3	US-09-467-423-179	Sequence 179, App
83	25	28.1	9	1	US-08-421-702A-113	Sequence 113, App
84	25	28.1	9	1	US-08-421-702A-116	Sequence 116, App
85	25	28.1	9	1	US-08-421-702A-119	Sequence 119, App
86	25	28.1	9	1	US-08-303-052A-55	Sequence 55, Appli
87	25	28.1	9	1	US-08-303-052A-113	Sequence 113, App
88	25	28.1	9	1	US-08-421-696A-19	Sequence 19, Appli
89	25	28.1	9	1	US-08-421-696A-113	Sequence 113, App
90	25	28.1	9	1	US-08-421-696A-116	Sequence 116, App
91	25	28.1	9	1	US-08-421-697A-113	Sequence 113, App
92	25	28.1	9	1	US-08-421-697A-116	Sequence 116, App
93	25	28.1	9	1	US-08-421-698A-19	Sequence 19, Appli
94	25	28.1	9	1	US-08-421-698A-113	Sequence 113, App
95	25	28.1	9	1	US-08-421-698A-116	Sequence 116, App
96	25	28.1	9	2	US-08-421-695A-19	Sequence 19, Appli
97	25	28.1	9	2	US-08-421-695A-55	Sequence 55, Appli
98	25	28.1	9	2	US-08-421-695A-114	Sequence 114, App
99	25	28.1	9	2	US-08-421-695A-114	Sequence 114, App
100	25	28.1	9	2	US-08-421-695A-114	Sequence 114, App

## ALIGNMENTS

RESULT 1  
US-09-641-803-2  
; Sequence 2, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-2

Query Match 100.0%; Score 89; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.8e-08; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0;

Qy 1 LQTQPQLLQVMPEPQGD 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 LQTQPQLLQVMPEPQGD 17

RESULT 2  
US-09-641-803-34  
; Sequence 34, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-34

Query Match 37.1%; Score 33; DB 4; Length 15;  
Best Local Similarity 53.8%; Pred. No. 57;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLQLQVMPEP 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 QPPQPLPPTVMFP 15

RESULT 3  
PCT-US91-05177-19  
; Sequence 19, Application PC/TUS9105177  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathy L  
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/05177  
; FILING DATE: 19910722  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/557,220  
; FILING DATE: 23-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 990008.544PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal  
PCT-US91-05177-19

Query Match 36.0%; Score 32; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQPLL 8  
| | | | | | | |  
Db 1 TPQPLL 6

RESULT 4  
US-08-162-081B-5  
; Sequence 5, Application US/08162081B  
; Patent No. 5824492  
; GENERAL INFORMATION:  
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
; APPLICANT: Stefano; Gout, Ivan Tarasovitch  
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
; THEIR PREPARATION AND USE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-162-081B-5

Query Match 34.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13  
| | | : | | :  
Db 4 PDPLVEVMLK 13

RESULT 5  
US-08-780-872-5  
Sequence 5, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-780-872-5

Query Match 34.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13  
| | | : | | :  
Db 4 PDPLVEVMLK 13

RESULT 6  
US-09-085-957-5  
Sequence 5, Application US/09085957  
Patent No. 6274327  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-085-957-5

Query Match 34.8%; Score 31; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQLLQVME 13

```
Db      |||:|:|:
      4 PDPLVEVMLK 13

RESULT 7
US-08-477-877B-30
; Sequence 30, Application US/0847787B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-877B-30

Query Match      34.8%; Score 31; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QTPQPLL 8
      |:|:|:|:
Db      8 QSPQPLI 14

RESULT 8
US-08-472-281A-30
; Sequence 30, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
```

```
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-472-281A-30

Query Match      34.8%; Score 31; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QTPQPLL 8
      |:|:|:|:
Db      8 QSPQPLI 14

RESULT 9
US-08-477-989B-30
; Sequence 30, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
```



COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,989B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-147  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-477-989B-30

Query Match 34.8%; Score 31; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
Db 8 QSPQPLI 14

RESULT 10  
US-09-017-205-35  
Sequence 35, Application US/09017205  
Patent No. 5965357  
GENERAL INFORMATION:  
APPLICANT: Marsden, Howard S  
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN  
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 5965357th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,205  
FILING DATE: 02-FEB-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide from HSV-2 glycoprotein G  
FRAGMENT TYPE: internal  
US-09-017-205-35

Query Match 32.6%; Score 29; DB 2; Length 18;  
Best Local Similarity 37.5%; Pred. No. 3e+02;  
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMPEQGD 17  
Db 1 KTLPLVVSATAMAPSVD 16

RESULT 11  
US-08-594-447-74  
Sequence 74, Application US/08594447  
Patent No. 5776716  
GENERAL INFORMATION:  
APPLICANT: Ron, Dorit  
APPLICANT: Napolitano, Eugene W.  
APPLICANT: Voronova, Anna P.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH  
TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,447  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /label= PRK1-3  
US-08-594-447-74

Query Match 31.5%; Score 28; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEPOG 16  
Db 1 MEPOG 5

RESULT 12  
US-08-541-964-73  
; Sequence 73, Application US/08541964  
; Patent No. 5783405  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; APPLICANT: Kauvar, Lawrence W.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS  
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,964  
; FILING DATE: 10-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.23  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /label= PRK1-3  
US-08-541-964-73  
Query Match 31.5%; Score 28; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 MEPOG 16  
DB 1 MEPOG 5  
RESULT 13  
US-08-665-647-88  
; Sequence 88, Application US/08665647  
; Patent No. 5935803  
; GENERAL INFORMATION:  
; APPLICANT: Dasquez, Nicki J.  
; APPLICANT: Ron, Dorit  
; APPLICANT: Voronova, Anna F.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,647  
; FILING DATE: 18-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.25  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /label= PRK1-3  
US-08-665-647-88  
Query Match 31.5%; Score 28; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 MEPOG 16  
DB 1 MEPOG 5  
RESULT 14  
US-08-981-392-53  
; Sequence 53, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514

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; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-53

Query Match      31.5%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLLVQVME 13
      |||||:
Db      1 PQLLVRTQE 10

RESULT 15
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
;             Henrique, Domingos Manuel Pinto
;             Lewis, Julian Hart
;             Artavanis-Tsakonas, Spyridon
;             Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
;                     VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53
Query Match      31.5%; Score 28; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLLVQVME 13
      |||||:
Db      1 PQLLVRTQE 10

RESULT 16
US-08-553-257A-21
; Sequence 21, Application US/08553257A
; Patent No. 5994083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.
; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandro
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,257A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IT94/00054
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: recombinant protein
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: of recombinant peptides on phage
; CLONE: phagic
; FEATURE:
; NAME/KEY: polypeptide
; IDENTIFICATION METHOD: selection with specific antibodies
US-08-553-257A-21
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Query Match 31.5%; Score 28; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

Qy 2 QTPQPLQVMMEPOGD 17  
Db 4 QVPOSRL---EPWGD 15

## RESULT 17

US-09-441-992-21  
; Sequence 21, Application US/09441992  
; Patent No. 6541210  
; GENERAL INFORMATION:  
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA  
; MOLECOLARE P. ANGELETTI S.p.A.  
; FELICI, Franco  
; LUZZAGO, Alessandra  
; NICOSIA, Alfredo  
; MONACI, Paolo  
; CORTESE, Riccardo  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS  
; OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR  
; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/441,992  
; FILING DATE: 18-NO. 6541210-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/553,257  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: RM93A000301  
; FILING DATE: 11-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: FELICI=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: recombinant protein  
; HYPOTHETICAL: yes  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; LIBRARY: of recombinant peptides on phage  
; CLONE: phagic  
; (ix) FEATURE  
; (A) NAME: polypeptide

US-09-441-992-21  
Query Match 31.5%; Score 28; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;

Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
Qy 2 QTPQPLQVMMEPOGD 17  
Db 4 QVPOSRL---EPWGD 15

## RESULT 18

US-08-602-999A-195  
; Sequence 195, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-195

Query Match 31.5%; Score 28; DB 3; Length 16;  
Best Local Similarity 41.7%; Pred. No. 3.8e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLQVMMEP 14  
Db 4 TPRPAVQRMNP 15

## RESULT 19

US-09-500-124-195  
; Sequence 195, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 195:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-195

Query Match 31.5%; Score 28; DB 4; Length 16;  
Best Local Similarity 41.7%; Pred. No. 3.8e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMEP 14  
|||:|  
Db 4 TPRPVPQRMNP 15

RESULT 20  
US-08-646-265A-125  
Sequence 125, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
TITLE OF INVENTION: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 125:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-125

Query Match 30.3%; Score 27; DB 3; Length 15;  
Best Local Similarity 57.1%; Pred. No. 5e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
||:|  
Db 8 QSPKPLI 14

RESULT 21  
US-09-947-372A-27  
Sequence 27, Application US/09947372A  
Patent No. 6613557  
GENERAL INFORMATION:  
APPLICANT: FRAZER, IAN  
APPLICANT: ZHOU, JIAN  
TITLE OF INVENTION: PAPILLOMAVIRUS VACCINE  
FILE REFERENCE: 065064/0137  
CURRENT APPLICATION NUMBER: US/09/947,372A  
CURRENT FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: 08/185,928  
PRIOR FILING DATE: 1994-01-19  
PRIOR APPLICATION NUMBER: PCT/AU92/02184  
PRIOR FILING DATE: 1992-07-20  
PRIOR APPLICATION NUMBER: AU PK7322  
PRIOR FILING DATE: 1991-07-19  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-947-372A-27

Query Match 30.3%; Score 27; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 5e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 LQVMMEPQGD 17  
:::|  
Db 1 IKMVSEPIGD 10

RESULT 22  
US-08-837-226-2  
Sequence 2, Application US/08837226  
Patent No. 6043216  
GENERAL INFORMATION:

APPLICANT: Toback, F. Gary  
APPLICANT: Lieske, John C.  
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING  
AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF  
CRYSTALS TO KIDNEY CELLS  
TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,226  
FILING DATE: 08-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/389,005  
FILING DATE: 15-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Martin, Alice O.  
REGISTRATION NUMBER: 35,601  
REFERENCE/DOCKET NUMBER: 7814/24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-837-226-2

Query Match 30.3%; Score 27; DB 3; Length 16;  
Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQLLQ 9  
Db 10 PQLYQ 15

RESULT 23  
US-09-537-226-2  
Sequence 2, Application US/09537226  
Patent No. 6482934  
GENERAL INFORMATION:  
APPLICANT: TOBACK, F. GARY  
APPLICANT: LIESKE, JOHN C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO  
KIDNEY CELLS  
TITLE OF INVENTION: KIDNEY CELLS  
FILE REFERENCE: 21459/90606  
CURRENT APPLICATION NUMBER: US/09/537,226  
CURRENT FILING DATE: 2000-03-28  
PRIOR APPLICATION NUMBER: 08/389,005  
PRIOR FILING DATE: 1995-02-15  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 2  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
peptide  
US-09-537-226-2

Query Match 30.3%; Score 27; DB 4; Length 16;  
Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQLLQ 9  
Db 10 PQLYQ 15

## RESULT 24

US-09-829-855-240  
Sequence 240, Application US/09829855  
Patent No. 6613520  
GENERAL INFORMATION:  
APPLICANT: Matthew, Ashby N.  
TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations  
FILE REFERENCE: ASHY-1  
CURRENT APPLICATION NUMBER: US/09/829,855  
CURRENT FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: US 60/196063  
PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: US 60/196258  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 244  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 240  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-2  
US-09-829-855-240

Query Match 29.8%; Score 26.5; DB 4; Length 18;  
Best Local Similarity 58.3%; Pred. No. 7.4e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 5 QPLQVMMPEQ 16  
Db 3 QP-LHVATPQ 13

## RESULT 25

US-08-475-955-182  
Sequence 182, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-873-8795  
; INFORMATION FOR SEQ ID NO: 182:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-475-955-182

Query Match 29.2%; Score 26; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.1e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 QVWMEPOG 16  
Db 1 QVWTPQG 8

RESULT 26  
US-08-475-955-185  
; Sequence 185, Application US/08475955  
; Patent No. 6641813  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; TITLE OF INVENTION: AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,955  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: April 13, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-873-8795  
; INFORMATION FOR SEQ ID NO: 185:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-475-955-185

Query Match 29.2%; Score 26; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 MEPOGD 17  
Db 1 MTPQGB 6

RESULT 27  
US-08-159-339A-1062  
; Sequence 1062, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1062:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-1062

Query Match

29.2%; Score 26; DB 3; Length 9;

Best Local Similarity 80.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

Qy 13 EPQGD 17  
:||||  
Db 1 QPQGD 5

RESULT 28  
US-08-737-109-5  
; Sequence 5, Application US/08737109  
; Patent No. 6455688  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: ELBOROUGH, Kieran Michael  
; APPLICANT: BRIGHT, Simon William Jonathan  
; APPLICANT: FENTIM, Philip Anthony  
; TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A  
; TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,109  
; FILING DATE: 21-OCT-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/00846  
; FILING DATE: 02-MAY-1994  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Avena sativa  
US-08-737-109-5

Query Match 29.2%; Score 26; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0;

Qy 11 MMEPQ 16  
:||||  
Db 2 VLEPQ 7

RESULT 29  
5204326-100  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHIRO;SHIMIZU, FUMIO  
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO:100:  
; LENGTH: 9

5204326-100

Query Match 29.2%; Score 26; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LQTPQ 5  
:||||  
Db 3 LQTPQ 7

RESULT 30  
5204326-100  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHIRO;SHIMIZU, FUMIO  
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO:100:  
; LENGTH: 9  
5204326-100

Query Match 29.2%; Score 26; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LQTPQ 5  
:||||  
Db 3 LQTPQ 7

RESULT 31  
US-08-159-339A-971  
; Sequence 971, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver



```
;
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-971

Query Match 29.2%; Score 26; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPOGD 17
Db 5 QPOGD 9

RESULT 32
US-08-159-339A-1070
; Sequence 1070, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1070:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1070

Query Match 29.2%; Score 26; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPOGD 17
Db 1 QPOGD 5

RESULT 33
US-09-023-173-9
; Sequence 9, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: N-terminal amino acid sequence of mature AAT
US-09-023-173-9

Query Match 29.2%; Score 26; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPOGD 17
Db 2 DPQGD 6

RESULT 34
US-09-023-339-7
; Sequence 7, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
```

; APPLICANT: Sutliff, Thomas D.  
; APPLICANT: Rodriguez, Raymond L.  
; TITLE OF INVENTION: Production of '1-Antitrypsin  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Dehlinger & Associates  
; STREET: P.O. Box 60850  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,339  
; FILING DATE: 13-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,991  
; FILING DATE: 13-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petithory, Joanne R  
; REGISTRATION NUMBER: P42,995  
; REFERENCE/DOCKET NUMBER: 0665-0003.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: N-terminal sequence of plant-produced mature AAT  
; US-09-023-339-7

Query Match 29.2%; Score 26; DB 3; Length 13;  
Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQGD 17  
;|||||  
Db 2 DPQGD 6

RESULT 35  
US-08-855-744-2  
; Sequence 2, Application US/08855744  
; Patent No. 6685930  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Tse Wen  
; TITLE OF INVENTION: METHODS AND SUBSTANCES FOR RECRUITING  
; TITLE OF INVENTION: THERAPEUTIC AGENTS TO SOLID TISSUES  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Tanox Biosystems, Inc.  
; STREET: 10301 Stella Link Rd.  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Hi Density Diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: DOS, Version 3.30  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,744  
; FILING DATE: 08-May-1997

; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/264,649  
; FILING DATE:  
; APPLICATION NUMBER: US/07/675,654  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirabel, Eric P.  
; REGISTRATION NUMBER: 31,211  
; REFERENCE/DOCKET NUMBER: TNX91-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713-664-2288  
; TELEFAX: 713-664-8914  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: Linear  
; US-08-855-744-2

Query Match 29.2%; Score 26; DB 4; Length 14;  
Best Local Similarity 62.5%; Pred. No. 6.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TPQPLLQV 10  
;|||:  
Db 4 TPSPGIQV 11

RESULT 36  
5204326-36  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO:36:  
; LENGTH: 14  
; 5204326-36

Query Match 29.2%; Score 26; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
;|||||  
Db 2 LQTPQ 6

RESULT 37  
5204326-95  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO:95:  
; LENGTH: 14  
; 5204326-95

Query Match 29.2%; Score 26; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|  
|  
|  
|  
Db 2 LQTPQ 6

RESULT 38  
5204326-36  
;PATENT NO. 5204326  
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
;NUMBER OF SEQUENCES: 147  
;CURRENT APPLICATION DATA:  
;APPLICATION NUMBER: US/07/493,359  
;FILING DATE: 14-MAR-1990  
;SEQ ID NO:36:  
;LENGTH: 14  
5204326-36

Query Match 29.2%; Score 26; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|  
|  
|  
|  
Db 2 LQTPQ 6

RESULT 39  
5204326-95  
;PATENT NO. 5204326  
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
;NUMBER OF SEQUENCES: 147  
;CURRENT APPLICATION DATA:  
;APPLICATION NUMBER: US/07/493,359  
;FILING DATE: 14-MAR-1990  
;SEQ ID NO:95:  
;LENGTH: 14  
5204326-95

Query Match 29.2%; Score 26; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|  
|  
|  
|  
Db 2 LQTPQ 6

RESULT 40  
US-08-096-044C-14  
;SEQUENCE 14, Application US/08096044C  
;PATENT NO. 6153192  
;GENERAL INFORMATION:  
;APPLICANT: Kopetzki, Erhard, Klein, Christian  
;TITLE OF INVENTION: PEPTIDES WITH CHARACTERISTIC  
;TITLE OF INVENTION: ANTIGENIC DETERMINANTS FOR  
;TITLE OF INVENTION: 1-MICROGLOBULIN  
;NUMBER OF SEQUENCES: 18  
;CORRESPONDENCE ADDRESS:  
;ADDRESSEE: Felfe & Lynch  
;STREET: 805 Third Avenue  
;CITY: New York  
;STATE: New York  
;COUNTRY: USA  
;ZIP: 10022

;COMPUTER READABLE FORM:  
;MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
;COMPUTER: IBM PS/2  
;OPERATING SYSTEM: PC-DOS  
;SOFTWARE: Wordperfect  
;CURRENT APPLICATION DATA:  
;APPLICATION NUMBER: US/08/096,044C  
;FILING DATE: July 22, 1993  
;CLASSIFICATION: 424  
;PRIOR APPLICATION DATA:  
;APPLICATION NUMBER: DE 40 24 919  
;FILING DATE: August 6, 1990  
;ATTORNEY/AGENT INFORMATION:  
;NAME: Bauer, John A.  
;REGISTRATION NUMBER: 32,554  
;REFERENCE/DOCKET NUMBER: HUBR 1000.1-PFF/JAB  
;TELECOMMUNICATION INFORMATION:  
;TELEPHONE: (212) 688-9200  
;TELEFAX: (212) 838-3884  
;INFORMATION FOR SEQ ID NO: 14:  
;SEQUENCE CHARACTERISTICS:  
;LENGTH: 15  
;TYPE: amino acid  
;STRANDEDNESS: single  
;TOPOLOGY: linear  
;US-08-096-044C-14

Query Match 29.2%; Score 26; DB 3; Length 15;  
Best Local Similarity 57.1%; Pred. No. 7.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
|  
|  
|  
|  
Db 6 QEPEPIL 12

Search completed: June 7, 2005, 23:23:11  
Job time : 25.1818 secs

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85 26 29.2 15 15 US-10-682-420-121 Sequence 121, App  
86 26 29.2 15 15 US-10-409-613-121 Sequence 121, App  
87 26 29.2 15 15 US-10-442-180-121 Sequence 121, App  
88 26 29.2 15 16 US-10-718-266-121 Sequence 121, App  
89 26 29.2 15 17 US-10-775-337-121 Sequence 121, App  
90 26 29.2 15 17 US-10-858-343-1 Sequence 1, Appli  
91 26 29.2 15 17 US-10-637-011-121 Sequence 121, App  
92 26 29.2 17 9 US-09-864-761-46994 Sequence 46994, A  
93 26 29.2 17 14 US-10-138-089-18 Sequence 18, Appl  
94 26 29.2 17 15 US-10-422-571-99 Sequence 99, Appl  
95 26 29.2 18 8 US-08-945-038-12 Sequence 12, Appl  
96 26 29.2 18 14 US-10-225-567A-1708 Sequence 1708, Ap  
97 26 29.2 18 17 US-10-803-738-27 Sequence 27, Appl  
98 25.5 28.7 12 15 US-10-649-873-122 Sequence 122, App  
99 25 28.1 9 15 US-10-334-726-124 Sequence 124, App  
100 25 28.1 9 17 US-10-487-259-7 Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-10-281-652-2  
; Sequence 2, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-2

Query Match 100.0%; Score 89; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17  
| | | | | | | | | | | | | | | | |  
Db 1 LQTPQLLQVNMPEQGD 17

RESULT 2  
US-10-691-157-2  
; Sequence 2, Application US/10691157  
; Publication No. US2004026681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265.00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-2

Query Match 100.0%; Score 89; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17  
| | | | | | | | | | | | | | | | |  
Db 1 LQTPQLLQVNMPEQGD 17

RESULT 3  
US-10-691-330-2  
; Sequence 2, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Kruzel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265.00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-2

Query Match 100.0%; Score 89; DB 17; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLLQVNMPEQGD 17  
| | | | | | | | | | | | | | | | |  
Db 1 LQTPQLLQVNMPEQGD 17

RESULT 4  
US-10-182-110-1  
; Sequence 1, Application US/10182110  
; Publication No. US20040171553A1  
; GENERAL INFORMATION:  
; APPLICANT: Regen Therapeutics plc  
; APPLICANT: Georgiades, Jerzy A.  
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use  
; FILE REFERENCE: AAT-14173  
; CURRENT APPLICATION NUMBER: US/10/182,110

; CURRENT FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: GB0001825.9  
; FILING DATE: 2000-01-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial

; FEATURE:  
; OTHER INFORMATION: Truncated version of a peptide found in colostrin

US-10-182-110-1

Query Match 62.9%; Score 56; DB 16; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.048;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15

Db 1 QPLLQVMMEPQ 11

#### RESULT 5

US-10-286-457-195  
; Sequence 195, Application US/10286457  
; Publication No. US20030166004A1

; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.

; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY

; FILE REFERENCE: GPCI-P01-178

; CURRENT APPLICATION NUMBER: US/10/286,457

; CURRENT FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: 60/334822

; PRIOR FILING DATE: 2001-11-01

; NUMBER OF SEQ ID NOS: 684

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 195

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based

; OTHER INFORMATION: ability to selectively bind to endothelial cells

US-10-286-457-195

Query Match 37.1%; Score 33; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQP 6

Db 2 LQTPQP 7

#### RESULT 6

US-10-281-652-34

; Sequence 34, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John

; APPLICANT: BOLDG, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265, 00220101

; CURRENT APPLICATION NUMBER: US/10/281,652

; CURRENT FILING DATE: 2002-10-28

; PRIOR APPLICATION NUMBER: US/09/641,803

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34

; LENGTH: 15

; TYPE: PRT

; ORGANISM: artificial

; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides

; OTHER INFORMATION: Synthetic Peptides

US-10-691-157-34

; SEQ ID NO 34

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: peptide

US-10-281-652-34

Query Match 37.1%; Score 33; DB 14; Length 15;

Best Local Similarity 53.8%; Pred. No. 2.6e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14

Db 3 QTPQPLLQVMMEP 15

#### RESULT 7

US-10-691-157-34

; Sequence 34, Application US/10691157

; Publication No. US2004026681A1

; GENERAL INFORMATION:  
; APPLICANT: BOLDG, Istvan

; APPLICANT: STANTON, G. John

; APPLICANT: GEORGIADES, Jerzy

; APPLICANT: HUGHES, Thomas

; APPLICANT: KRUEL, Marian

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS

; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES

; FILE REFERENCE: 265, 00440101

; CURRENT APPLICATION NUMBER: US/10/691,157

; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652

; PRIOR FILING DATE: 2002-10-28

; PRIOR APPLICATION NUMBER: 09/641,803

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/420,369

; PRIOR FILING DATE: 2002-10-22

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34

; LENGTH: 15

; TYPE: PRT

; ORGANISM: artificial

; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides

US-10-691-157-34

Query Match 37.1%; Score 33; DB 16; Length 15;

Best Local Similarity 53.8%; Pred. No. 2.6e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14

Db 3 QTPQPLLQVMMEP 15

#### RESULT 8

US-10-691-330-34

; Sequence 34, Application US/10691330

; Publication No. US20050042300A1

; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan

; APPLICANT: Stanton, G. John

; APPLICANT: Georgiades, Jerzy A.

; APPLICANT: Hughes, Thomas K., Jr.

; APPLICANT: Kruzel, Marian

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS

; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE

; FILE REFERENCE: 265, 00390101

; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-34

Query Match 37.1%; Score 33; DB 17; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLQVMMEP 14  
Db 3 QPPQLPPTVMFP 15

RESULT 9  
US-10-346-162-130  
; Sequence 130, Application US/10346162  
; Publication No. US20030224390A1  
; GENERAL INFORMATION:  
; APPLICANT: KARO BIO USA, INC.  
; APPLICANT: FOMKES, Dana M.  
; APPLICANT: BARNETT, Thomas R.  
; APPLICANT: BUEHRER, Benjamin  
; TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: PAIGE=1H  
; CURRENT APPLICATION NUMBER: US/10/346,162  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US 09/614,865  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 09/860,688  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-346-162-130

Query Match 33.7%; Score 30; DB 15; Length 16;  
Best Local Similarity 45.5%; Pred. No. 8.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEPQG 16  
Db 5 PLLMALLAPPG 15

RESULT 10  
US-09-870-216C-3  
; Sequence 3, Application US/09870216C  
; Publication No. US20040138135A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER  
; FILE REFERENCE: 68126881210100  
; CURRENT APPLICATION NUMBER: US/09/870,216C  
; CURRENT FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/209,391  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/226,256

; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/257,008  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-216C-3

Query Match 32.6%; Score 29; DB 11; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+06;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14  
Db 2 LQLLMEP 8

RESULT 11  
US-10-017-327-3  
; Sequence 3, Application US/10017327  
; Publication No. US20020155471A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND  
; TITLE OF INVENTION: METHODS FOR USING SAME  
; FILE REFERENCE: GZ 2101.20  
; CURRENT APPLICATION NUMBER: US/10/017,327  
; CURRENT FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-327-3

Query Match 32.6%; Score 29; DB 13; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+06;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14  
Db 2 LQLLMEP 8

RESULT 12  
US-10-073-054-20  
; Sequence 20, Application US/10073054  
; Publication No. US20030167485A1  
; GENERAL INFORMATION:  
; APPLICANT: Garvan Institute of Medical Research  
; APPLICANT: HERZOG, Herbert  
; TITLE OF INVENTION: No. US20030167485A1el G-protein coupled receptor-encoding gene an  
; TITLE OF INVENTION: therefor  
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
; CURRENT APPLICATION NUMBER: US/10/073,054  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US 09/308,696  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00805  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: AU P0386  
; PRIOR FILING DATE: 1997-09-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: N-terminal peptide  
US-10-073-054-20



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Query Match      32.6%; Score 29; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQPLQ 9
DB 2 TPQSLQ 8

RESULT 13
US-10-469-101-53
; Sequence 53, Application US/10469101
; Publication No. US20040071688A1
; GENERAL INFORMATION:
; APPLICANT: CARTER, Graham
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED THROMBOPOIETIN WITH REDUCED
; FILE REFERENCE: MER-109
; CURRENT APPLICATION NUMBER: US/10/469,101
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: EP 01104702.4
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/EP02/01931
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-469-101-53

Query Match      32.6%; Score 29; DB 15; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 QPLLQVMEPQG 16
DB 1 QSLIGTQLPQG 12

RESULT 14
US-09-864-761-40147
; Sequence 40147, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40147
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005343.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
US-09-864-761-40147

Query Match      32.6%; Score 29; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLLQV 10
DB 3 QPLLQV 8

RESULT 15
US-10-013-312-33
; Sequence 33, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-33

```

Query Match 31.5%; Score 28; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 3 TPSPIIQ 9

## RESULT 16

US-10-013-312-412  
; Sequence 412, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 412  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-412

Query Match 31.5%; Score 28; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

## RESULT 17

US-10-013-312-502  
; Sequence 502, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 502  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-502

Query Match 31.5%; Score 28; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

## RESULT 18

US-10-013-312-605  
; Sequence 605, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 605  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-605

Query Match 31.5%; Score 28; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

## RESULT 19

US-10-013-312-1358  
; Sequence 1358, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1358  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1358

Query Match 31.5%; Score 28; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

## RESULT 20

US-10-013-312-1522  
; Sequence 1522, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:

```
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013.312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1522
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1522

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TPQPLLQ 9
Db      2 TPSP1IQ 8

RESULT 21
US-10-013-312-1598
; Sequence 1598, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013.312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1598

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TPQPLLQ 9
Db      1 TPSP1IQ 7

RESULT 22
US-10-013-312-1693
; Sequence 1693, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013.312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1693
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1693

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TPQPLLQ 9
Db      1 TPSP1IQ 7

RESULT 23
US-10-013-312-1721
; Sequence 1721, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013.312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1721
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1721

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TPQPLLQ 9
Db      1 TPSP1IQ 7

RESULT 24
US-10-013-312-1810
; Sequence 1810, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013.312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1810
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1810

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPIIQ 7

RESULT 25
US-10-013-312-1928
; Sequence 1928, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1928
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1928

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPIIQ 7

RESULT 26
US-10-013-312-1983
; Sequence 1983, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1983
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1983

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 1 TPSPIIQ 7

RESULT 27
US-10-013-312-2020
; Sequence 2020, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2020
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2020

Query Match      31.5%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9
Db 3 TPSPIIQ 9

RESULT 28
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Teakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53

Query Match      31.5%; Score 28; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLPLQVME 13
Db      1 PQLPLRTEQE 10

RESULT 29
US-09-783-931-53
; Sequence 53, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
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; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-783-931-53

Query Match      31.5%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 PQLPLQVME 13
Db      1 PQLPLRTEQE 10

RESULT 30
US-10-013-312-82
; Sequence 82, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193F1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-82

Query Match      31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TPQPLLQ 9
Db      3 TPSPFIQ 9

RESULT 31
US-10-013-312-196
; Sequence 196, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 193F1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 196
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-196

Query Match      31.5%; Score 28; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

## RESULT 32

US-10-013-312-459  
; Sequence 459, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 459  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-459

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

## RESULT 33

US-10-013-312-560  
; Sequence 560, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 560  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-560

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

## RESULT 34

US-10-013-312-690

; Sequence 690, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 690  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-690

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

## RESULT 35

US-10-013-312-2072  
; Sequence 2072, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2072  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2072

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

## RESULT 36

US-10-013-312-2241  
; Sequence 2241, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2241  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2241

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||:|  
Db 2 TPSPILQ 8

RESULT 37  
US-10-013-312-2432  
; Sequence 2432, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2432  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2432

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||:|  
Db 1 TPSPILQ 7

RESULT 38  
US-10-013-312-2450  
; Sequence 2450, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2450  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2450

Query Match 31.5%; Score 28; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||:|  
Db 2 TPSPILQ 8

RESULT 39  
US-10-234-816-33  
; Sequence 33, Application US/10234816  
; Publication No. US20030157514A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRAIN HOMOLOGY DOMAIN AND PR  
; FILE REFERENCE: D0117 NP  
; CURRENT APPLICATION NUMBER: US/10/234,816  
; CURRENT FILING DATE: 2002-09-04  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-234-816-33

Query Match 31.5%; Score 28; DB 14; Length 13;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTQPPLL 8  
:|:|:|  
Db 5 ETPRPLM 11

RESULT 40  
US-10-185-425-24  
; Sequence 24, Application US/10185425  
; Publication No. US20030053984A1  
; GENERAL INFORMATION:  
; APPLICANT: Apotech Research and Development Ltd.  
; APPLICANT: Tschoep, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Holler, Nils  
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer  
; FILE REFERENCE: 1708.001US1  
; CURRENT APPLICATION NUMBER: US/10/185,425  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: PCT/EP00/13032  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: DE 199 63 859.4  
; PRIOR FILING DATE: 1999-12-30  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Linker  
US-10-185-425-24

Query Match 31.5%; Score 28; DB 14; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 PQLLQVMEPQ 15  
|||  
Db 3 PPKPKPKPEPE 14

Search completed: June 7, 2005, 23:31:32  
Job time : 78.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 15.7636 Seconds  
(without alignments)  
103.763 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMMEPQGD 17

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.1	14	2 C44823	synaptosomal-assoc
2	25	28.1	18	2 A35704	cytochrome P450 ol
3	25	28.1	18	2 F49215	urease (EC 3.5.1.5
4	24	27.0	10	2 A61218	alpha-gliadin 4Ha
5	24	27.0	15	2 A61391	alpha-1-antitrypsi
6	23	25.8	11	2 PC2330	cycloinooligosac
7	23	25.8	12	2 S70344	amine oxidase (cop
8	23	25.8	15	2 E56819	PS I complex subun
9	23	25.8	16	2 A46236	transforming prote
10	23	25.8	16	2 P80210	28K protein 4209 -
11	23	25.8	18	2 I59649	human leukocyte an
12	21	23.6	10	2 B61218	alpha-gliadin 6Ha
13	21	23.6	12	2 PH1567	cerebrin 28 - huma
14	21	23.6	14	2 PH1566	cerebrin 30 - huma
15	21	23.6	14	2 PN0147	omega-gliadine 1 a
16	21	23.6	15	2 A42413	Ig heavy chain V r
17	21	23.6	15	2 A40634	orf19 3' of eryk -
18	21	23.6	17	2 PC1318	large granule L6 c
19	21	23.6	18	2 PN0149	beta-Gliadine 13 -
20	21	23.6	18	2 S78767	ribosomal protein
21	20	22.5	10	2 PX0030	triacylglycerol li
22	20	22.5	10	2 PQ0788	NADH2 dehydrogenas
23	20	22.5	13	2 D39690	neural cell adhesi
24	20	22.5	14	2 PC7075	guanylate cyclase
25	20	22.5	15	2 PA0021	protein QA300016 -
26	20	22.5	15	2 PN0148	omega-gliadine 3 -
27	20	22.5	15	2 PL0110	complement factor
28	20	22.5	15	2 A41436	alpha-macroglobuli
29	20	22.5	16	2 S00123	dihydrolipoamide S

30	20	22.5	16	2 D83794	hypothetical prote
31	20	22.5	17	2 S33609	extensin - maize (
32	20	22.5	17	2 B31769	T-cell receptor de
33	20	22.5	18	2 S10452	hypothetical prote
34	20	22.5	18	2 I78841	thrombopoietin rec
35	19	21.3	8	2 S21288	lectin - potato (f
36	19	21.3	9	2 S70345	amine oxidase (cop
37	19	21.3	10	2 D33098	214K exoantigen (v
38	19	21.3	10	2 A61007	hementin (EC 3.4.-
39	19	21.3	11	2 S42587	cell protein - Bsc
40	19	21.3	11	2 S21127	precorrin methyltr
41	19	21.3	11	2 PN0044	protein kinase C i
42	19	21.3	12	2 A61309	glycoprotein hormo
43	19	21.3	13	2 S36668	hypothetical prote
44	19	21.3	14	2 I54945	gene C protein - E
45	19	21.3	14	2 A39239	actin 8 - slime mo
46	19	21.3	14	2 S12904	protein kinase (EC
47	19	21.3	15	2 A56891	gamma 1 gliadin -
48	19	21.3	15	2 F44823	synaptosomal-assoc
49	19	21.3	16	2 PH0763	T-cell receptor be
50	19	21.3	16	2 A45454	ankyrin-binding gl
51	19	21.3	16	2 A24099	crystal protein, 2
52	19	21.3	17	2 S41207	F420-non-reducing-
53	19	21.3	17	2 S15064	hypothetical prote
54	19	21.3	17	2 D48138	d(TTAGGG)n-binding
55	19	21.3	18	2 I52614	u-plasminogen acti
56	19	21.3	18	2 S52125	gamma2-gliadin P25
57	18.5	20.8	14	2 S6049	kidney stone prote
58	18.5	20.8	14	2 S00150	ovostatin - duck (
59	18.5	20.8	15	2 B4136	ovostatin - green
60	18.5	20.8	18	2 A61392	brain-associated s
61	18	20.2	9	2 A60108	exotoxin A - Strep
62	18	20.2	10	2 A61622	vitellogenin, 190K
63	18	20.2	11	2 A34662	Achatina cardio-ex
64	18	20.2	12	2 B44818	extracellular lipa
65	18	20.2	12	2 S67528	napiin - rape (frag
66	18	20.2	12	2 S70337	napiin small chain
67	18	20.2	12	2 PN0046	ATP synthase D cha
68	18	20.2	12	4 JX0315	aminotransferase c
69	18	20.2	13	2 A44818	extracellular lipa
70	18	20.2	13	2 S09716	2S albumin large c
71	18	20.2	13	2 PH1772	T cell receptor al
72	18	20.2	13	2 B47415	mannose-1-phosphat
73	18	20.2	13	2 B56864	dipeptidyl-peptida
74	18	20.2	14	2 S02078	ribulose-bisphosph
75	18	20.2	15	2 B39109	hypothetical 1.5K
76	18	20.2	15	2 PA0088	protein QP200051 -
77	18	20.2	15	2 A45103	7 alpha-hydroxy-4-
78	18	20.2	15	2 I78838	flc3 ligand isofor
79	18	20.2	15	2 A57003	hypothetical prote
80	18	20.2	16	2 PH0767	T-cell receptor be
81	18	20.2	16	2 PD0002	inulin fructotrans
82	18	20.2	17	2 A60570	Ig mu heavy chain
83	18	20.2	17	2 A35550	adrenocortical cel
84	18	20.2	17	2 B25348	glycogen(starch) s
85	18	20.2	18	2 S46418	Nr1 protein - cur
86	18	20.2	18	2 S28408	platelet-derived g
87	18	20.2	18	2 I46653	T-cell receptor de
88	18	20.2	18	2 A54195	Na+/K+-exchanging
89	17	19.1	8	2 S71299	IC12 protein - Par
90	17	19.1	8	2 S53008	citrate synthase -
91	17	19.1	9	2 A41978	calliPMRFamide 1 -
92	17	19.1	9	2 S26508	collagen alpha 2 (V
93	17	19.1	9	2 PC7074	translation elonga
94	17	19.1	10	2 S33844	alpha-2-macroglobu
95	17	19.1	10	2 S71948	matrix metalloprot
96	17	19.1	10	2 B59272	peptide-N4-(N-acet
97	17	19.1	10	2 S68128	hypothetical prote
98	17	19.1	11	2 S68637	acetylcholinestera
99	17	19.1	11	2 S23306	substance P - Atla
100	17	19.1	12	2 G49215	urease (EC 3.5.1.5

## ALIGNMENTS

RESULT 1  
C44823  
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)  
N:Alternate names: superprotein peptide 8  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C:Accession: C44823  
R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A:Reference number: A44823; MUID:92044785; PMID:1941090  
A:Accession: C44823  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <LOE>  
A:Experimental source: visual tissue  
A:Note: sequence extracted from NCBI backbone (NCBIP:64253)  
C:Keywords: membrane trafficking

Query Match 28.1%; Score 25; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 VMMEPQGD 17  
||: ||:  
Db 3 VMLDQGE 10

RESULT 2  
A35704  
cytochrome P450 olf2 - bovine (fragment)  
N:Contains: oxidoreductase (EC 1.-.-.-)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: A35704  
R:Jazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.  
Biochemistry 29, 7433-7440, 1990  
A:Title: Identification and biochemical analysis of novel olfactory-specific cytochrome  
A:Reference number: A35704; MUID:91027757; PMID:2121272  
A:Accession: A35704  
A:Molecule type: protein  
A:Residues: 1-18 <LAZ>  
A:CROSS-references: UNIPROT:P22779  
C:Genetics:  
A:Gene: CYP2A  
A:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protein

Query Match 28.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 46.2%; Pred. No. 6.7e+02;  
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 PQLLQVMMEPOG 16  
||: ||:  
Db 5 PGFQQQAFKELQG 17

RESULT 3  
F49215  
urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772) (fragment)  
C:Species: Helicobacter mustelae  
C>Date: 19-Dec-1993 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: F49215  
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.  
Infect. Immun. 60, 5259-5266, 1992  
A:Title: Purification and characterization of the urease enzymes of Helicobacter species  
A:Reference number: A49215; MUID:93084378; PMID:1452359  
A:Accession: F49215  
A:Status: preliminary  
A:Molecule type: protein

A:Residues: 1-18 <TUR>  
A:CROSS-references: UNIPROT:Q9RSF6  
A:Note: sequence extracted from NCBI backbone (NCBIP:119487)  
C:Superfamily: urease, fused gamma/beta subunit; urease 11k chain homology; urease 12k chain homology; hydrolase  
C:Keywords: hydrolase

Query Match 28.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 6.7e+02;  
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 TPQPLLQVMMEPOGD 17  
||: ||:  
Db 2 TPKELDKWMLHVAGE 16

RESULT 4  
A61218  
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Dasypyrum villosum  
C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: A61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia  
A:Reference number: A61218; MUID:91315394; PMID:1859356  
A:Accession: A61218  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHE>  
A:CROSS-references: UNIPROT:Q7MLF7  
C:Keywords: seed; storage protein

Query Match 27.0%; Score 24; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQLLQ 9  
||: ||:  
Db 2 LRVFVPLQ 10

RESULT 5  
A61391  
alpha-1-antitrypsin homolog - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: A61391  
R:Tanaka, N.; Sekiya, S.; Takamizawa, H.; Kato, N.; Moriyama, Y.; Fujimura, S.  
Jpn. J. Cancer Res. 82, 693-700, 1991  
A:Title: Characterization of a 54 kDa, alpha-1-antitrypsin-like protein isolated from as  
A:Reference number: A61391; MUID:91310496; PMID:1906855  
A:Accession: A61391  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <TAN>  
A:CROSS-references: UNIPROT:Q7M4R2

Query Match 27.0%; Score 24; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17  
||| |||  
Db 3 PQGD 6

RESULT 6  
PC2330  
cyclooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-255)  
C:Species: Bacillus circulans  
C>Date: 21-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: PC2330  
R:Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.

Biosci., Biotechnol. Biochem. 59, 31-34, 1995  
 A:Title: Purification and characterization of cycloolmulooligosaccharide fructanotransferase  
 A:Reference number: PC2330; MUID:95201377; PMID:7765973  
 A:Accession: PC2330  
 A:Molecule type: protein  
 A:Residues: 1-11 <KUS>  
 A:Cross-references: UNIPROT:Q7M0L3  
 C:Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular  
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 25.8%; Score 23; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 MEPOG 16  
 | | | |  
 Db 7 NNPOG 11

RESULT 7  
 S70344  
 amine oxidase (copper-containing) (EC 1.4.3.6) I - Aspergillus niger (fragments)  
 C:Species: Aspergillus niger  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C:Accession: S70344  
 R:Frederick, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.  
 Biochim. Biophys. Acta 1295, 59-72, 1996  
 A:Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the  
 A:Reference number: S70344; MUID:96283794; PMID:8679675  
 A:Accession: S70344  
 A:Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7; 8-12 <FRE>  
 C:Keywords: oxidoreductase

Query Match 25.8%; Score 23; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 9.2e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 VMPEPG 16  
 | | | |  
 Db 1 VVIEPYG 7

RESULT 8  
 E56819  
 PS I complex subunit 8 - cucumber (fragment)  
 C:Species: Cucumis sativus (cucumber)  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Jul-2004  
 C:Accession: E56819  
 R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.  
 Biochim. Biophys. Acta 1059, 141-148, 1991  
 A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-ter  
 A:Reference number: A56819; MUID:91355209; PMID:1883835  
 A:Accession: E56819  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <IWA>  
 A:Cross-references: UNIPROT:P42052  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:58606)

Query Match 25.8%; Score 23; DB 2; Length 15;  
 Best Local Similarity 30.8%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LQTPQLQVME 13  
 | | | |  
 Db 1 IQADXTFQVIQD 13

RESULT 9  
 A46236  
 transforming protein myc, form 1 - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C:Accession: A46236  
 R:Hann, S.R.; Sloan-Brown, K.; Spotts, G.D.  
 Genes Dev. 6, 1229-1240, 1992  
 A:Title: Translational activation of the non-AUG-initiated c-myc 1 protein at high cell  
 A:Reference number: A46236; MUID:92331929; PMID:1628829  
 A:Accession: A46236  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <HAN>  
 A:Cross-references: GB:X01023  
 C:Genetics:  
 A:Start codon: CTG  
 C:Keywords: alternative initiators

Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5  
 | | | |  
 Db 7 LETPQ 11

RESULT 10  
 PS0210  
 28K protein 4209 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C:Accession: PS0210  
 R:Tsuigita, A.; Miyatake, N.  
 Submitted to JIPID, April 1993  
 A:Reference number: PS0208  
 A:Accession: PS0210  
 A:Molecule type: protein  
 A:Residues: 1-16 <TSA>  
 A:Cross-references: UNIPROT:Q7M281  
 A:Experimental source: germ, bran, strain Nihonbare  
 C:Comment: molecular weight 28K, pI 7.3.

Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 37.5%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 VMPEPGD 17  
 | | | |  
 Db 8 IVPNPEGD 15

RESULT 11  
 I59649  
 human leukocyte antigen alpha chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I59649  
 R:Fogdell, A.; Olerup, O.  
 Tissue Antigens 44, 19-24, 1994  
 A:Title: The DOA1\*0104 allele is carried by DRB1\*1001- and DRB1\*1401-positive haplotypes  
 A:Reference number: I59649; MUID:95064785; PMID:7974465  
 A:Accession: I59649  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-18 <RES>  
 A:Cross-references: UNIPROT:Q30216; GB:S75685; NID:9913771; PIDN:AAB32621.1; PID:9913772  
 C:Genetics:  
 A:Gene: GDB:HLA-DQA1  
 A:Cross-references: GDB:120638; OMIM:146880  
 A:Map position: 6p21.3-6p21.3

Query Match 25.8%; Score 23; DB 2; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 LQVMMEPQ 16  
| | | | |  
Db 5 LTTWSPCG 13

## RESULT 12

B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Dasyphyrum villosum  
C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: B61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A>Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
A:Reference number: A61218; MUID:91315394; PMID:1859356  
A:Accession: B61218  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHE>  
A:Cross-references: UNIPROT:Q7M1F6  
C:Keywords: seed; storage protein

Query Match 23.6%; Score 21; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLQ 9  
: : | | |  
Db 1 VRVPVPLQ 9

## RESULT 13

PH1567  
cerebrin 28 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: PH1567  
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993  
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance liquid chromatography  
A:Reference number: PH1566; MUID:93329419; PMID:8336140  
A:Accession: PH1567  
A:Molecule type: protein  
A:Residues: 1-12 <LEO>  
A:Cross-references: UNIPROT:P41222

Query Match 23.6%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 PLLQVMMEP 14  
| | | | |  
Db 2 PPAQVSVQP 10

## RESULT 14

PH1566  
cerebrin 30 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: PH1566  
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993  
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance liquid chromatography  
A:Reference number: PH1566; MUID:93329419; PMID:8336140  
A:Accession: PH1566  
A:Molecule type: protein  
A:Residues: 1-14 <LEO>

Query Match 23.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 44.4%; Pred. No. 2.4e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 PLLQVMMEP 14  
| | | | |  
Db 2 PPAQVSVQP 10

## RESULT 15

PN0147  
omega-gliadin 1 and 2 - Aegilops longissima (fragment)  
C:Species: Aegilops longissima  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: PN0147; PN0146  
R:Odintsova, T.I.; Egorov, T.A.  
Biokhimiya 55, 509-516, 1990  
A>Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the omega-gliadin gene  
A:Reference number: PN0146; MUID:90283493; PMID:2354218  
A:Accession: PN0147  
A:Molecule type: protein  
A:Residues: 1-14 <ODI>  
A:Cross-references: UNIPROT:Q7M1V5  
A:Experimental source: strain K-202  
A>Note: Omega-gliadin 2 (amino-terminal fragment)  
A:Accession: PN0146  
A:Molecule type: protein  
A:Residues: 1-9 <OD2>  
A:Experimental source: strain K-202  
A>Note: omega-gliadin 1 (amino-terminal fragment)

Query Match 23.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
| | | |  
Db 11 LQTP 14

## RESULT 16

A42413  
Ig heavy chain V region (LBL-copurifying) - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C:Accession: A42413  
R:Bao, Z.; Muschler, J.; Horwitz, A.F.  
J. Biol. Chem. 267, 4974-4980, 1992  
A>Title: LBL, a novel, developmentally regulated, laminin-binding lectin.  
A:Reference number: A42413; MUID:92165867; PMID:1531660  
A:Accession: A42413  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <BAO>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.6%; Score 21; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
| | | |  
Db 11 LQTP 14

## RESULT 17

A40634  
orf19 3' of eryK - Saccharopolyspora erythraea (fragment)  
C:Species: Saccharopolyspora erythraea  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A40634  
R:Stassi, D.; Donadio, S.; Staver, M.J.; Katz, L.  
J. Bacteriol. 175, 182-189, 1993  
A>Title: Identification of a Saccharopolyspora erythraea gene required for the final hyphae development  
A:Reference number: A40634; MUID:93106953; PMID:8416893  
A:Accession: A40634

A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-15 <STA>  
A;Cross-references: UNIPROT:Q04794  
A;Note: sequence extracted from NCBI backbone (NCBIN:121243, NCBI:121244)

Query Match 23.6%; Score 21; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQ 6  
: ||:  
Db 7 VSTRP 12

RESULT 18  
PC1318  
large granule L6 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)  
C;Species: Tachyplesus tridentatus  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: PC1318  
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-316, 1993  
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1318  
A;Molecule type: protein  
A;Residues: 1-17 <SHI>  
A;Cross-references: UNIPROT:P82151; UNIPROT:Q9USE9  
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 23.6%; Score 21; DB 2; Length 17;  
Best Local Similarity 30.8%; Pred. No. 2.9e+03;  
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QTPQFLQVMEP 14  
: ||:  
Db 5 QIPGKLMHITATP 17

RESULT 19  
PN0149  
beta-Gliadine 13 - Aegilops longissima (fragment)  
C;Species: Aegilops longissima  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: PN0149  
R;Odintsova, T. I.; Egorov, T. A.  
Biokhimiya 55, 509-516, 1990  
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of  
A;Reference number: PN0146; MUID:90283493; PMID:2354218  
A;Accession: PN0149  
A;Molecule type: protein  
A;Residues: 1-18 <ODI>  
A;Cross-references: UNIPROT:Q7M1Z6  
A;Experimental source: strain K-202  
C;Superfamily: gliadin

Query Match 23.6%; Score 21; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 3.1e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQLLQ 9  
: ||:  
Db 1 VRVPVPLQ 9

RESULT 20  
S78767  
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: S78767  
R;Graack, H. R.

A;Status: preliminary  
A;Reference number: S78760  
A;Accession: S78767  
A;Molecule type: protein  
A;Residues: 1-18 <GRA>  
C;Keywords: mitochondrial  
R;1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>

Query Match 23.6%; Score 21; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 3.1e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LLQVMEPQ 15  
: ||:  
Db 6 ILKAMQRP 14

RESULT 21  
PX0030  
triacylglycerol lipase (EC 3.1.1.3) II - yeast (Geotrichum candidum) (fragments)  
C;Species: Geotrichum candidum  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: PX0030  
R;Sugihara, A.; Shimada, Y.; Tominaga, Y.  
J. Biochem. 107, 426-430, 1990  
A;Title: Separation and characterization of two molecular forms of Geotrichum candidum I  
A;Reference number: PX0030; MUID:90256718; PMID:2341377  
A;Accession: PX0030  
A;Molecule type: protein  
A;Residues: 1-10 <SUG>  
A;Cross-references: UNIPROT:P22394  
C;Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains two  
C;Keywords: carboxylic ester hydrolase

Query Match 22.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.4e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QTPQPL 8  
: ||:  
Db 1 EAPRPL 7

RESULT 22  
PQ0788  
NADH2 dehydrogenase (EC 1.6.99.3) 20K chain - fava bean mitochondrion (fragment)  
N;Alternate names: complex I 20K chain; NADH-ubiquinone reductase 20K chain  
C;Species: mitochondrion Vicia faba (fava bean)  
C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: PQ0788  
R;Leternme, S.; Boutry, M.  
Plant Physiol. 102, 435-443, 1993  
A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH  
A;Reference number: PQ0775; MUID:94151437; PMID:8108509  
A;Accession: PQ0788  
A;Molecule type: protein  
A;Residues: 1-10 <LET>  
A;Cross-references: UNIPROT:Q7M2G4  
C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th  
ranging from 5K to 75K.  
C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by  
C;Genetics:  
A;Genome: mitochondrion  
C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 22.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.4e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLQV 10  
: ||||  
Db 5 QVLLQV 10

RESULT 23  
D39690  
neural cell adhesion molecule, cardiac splice form +, -, + - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C:Accession: D39690  
Mol. Cell. Biol. 11, 1654-1661, 1991  
R:Reyes, A.A.; Small, S.J.; Akeson, R.  
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
A:Reference number: A39690; MUID:91141516; PMID:1996115  
A:Accession: D39690  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-13 <REV>  
A:Cross-references: GB:M63970  
A:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin  
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 22.5%; Score 20; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 1

Qy 14 PQGD 17  
|||:  
Db 8 PQGE 11

RESULT 24  
PC7075  
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: PC7075  
R:Taugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of brain  
A:Reference number: PC7072  
A:Accession: PC7075  
A:Molecule type: protein  
A:Residues: 1-14 <TSU>  
A:Cross-references: UNIPROT:Q7M058  
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C:Keywords: brain; phosphorus-oxygen lyase

Query Match 22.5%; Score 20; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 3.5e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 1

Qy 14 PQGD 17  
|||:  
Db 9 PQGE 12

RESULT 25  
PA0021  
protein QA300016 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0021  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
A:Reference number: PA0001  
A:Accession: PA0021  
A:Molecule type: protein  
A:Residues: 1-15 <RAM>  
A:Experimental source: leaf

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.7e+03; Mismatches 3; Indels 0; Gaps 0;  
Matches 3; Conservative 1

Qy 9 QVMEPQ 15  
: : : : :  
Db 5 EXVIEPQ 11

RESULT 26  
PN0148  
omega-gliadine 3 - Aegilops longissima (fragment)  
C:Species: Aegilops longissima  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PN0148  
R:Odintsova, T.I.; Egorov, T.A.  
Biokhimiia 55, 509-516, 1990  
A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of  
A:Reference number: PN0146; MUID:90283493; PMID:2354218  
A:Accession: PN0148  
A:Molecule type: protein  
A:Residues: 1-15 <ODI>  
A:Experimental source: strain K-202  
A:Note: 11-Gln was also found

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.7e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0

Qy 1 LQTPQ 5  
| : : :  
Db 11 LXTPQ 15

RESULT 27  
PL0110  
complement factor B1-Bb and B2-Bb - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 15-Nov-1996  
C:Accession: PL0110  
R:Matsushita, M.; Okada, H.  
Mol. Immunol. 26, 669-676, 1989  
A:Title: Two forms of guinea pig factor B of the alternative complement pathway with dif  
A:Reference number: A93136; MUID:89384686; PMID:2779589  
A:Accession: PL0110  
A:Molecule type: protein  
A:Residues: 1-15 <MAT>  
C:Keywords: complement alternate pathway; glycoprotein

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 28.6%; Pred. No. 3.7e+03; Mismatches 4; Indels 0; Gaps 0;  
Matches 2; Conservative 4

Qy 10 VVMEPQ 16  
: : : : :  
Db 2 ILDPAG 8

RESULT 28  
A41436  
alpha-macroglobulin - green sea turtle (fragment)  
C:Species: Chelonia mydas (green sea turtle)  
C:Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 09-Jul-2004  
C:Accession: A41436  
R:Osada, T.; Sasaki, T.; Ikai, A.  
J. Biochem. 103, 212-217, 1988  
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin  
A:Reference number: A41436; MUID:88227890; PMID:2453503  
A:Accession: A41436  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OSA>  
A:Cross-references: UNIPROT:Q7LZ35

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 3.7e+03; Mismatches 3; Indels 0; Gaps 0;  
Matches 3; Conservative 3

QY 4 P0PLQVNM 12  
|:|:|:  
Db 2 PEPQWVLV 10

RESULT 29  
S00123  
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - bovine (fragment)  
N:Alternate names: 2-oxoglutarate dehydrogenase complex chain E2; transsuccinylase  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00123  
R:Bradford, A.P.; Aitken, A.; Beg, F.; Cook, K.G.; Yeaman, S.J.  
FEBS Lett. 222, 211-214, 1987  
A:Title: Amino acid sequence surrounding the lipoid acid cofactor of bovine kidney 2-oxo-  
A:Reference number: S00123; MUID:88005143; PMID:3115829  
A:Accession: S00123  
A:Molecule type: protein  
A:Residues: 1-16 <BRA>  
A:Cross-references: UNIPROT:P11179  
C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
C:Keywords: acyltransferase; coenzyme A; lipoamide; mitochondrion; oxidoreductase; tria  
F:1-16/Domain: lipoyl/biotin-binding homology (fragment) <LPB>  
F:5/Binding site: lipoamide (lys) (covalent) #status experimental

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 4e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQP 6  
|:|:|:  
Db 8 VQVPSP 13

RESULT 30  
D83794  
hypothetical protein BH1156 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: D83794  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: D83794  
A:Status: preliminary  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <STO>  
A:Cross-references: UNIPROT:Q9KQD5; GB:AP001511; GB:BA000004; NID:gi0173727; PIDN:BA048  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1156

Query Match 22.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MMEPQG 16  
|:|:|:  
Db 10 MMELEG 15

RESULT 31  
S33609  
extensin - maize (fragment)  
C:Species: Zea mays (maize)  
C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C:Accession: S33609  
R:Murphy, J.M.; Hood, E.E.  
Plant Mol. Biol. 21, 885-893, 1993  
A:Title: Molecular basis for extensin size heterogeneity in two maize varieties.  
A:Reference number: S33609; MUID:93222485; PMID:8467081

A:Accession: S33609  
A:Molecule type: protein  
A:Residues: 1-17 <MUR>  
C:Keywords: glycoprotein; hydroxyproline

Query Match 22.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 75.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQP 6  
|:|:|:  
Db 13 TPKP 16

RESULT 32  
B31769  
T-cell receptor delta-2 chain J region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 05-Nov-1999  
C:Accession: B31769  
R:Loh, E.Y.; Cwiria, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.  
Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988  
A:Title: Human T-cell-receptor delta chain: genomic organization, diversity, and express  
A:Reference number: A94221; MUID:89071766; PMID:2974163  
A:Accession: B31769  
A:Molecule type: DNA  
A:Residues: 1-17 <LOH>  
A:Cross-references: GB:L36386; NID:G540455; PIDN:AAA61108.1; PID:G540456  
C:Keywords: T-cell receptor

Query Match 22.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVMMEP 14  
|:|:|:  
Db 12 QLIVPEP 17

RESULT 33  
S10452  
hypothetical protein (bpha 5' region) - Aspergillus niger  
C:Species: Aspergillus niger  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1997  
C:Accession: S10452  
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken  
submitted to the EMBL Data Library, March 1990  
A:Reference number: S10452  
A:Accession: S10452  
A:Molecule type: DNA  
A:Residues: 1-18 <VAN>  
A:Cross-references: EMBL:X52521; NID:G2336; PID:G2337

Query Match 22.5%; Score 20; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 4.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQPL 7  
|:|:|:  
Db 2 TDQPL 6

RESULT 34  
I78841  
thrombopoietin receptor - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I78841  
R:Alexander, W.S.; Dunn, A.R.  
Oncogene 10, 795-803, 1995  
A:Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep  
A:Reference number: I58350; MUID:95166571; PMID:7862460  
A:Accession: I78841

A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-18 <RES>  
A:Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991  
C:Genetics:  
A:Gene: C-mpl1

Query Match 22.5%; Score 20; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 4.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PQPLQV 10  
| | | |  
DB 5 PAPFLTV 11

RESULT 35  
S21288  
lectin - potato (fragment)  
C:Species: Solanum tuberosum (potato)  
C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C:Accession: S21288  
R:Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.  
Biochem. J. 283, 813-821, 1992  
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization  
A:Reference number: S21288; MUID:92272683; PMID:1590771  
A:Accession: S21288  
A:Molecule type: protein  
A:Residues: 1-8 <MIL>  
A:Cross-references: UNIPROT:Q7M1V6  
A:Experimental source: var. Ulster Sceptre  
C:Function:  
A:Description: may be involved in defence mechanism of the plant  
C:Keywords: hydroxyproline; lectin

Query Match 21.3%; Score 19; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQP 6  
| | |  
DB 4 TPSP 7

RESULT 36  
S70345  
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)  
C:Species: Aspergillus niger  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C:Accession: S70345  
R:Prebort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.  
Biochim. Biophys. Acta 1295, 59-72, 1996  
A:Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the  
A:Reference number: S70344; MUID:96283794; PMID:8679675  
A:Accession: S70345  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5;6-9 <PRE>  
C:Keywords: oxidoreductase

Query Match 21.3%; Score 19; DB 2; Length 9;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 VMPEQGD 17  
| : | | |  
DB 1 VVIEPNX 8

RESULT 37  
D33098  
214K exoantigen (version 1) - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: D33098  
R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: D33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <NIC>

Query Match 21.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 MMPEP 14  
| : | |  
DB 4 MLEP 7

RESULT 38  
A61007  
hementin (EC 3.4.-.-) - Amazon leech (fragment)  
C:Species: Haementeria ghilianii (Amazon leech)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A61007  
R:Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.  
J. Chromatogr. 502, 359-369, 1990  
A:Title: Purification and characterization of hementin, a fibrinogenolytic protease from  
A:Reference number: A61007; MUID:90256973; PMID:2187898  
A:Accession: A61007  
A:Molecule type: protein  
A:Residues: 1-10 <SWA>  
A:Cross-references: UNIPROT:Q7M3P9  
C:Keywords: anticoagulant; hydrolase; saliva

Query Match 21.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.5e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 MMPEQGD 17  
| : | | |  
DB 3 LTPSPD 9

RESULT 39  
S42587  
celf protein - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C:Accession: S42587  
R:Guzzo, A.; DuBow, M.S.  
Mol. Gen. Genet. 242, 455-460, 1994  
A:Title: A luxAB transcriptional fusion to the cryptic celf gene of Escherichia coli dis  
A:Reference number: S42587; MUID:94166755; PMID:8121401  
A:Accession: S42587  
A:Molecule type: DNA  
A:Residues: 1-11 <GUZ>  
C:Genetics:  
A:Gene: celf

Query Match 21.3%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TPQP 6  
| | |  
DB 6 TPHP 9

RESULT 40  
S21127  
precorrin methyltransferase - Salmonella typhimurium  
C:Species: Salmonella typhimurium



C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C:Accession: S21127  
R:Roessner, C.A.; Warren, M.J.; Santander, P.J.; Atshaves, B.P.; Ozaki, S.; Stolowich, N.  
FEBS Lett. 301, 73-78, 1992  
A>Title: Expression of 9 Salmonella typhimurium enzymes for cobinamide synthesis. Ident  
A:Reference number: S21127; MUID:93083628; PMID:1451790  
A:Accession: S21127  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <ROE>

Query Match 21.3%; Score 19; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.9e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQPL 7  
:| | | :  
Db 4 LQTPQTI 10

Search completed: June 7, 2005, 23:20:36  
Job time : 17.7636 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 74.8 Seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-2

Perfect score: 89

Sequence: 1 LQTPQLQVMEPQGD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	36.0	18	2 Q9TWM9	Q9twm9 tetrahymena
2	28	31.5	17	2 Q7Y013	Q7y013 zea mays (m
3	27	30.3	16	2 Q8LVE0	Q8lve0 trapa maxim
4	27	30.3	16	2 Q8LVE1	Q8lve1 punica gran
5	27	30.3	16	2 Q8LVE2	Q8lve2 lythrum sal
6	27	30.3	16	2 Q8MC15	Q8mc15 fuchsia hyb
7	27	30.3	16	2 Q8MC17	Q8mc17 ludwigia hy
8	27	30.3	16	2 Q8MC19	Q8mc19 quisqualis
9	27	30.3	16	2 Q8MC21	Q8mc21 combretum w
10	27	30.3	16	2 Q8MC23	Q8mc23 sonneratia
11	27	30.3	16	2 Q8MC25	Q8mc25 sonneratia
12	27	30.3	16	2 Q8MC27	Q8mc27 lagerstroem
13	27	30.3	16	2 Q8MC29	Q8mc29 duabanga gr
14	27	30.3	16	2 Q8MC31	Q8mc31 lagerstroem
15	27	30.3	16	2 Q8MC33	Q8mc33 rotala indi
16	27	30.3	16	2 Q8MC35	Q8mc35 heimia myrt
17	27	30.3	16	2 Q8MC37	Q8mc37 lawsonia in
18	27	30.3	16	2 Q8MC39	Q8mc39 amannia ba
19	27	30.3	16	2 Q8MC41	Q8mc41 nesaea lued
20	27	30.3	16	2 Q8MC43	Q8mc43 sonneratia
21	27	30.3	16	2 Q8MC45	Q8mc45 decodon ver
22	27	30.3	16	2 Q8MC47	Q8mc47 peplis port
23	27	30.3	16	2 Q8MC49	Q8mc49 pemphis aci
24	27	30.3	16	2 Q8MC51	Q8mc51 cuphea lanc
25	27	30.3	16	2 Q8MC53	Q8mc53 woodfordia
26	27	30.3	16	2 Q8MC58	Q8mc58 daphniphyll
27	27	30.3	16	2 Q8MET0	Q8met0 cercidiphyll
28	27	30.3	16	2 Q8MET2	Q8met2 saxifraga s
29	27	30.3	17	2 Q8LCL9	Q8lcl9 homo sapien
30	27	30.3	17	2 Q7LVQ4	Q7lvq4 homo sapien
31	27	30.3	17	2 Q9XQN9	Q9xqn9 sinapis alb

#### ALIGNMENTS

32	26	29.2	17	2	Q90XE2	Q90xe2 gallus gall
33	26	29.2	18	2	Q67216	Q67216 pennisetum
34	25	28.1	16	2	Q9UCH1	Q9uch1 homo sapien
35	25	28.1	16	2	Q9TRB4	Q9trb4 bos taurus
36	25	28.1	17	2	Q9APT4	Q9apt4 pseudomonas
37	25	28.1	18	1	CPAX_BOVIN	P22779 bos taurus
38	25	28.1	18	1	Q9R5F6	Q9r5f6 helicobacte
39	24	27.0	10	2	Q7M1F7	Q7m1f7 haynaldia v
40	24	27.0	15	2	Q6LCI3	Q6lci3 homo sapien
41	24	27.0	15	2	Q7M4R2	Q7m4r2 homo sapien
42	23	25.8	11	2	Q44237	Q44237 anabaena sp
43	23	25.8	11	2	Q7M0L3	Q7m0l3 bacillus ci
44	23	25.8	13	2	Q9UEE2	Q9uee2 homo sapien
45	23	25.8	15	1	PSAO_CUCSA	P42052 cucumis sat
46	23	25.8	16	2	Q9ERT5	Q9ert5 homo sapien
47	23	25.8	16	2	Q7M281	Q7m281 oryza sativ
48	23	25.8	16	2	Q84RM4	Q84rm4 boea crassi
49	23	25.8	17	2	Q7X3X0	Q7x3x0 streptomyce
50	23	25.8	18	2	Q30216	Q30216 homo sapien
51	22	24.7	12	2	Q8CG32	Q8cg32 rattus sp.
52	22	24.7	13	2	Q88176	Q88176 mus musculu
53	22	24.7	13	2	Q8CIW3	Q8ciw3 mus musculu
54	22	24.7	14	1	TAT_HV1W2	P12509 human immun
55	22	24.7	14	1	TAT_HV128	P12511 human immun
56	22	24.7	16	1	CPAB_BOVIN	P81187 bos taurus
57	22	24.7	16	2	Q9NNZ2	Q9nnz2 homo sapien
58	22	24.7	16	2	Q64KCO	Q64kco sporophila
59	22	24.7	18	2	Q81CS8	Q81cs8 bacillus ce
60	21	23.6	8	2	Q9T2V3	Q9t2v3 begonia for
61	21	23.6	10	1	FAR6_PANRE	P82660 panagrellus
62	21	23.6	10	2	Q7M1F6	Q7m1f6 haynaldia v
63	21	23.6	10	2	Q7TSC5	Q7tsc5 mus musculu
64	21	23.6	14	2	Q7M1V5	Q7m1v5 aegilops lo
65	21	23.6	15	2	Q9X635	Q9x635 escherichia
66	21	23.6	15	2	Q9X637	Q9x637 klebsiella
67	21	23.6	16	1	FOR1_MYRGU	P81438 myrmecia gu
68	21	23.6	16	2	Q7SM54	Q7sm54 human c-lym
69	21	23.6	17	2	Q8V9K6	Q8v9k6 homo sapien
70	21	23.6	17	2	Q9EL24	Q9el24 human immun
71	21	23.6	18	1	LCTN_LAMGL	P83315 lama glama
72	21	23.6	18	2	Q7M1Z6	Q7m1z6 aegilops lo
73	21	23.6	18	2	Q9R5S8	Q9r5s8 treponema d
74	20	22.5	8	2	Q7AUJ4	Q7auj4 acinetobact
75	20	22.5	10	2	Q9UNF2	Q9unf2 homo sapien
76	20	22.5	10	2	Q7M2G4	Q7m2g4 vicia faba
77	20	22.5	11	1	RANC_RANPI	P08951 rana pipien
78	20	22.5	12	2	Q6X7V1	Q6x7v1 canis famil
79	20	22.5	13	2	Q6T675	Q6t675 papio anubi
80	20	22.5	13	2	Q81769	Q81769 hepatitis c
81	20	22.5	14	2	Q7RR89	Q7rr89 plasmodium
82	20	22.5	14	2	Q7M058	Q7m058 mus musculu
83	20	22.5	15	2	Q9TNQ1	Q9tnq1 mus sp. bet
84	20	22.5	15	2	Q9S8N8	Q9s8n8 hordeum vul
85	20	22.5	15	2	Q9QV72	Q9qv72 mus sp. i
86	20	22.5	15	2	Q7LZ35	Q7lzf35 chelonina gy
87	20	22.5	16	1	FOR2_MYRGU	P81437 myrmecia gu
88	20	22.5	16	1	ODOO_BOVIN	P11179 bos taurus
89	20	22.5	16	2	Q9TWK1	Q9twk1 mytilus edu
90	20	22.5	16	2	Q9TR99	Q9tr99 canis famil
91	20	22.5	16	2	Q9T2R0	Q9t2r0 solanum tub
92	20	22.5	16	2	Q9K0D5	Q9k0d5 bacillus ha
93	20	22.5	17	2	Q79E46	Q79e46 coxiella bu
94	20	22.5	17	2	Q9JLA7	Q9jla7 mus musculu
95	20	22.5	18	2	Q9UR73	Q9ur73 trichoderma
96	20	22.5	18	2	Q7LUR5	Q7lur5 homo sapien
97	20	22.5	18	2	Q9BRH2	Q9brh2 homo sapien
98	20	22.5	18	2	Q9UCF9	Q9ucf9 homo sapien
99	20	22.5	18	2	Q97773	Q97773 cercopithec
100	20	22.5	18	2	Q7YRH7	Q7yrh7 sus scrofa

```
RESULT 1
Q9TWM9 PRELIMINARY; PRT; 18 AA.
ID Q9TWM9
AC Q9TWM9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE NKTAG antigen (Fragment).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=94323706; PubMed=7519359;
RA Leary J.H.3rd, Evans D.L., Jaso-Friedmann L.;
RT "Partial amino acid sequence of a novel protozoan parasite antigen
RT that inhibits non-specific cytotoxic cell activity.";
RL Scand. J. Immunol. 40:158-164(1994).
SQ SEQUENCE 18 AA; 2082 MW; 13BCB737B1FF92A3 CRC64;

Query Match 36.0%; Score 32; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 LQVMEPQGD 17
Db 3 LQLPFPQGD 12

RESULT 2
Q7Y0I3 PRELIMINARY; PRT; 17 AA.
ID Q7Y0I3
AC Q7Y0I3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Isoamylase (Fragment).
GN Name=sul;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S. IV.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY290391; AAP45416.1; -.
DT NON_TER 17
SQ SEQUENCE 17 AA; 1810 MW; E2913BED794C0670 CRC64;

Query Match 31.5%; Score 28; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLQV 10
Db 8 VSSPRPLLAV 17

RESULT 3
Q8LVE0 PRELIMINARY; PRT; 16 AA.
ID Q8LVE0
AC Q8LVE0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Trapa maximowiczii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Trapa.
OX NCBI_TaxID=162053;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035729; AAL14139.1; -.
DR EMBL; AY035730; AAL14141.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLQVME 13
Db 3 IRSPEPEVKILVD 15

RESULT 4
Q8LVE1 PRELIMINARY; PRT; 16 AA.
ID Q8LVE1
AC Q8LVE1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Punica granatum (Pomegranate).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Punica.
OX NCBI_TaxID=22663;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035724; AAL14129.1; -.
DR EMBL; AY035742; AAL14185.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLQV 13
Db 3 IRSPEPEVKILVD 15

RESULT 5
Q8LVE2 PRELIMINARY; PRT; 16 AA.
ID Q8LVE2
AC Q8LVE2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE PsaA (Fragment).  
 GN Name=psaA;  
 OS Lythrum salicaria (Purple loosestrife).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lythrum.  
 OX NCBI\_TaxID=13129;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035727; AAL41413.1; -.  
 DR EMBL; AF421495; AAM45853.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast. 16  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13  
 ::||| :::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 6

ID Q8MC15 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC15;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN Name=psaA;  
 OS Fuchsia hybrid cultivar.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Onagraceae; Fuchsia.  
 OX NCBI\_TaxID=133545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035746; AAL414173.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast. 16  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13  
 ::||| :::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 7

Q8MC17 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC17  
 AC Q8MC17;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN Name=psaA;  
 OS Ludwigia hyssopifolia.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Onagraceae; Ludwigia.  
 OX NCBI\_TaxID=155013;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035745; AAL414171.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast. 16  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13  
 ::||| :::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 8

Q8MC19 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC19  
 AC Q8MC19;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN Name=psaA;  
 OS Quisqualis indica (Rangoon creeper).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Combretaceae; Quisqualis.  
 OX NCBI\_TaxID=3956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035744; AAL414169.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast. 16  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13  
 ::||| :::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 9

Q8MC21 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC21  
 AC Q8MC21;

DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name=psaA;  
OS Combretrum wallichii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Combretaceae; Combretrum.  
OX NCBI\_TaxID=131243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035743; AAL14167.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
  
Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQLQVWME 13  
:::|:| :|:::  
Db 3 IRSPEVKILVD 15  
  
RESULT 10  
Q8MC23  
ID Q8MC23 PRELIMINARY; PRT; 16 AA.  
AC Q8MC23;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name=psaA;  
OS Sonneratia alba.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122812;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035741; AAL14163.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
  
Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQLQVWME 13  
:::|:| :|:::  
Db 3 IRSPEVKILVD 15  
  
RESULT 11  
Q8MC25  
ID Q8MC25 PRELIMINARY; PRT; 16 AA.

Q8MC25;  
AC 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name=psaA;  
OS Sonneratia apetala.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035740; AAL14161.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
  
Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQLQVWME 13  
:::|:| :|:::  
Db 3 IRSPEVKILVD 15  
  
RESULT 12  
Q8MC27  
ID Q8MC27 PRELIMINARY; PRT; 16 AA.  
AC Q8MC27;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name=psaA;  
OS Lagerstroemia villosa.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Lagerstroemia.  
OX NCBI\_TaxID=162025;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035739; AAL14159.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
  
Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQLQVWME 13  
:::|:| :|:::  
Db 3 IRSPEVKILVD 15  
  
RESULT 13  
Q8MC29

Q8MC29 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC29;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Duabanga grandiflora.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Duabanga.  
 OX NCBI\_TaxID=122808;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035738; AAL14157.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13  
 :::||| ::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 14

Q8MC31 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC31;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Lagerstroemia speciosa (Queen crape myrtle).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=122810;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035737; AAL14155.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13  
 :::||| ::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 15

Q8MC33 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC33;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Rotala indica.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Rotala.  
 OX NCBI\_TaxID=162024;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035736; AAL14153.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13  
 :::||| ::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 16

Q8MC35 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC35;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Heimia myrtifolia.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Heimia.  
 OX NCBI\_TaxID=135798;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035735; AAL14151.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTQPPLQVWME 13  
 :::||| ::::  
 Db 3 IRSPEPEVKILVD 15

## RESULT 17

Q8MC37  
ID Q8MC37 PRELIMINARY; PRT; 16 AA.  
AC Q8MC37;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name-psaA;  
OS Lawsonia inermis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Lawsonia.  
OX NCBI\_TaxID=141191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035734; AAL14149.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13  
:::|:| :|:|:|  
Db 3 IRSPEPEVKILVD 15

## RESULT 18

Q8MC39  
ID Q8MC39 PRELIMINARY; PRT; 16 AA.  
AC Q8MC39;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name-psaA;  
OS Ammannia baccifera.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Ammannia.  
OX NCBI\_TaxID=162022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035733; AAL14147.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13  
:::|:| :|:|:|  
Db 3 IRSPEPEVKILVD 15

## RESULT 19

Q8MC41  
ID Q8MC41 PRELIMINARY; PRT; 16 AA.  
AC Q8MC41;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name-psaA;  
OS Nesaea luederitzi.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Nesaea.  
OX NCBI\_TaxID=162020;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035732; AAL14145.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13  
:::|:| :|:|:|  
Db 3 IRSPEPEVKILVD 15

## RESULT 20

Q8MC43  
ID Q8MC43 PRELIMINARY; PRT; 16 AA.  
AC Q8MC43;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name-psaA;  
OS Sonneratia caseolaris.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122814;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035731; AAL14143.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLQVWME 13  
:::|:| :|:|:|  
Db 3 IRSPEPEVKILVD 15



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Db          3 IRSPEPEVKILVD 15

RESULT 21
Q8MC45
ID Q8MC45 PRELIMINARY; PRT; 16 AA.
AC Q8MC45;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Decodon verticillatus (Swamp loosestrife).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Decodon.
OX NCBI_TaxID=162018;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035728; AAL14137.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
Db 3 IRSPEPEVKILVD 15

RESULT 22
Q8MC47
ID Q8MC47 PRELIMINARY; PRT; 16 AA.
AC Q8MC47;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Peplis portula.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Peplis.
OX NCBI_TaxID=162016;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035726; AAL14133.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
Db 3 IRSPEPEVKILVD 15

RESULT 23
Q8MC49
ID Q8MC49 PRELIMINARY; PRT; 16 AA.
AC Q8MC49;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Pemphis acidula.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Pemphis.
OX NCBI_TaxID=126635;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035725; AAL14131.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
Db 3 IRSPEPEVKILVD 15

RESULT 24
Q8MC51
ID Q8MC51 PRELIMINARY; PRT; 16 AA.
AC Q8MC51;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN Name=psaA;
OS Cuphea lanceolata.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Cuphea.
OX NCBI_TaxID=3930;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035723; AAL14127.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 15.4%; Pred. No. 1.9e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQLQVWME 13
Db 3 IRSPEPEVKILVD 15

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Db 3 IRSPEVKILVD 15  
:::|:| :|:|:|

RESULT 25  
Q8MC53  
ID Q8MC53 PRELIMINARY; PRT; 16 AA.  
AC Q8MC53;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN Name=psaA;  
OS Woodfordia fruticosa.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Woodfordia.  
OX NCBI\_TaxID=141189;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035722; AAL14125.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LQTPQLQVME 13  
:::|:| :|:|:|  
Db 3 IRSPEVKILVD 15

RESULT 26  
Q8MES8  
ID Q8MES8 PRELIMINARY; PRT; 16 AA.  
AC Q8MES8;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN Name=PsaA;  
OS Daphniophyllum calycinum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Daphniophyllaceae; Daphniophyllum.  
OX NCBI\_TaxID=182071;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
RT "Phylogeny of the Altingiaceae based on cpDNA matK, *psaA* and *rDNA*  
ITS sequences.";  
RL Plant Syst. Evol. 230:13-24(2001).  
DR EMBL; AF377997; AAM45516.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LQTPQLQVME 13

Db 3 IRSPEVKILVD 15  
:::|:| :|:|:|

RESULT 27  
Q8MET0  
ID Q8MET0 PRELIMINARY; PRT; 16 AA.  
AC Q8MET0;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN Name=PsaA;  
OS Cercidiphyllum japonicum (Katsura tree).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.  
OX NCBI\_TaxID=13413;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
RT "Phylogeny of the Altingiaceae based on cpDNA matK, *psaA* and *rDNA*  
ITS sequences.";  
RL Plant Syst. Evol. 230:13-24(2001).  
DR EMBL; AF377996; AAM45514.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LQTPQLQVME 13  
:::|:| :|:|:|  
Db 3 IRSPEVKILVD 15

RESULT 28  
Q8MET2  
ID Q8MET2 PRELIMINARY; PRT; 16 AA.  
AC Q8MET2;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN Name=PsaA;  
OS Saxifraga stolonifera.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Saxifragaceae; Saxifraga.  
OX NCBI\_TaxID=182070;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
RT "Phylogeny of the Altingiaceae based on cpDNA matK, *psaA* and *rDNA*  
ITS sequences.";  
RL Plant Syst. Evol. 230:13-24(2001).  
DR EMBL; AF377995; AAM45512.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 2; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.9e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LQTPQLQVME 13  
:::|:| :|:|:|

```

Db          3 IRSPEPEVKILVD 15

RESULT 29
Q6LC19
ID          PRELIMINARY;      PRT;      17 AA.
AC          Q6LC19;
DT          05-JUL-2004 (TREMBlrel. 27, Created)
DT          05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE          Class II transactivator (Fragment).
GN          Name=CIITA;
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=98211702; PubMed=9551976;
RA          Piskurich J.F., Wang Y., Linhoff M.W., White L.C., Ting J.P.;
RT          "Identification of distinct regions of 5' flanking DNA that mediate
RT          constitutive, IFN-gamma, STAT1, and TGF-beta-regulated expression of
RT          the class II transactivator gene.";
RL          J. Immunol. 160:233-240(1998).
DR          EMBL; U94773; AAC39714.1; -.
FT          NON_TER      17
SQ          SEQUENCE 17 AA; 1876 MW; 8ED60CDAF7606B70 CRC64;

Query Match      30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy          4 POPLLQVMMBPQ 15
Db          6 PRPAGSYLSEFQ 17

RESULT 30
Q71VQ4
ID          PRELIMINARY;      PRT;      17 AA.
AC          Q71VQ4;
DT          05-JUL-2004 (TREMBlrel. 27, Created)
DT          05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE          MHC class II transactivator type III (Fragment).
GN          Name=C2TA;
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=97327562; PubMed=9184229; DOI=10.1093/emboj/16.10.2851;
RA          Muhlethaler-Mottet A., Otten L.A., Steinle V., Mach B.;
RT          "Expression of MHC class II molecules in different cellular and
RT          functional compartments is controlled by differential usage of
RT          multiple promoters of the transactivator CIITA.";
RL          EMBO J. 16:2851-2860(1997).
DR          EMBL; AF000003; AAB92363.1; -.
FT          NON_TER      17
SQ          SEQUENCE 17 AA; 1876 MW; 8ED60CDAF7606B70 CRC64;

Query Match      30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy          4 POPLLQVMMBPQ 15
Db          6 PRPAGSYLSEFQ 17

RESULT 31
Q9XQN9

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ID          Q9XQN9
AC          Q9XQN9;
DT          01-NOV-1999 (TREMBlrel. 12, Created)
DT          01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT          01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE          Photosystem I P700 chlorophyll (Fragment).
GN          Name=psaA;
OS          Sinapis alba (White mustard) (Brassica hirta).
OG          Chloroplast.
OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC          eurosids II; Brassicales; Brassicaceae; Sinapis.
OX          NCBI_TaxID=3728;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          TISSUE=Cotyledons;
RX          MEDLINE=20136375; PubMed=10672444;
RA          Sumner H., Pfannschmidt T., Link G.;
RT          "Transcripts and sequence elements suggest differential promoter usage
RT          within the ycf3-psaA gene cluster on mustard (Sinapis alba L.)
RT          chloroplast DNA.";
RL          Curr. Genet. 37:45-52(2000).
DR          EMBL; AJ242660; CAB45538.1; -.
DR          GO; GO:0009507; C:chloroplast; IEA.
KW          Chloroplast.
FT          NON_TER      17
SQ          SEQUENCE 17 AA; 2008 MW; 99517FE691B89355 CRC64;

Query Match      30.3%; Score 27; DB 2; Length 17;
Best Local Similarity 15.4%; Pred. No. 2.1e+03;
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy          1 LQTPQLQVMMVE 13
Db          3 IRSPEPEVKILVD 15

RESULT 32
Q90XE2
ID          PRELIMINARY;      PRT;      17 AA.
AC          Q90XE2;
DT          01-DEC-2001 (TREMBlrel. 19, Created)
DT          01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT          01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE          Transforming growth factor beta 4 (Fragment).
OS          Gallus gallus (Chicken).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC          Gallus.
OX          NCBI_TaxID=9031;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=22533207; PubMed=12646161; DOI=10.1016/S0006-291X(03)00300-0;
RA          Pan H.J., Halper J.;
RT          "Cloning, expression, and characterization of chicken transforming
RT          growth factor beta 4.";
RL          Biochem. Biophys. Res. Commun. 303:24-30(2003).
DR          EMBL; AF395834; AAL05481.1; -.
FT          NON_TER      17
SQ          SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;

Query Match      29.2%; Score 26; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy          4 POPLLQVMM 12
Db          3 PSPLLALL 11

RESULT 33
Q67216
ID          Q67216

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AC Q67216;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Photosystem I apoprotein A1 (Fragment).  
GN Name=psaA;  
OS Pennisetum americanum (Pearl millet).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Paniceae; Pennisetum.  
OX NCBI\_TaxID=4543;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nallar S.C., Nekalapudi S.C., Podile A.R.;  
RT "Pennisetum glaucum clone PGB788 coding for IRF170.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY694132; AAU12166.1; -;  
KW GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER.  
SQ SEQUENCE 18 AA; 2111 MW; 008B617FE6945893 CRC64;  
  
Query Match 29.2%; Score 26; DB 2; Length 18;  
Best Local Similarity 15.4%; Pred. No. 3.2e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQLQVWME 13  
: : : : :  
DB 3 IRSPEVKIVVD 15  
  
RESULT 34  
Q9UCH1 PRELIMINARY; PRT; 16 AA.  
ID Q9UCH1  
AC Q9UCH1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE LIPOAMIDASE (EC 3.1.1.13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93228634; PubMed=8471055;  
RA Hui D.Y., Hayakawa K., Oizumi J.;  
RT "Lipoamidase activity in normal and mutagenized pancreatic cholesterol  
esterase (bile salt-stimulated lipase).";  
RL Biochem. J. 291:65-69(1993).  
DR GO:0004771; F:sterol esterase activity; IEA.  
SQ SEQUENCE 16 AA; 1844 MW; 147321FA60374B3C CRC64;  
  
Query Match 28.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 4.2e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 LQTPQP 6  
: : : :  
DB 3 LENPQP 8  
  
RESULT 35  
Q9TRB4 PRELIMINARY; PRT; 16 AA.  
ID Q9TRB4  
AC Q9TRB4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE ATP-dependent 20 S proteasome activator (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94342244; PubMed=8063704;  
RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,  
RA Afendis S.J., Swaffield J.C., Slaughter C.A.;  
RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an  
RT ATPase containing multiple members of a nucleotide-binding protein  
RT family.";  
RL J. Biol. Chem. 269:20878-20884(1994).  
SQ SEQUENCE 16 AA; 1878 MW; F70F74211EE26EDE CRC64;  
  
Query Match 28.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 36.4%; Pred. No. 4.2e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 4 PQLLQVWMEP 14  
: : : : :  
DB 4 PEPNFQLLDNP 14  
  
RESULT 36  
Q9APT4 PRELIMINARY; PRT; 17 AA.  
ID Q9APT4  
AC Q9APT4  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21142509; PubMed=11208781; DOI=10.1128/JB.183.3.843-853.2001;  
RA Liang X., Phan X.Q.T., Olson M.V., Lory S.;  
RT "Identification of a genomic island present in the majority of  
RT pathogenic isolates of Pseudomonas aeruginosa.";  
RL J. Bacteriol. 183:843-853(2001).  
DR EMBL; AF241171; AAK01539.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 17 AA; 1954 MW; 68FDF0471E399969 CRC64;  
  
Query Match 28.1%; Score 25; DB 2; Length 17;  
Best Local Similarity 36.4%; Pred. No. 4.5e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 4 PQLLQVWMEP 14  
: : : : :  
DB 3 PWEVLDALEP 13  
  
RESULT 37  
CPAX\_BOVIN STANDARD; PRT; 18 AA.  
ID CPAX\_BOVIN  
AC P22779;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cytochrome P450 2A (OLP2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91027757; PubMed=2121272;  
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;  
RT "Identification and biochemical analysis of novel olfactory-specific

```

RT Cytochrome P-45011A and UDP-glucuronosyl transferase."
RL Biochemistry 29:7433-7440(1990).
CC -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC monooxygenases. In liver microsomes, this enzyme is involved in an
CC NADPH-dependent electron transport pathway. It oxidizes a variety
CC of structurally unrelated compounds, including steroids, fatty
CC acids, and xenobiotics.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR PIR: A35704; A35704.
DR InterPro: IPR001128; Cytochrome P450.
DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
KW Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KW Heme; Membrane; Microsome; Monooxygenase; Olfaction; Oxidoreductase.
FT NON_TER 1 1
FT VARIANT 6 6 G -> D.
FT VARIANT 11 11 A -> E.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;
Query Match 28.1%; Score 25; DB 1; Length 18;
Best Local Similarity 46.2%; Pred. No. 4.8e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4 PQLQVMEPQG 16
Db 5 PGQQQAFKELQG 17
RESULT 38
ID Q9RSF6 PRELIMINARY; PRT; 18 AA.
AC Q9RSF6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Helicobacter small subunit (Fragment).
OS Helicobacter mustelae.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=217;
RN [1]
RP SEQUENCE.
RX MEDLINE=93084378; PubMed=1452359;
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RA "Purification and characterization of the urease enzymes of
RT Helicobacter species from humans and animals.";
RL Infect. Immun. 60:5259-5266(1992).
DR PIR: F49215; F49215.
DR HSSP; P14916; 1E9Y.
DR GO; GO:0016151; P:nickel ion binding; IEA.
DR GO; GO:0009039; P:urease activity; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro: IPR002026; Urease Gamma.
DR Pfam: PF00547; Urease Gamma; 1.
SQ SEQUENCE 18 AA; 2060 MW; 29C9E0AB77E21805 CRC64;
Query Match 28.1%; Score 25; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 4.8e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 3 TPQLQVMEPQGD 17
Db 2 TPKELDKWMLHYAGE 16
RESULT 39
ID Q7MLF7 PRELIMINARY; PRT; 10 AA.
AC Q7MLF7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-gliadin 4Ha (Fragment).
OS Haynaldia villosa.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE.
RX MEDLINE=91315394; PubMed=1859356;
RA Shawry P.R., Sabelli P.A., Parmar S., Lafandra D.;
RA "alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha
RT of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).";
RL Biochem. Genet. 29:207-211(1991).
DR PIR: A61218; A61218.
FT NON_TER 1 1
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1162 MW; 72F11BC772D72D4 CRC64;
Query Match 27.0%; Score 24; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LQTPQPLQ 9
Db 2 LRVEVPQLQ 10
RESULT 40
ID Q6LCI3 PRELIMINARY; PRT; 15 AA.
AC Q6LCI3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+-phosphate cotransporter type II (Fragment).
GN Name=NPT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93317607; PubMed=8327470;
RA Magagnoli S., Werner A., Markovich D., Sorribas V., Stange G.,
RA Biber J., Murer H.;
RA "Expression cloning of human and rat renal cortex Na/Pi cotransport.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96293539; PubMed=8693007; DOI=10.1073/pnas.93.14.7409;
RA Hartmann C.M., Hewson A.S., Kos C.H., Hilfinger H., Soumounou Y.,
RA Murer H., Tenenhouse H.S.;
RA "Structure of murine and human renal type II Na+-phosphate
RT cotransporter genes (Npt2 and NPT2).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414(1996).
DR EMBL; U56684; AAD14856.1; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1770 MW; 23810E2056D88B8B CRC64;
Query Match 27.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 7 LLQVMEP 14
Db 1 LLKIIEP 8
Search completed: June 7, 2005, 23:18:51
Job time : 78.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 96.8727 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPLQPFQVQS 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

- Database : A\_Geneseq\_16Dec04.\*
- 1: Geneseqp1980s.\*
  - 2: Geneseqp1990s.\*
  - 3: Geneseqp2000s.\*
  - 4: Geneseqp2001s.\*
  - 5: Geneseqp2002s.\*
  - 6: Geneseqp2003s.\*
  - 7: Geneseqp2003bs.\*
  - 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	4	AAB72502 Colostrin
2	98	100.0	18	4	AAB59325 Ewe colos
3	98	100.0	18	4	AAB72248 Colostrin
4	98	100.0	18	4	AAB72534 Colostrin
5	98	100.0	18	5	AAB14579 Neural ce
6	98	100.0	18	5	AAM51038 Colostrin
7	98	100.0	18	5	AAB20230 Colostrin
8	98	100.0	18	8	ADN60297 Constitue
9	98	100.0	18	5	ADN74401 Ovine col
10	41	41.8	15	5	ABG67986 Human ADP
11	41	41.8	15	6	ADA24138 Alzheimer
12	39	39.8	16	2	AR49858 Sequence
13	39	39.8	16	6	ABP83082 G protein
14	37	37.8	13	7	ADM75689 Potential
15	37	37.8	13	7	ADM74895 Potential
16	36	36.7	15	5	AAM47777 Short cha
17	35	35.7	12	5	ABG67771 Human ADP
18	35	35.7	12	6	ADA23910 Alzheimer
19	35	35.7	13	3	AAB26624 Partial s
20	34	34.7	13	5	ABB97740 Human pro
21	34	34.7	13	5	ABB97739 Human pro
22	34	34.7	13	7	ADM75160 Potential
23	33	33.7	15	3	AAB21134 Src homol
24	33	33.7	18	2	AAI41624 Mammalian
25	33	33.7	18	6	AAE34138 T-cell st

26	33	33.7	18	6	AAE34142	Aae34142 T-cell st
27	33	33.7	18	6	AAE34133	Adm44636 Human mat
28	32	32.7	9	7	ADM48666	Aab21124 Src homol
29	32	32.7	11	3	AAE21124	Aab21133 Src homol
30	32	32.7	11	3	AAE21133	Aau01841 Wheat pep
31	32	32.7	17	4	AAU01841	Aau01840 Wheat pep
32	32	32.7	17	4	AAU01840	Adh14690 Gliadin r
33	32	32.7	17	8	ADH14690	Adh14691 Gliadin r
34	32	32.7	17	8	ADH14691	Aaw38909 Peptide r
35	32	32.7	18	2	AAW38909	Adh14808 Gliadin r
36	31.5	32.1	17	8	ADH14808	Adh14809 Gliadin r
37	31.5	32.1	17	8	ADH14809	Adh14821 Gliadin r
38	31.5	32.1	18	8	ADH14821	AAG97089 Human com
39	31	31.6	10	4	AAG97089	Aaw17451 Consensus
40	31	31.6	11	2	AAW17451	ABP61522 Human KRP
41	31	31.6	11	5	ABP61522	Aaw45819 Peptide r
42	31	31.6	15	2	AAW45819	Aaw45614 Peptide r
43	31	31.6	15	2	AAW45614	Aaw09376 Proline-r
44	31	31.6	16	2	AAW09376	Aaw09377 Proline-r
45	31	31.6	16	2	AAW09377	Aaw12220 Human ace
46	31	31.6	17	2	AAW12220	Aaw09378 Proline-r
47	31	31.6	18	2	AAW09378	Aar44563 Encoded b
48	30.5	31.1	11	2	AAE44563	Adf14527 Epitope o
49	30.5	31.1	14	7	ADF14527	Adf14528 Epitope o
50	30.5	31.1	14	7	ADF14528	ABP55802 B15 class
51	30	30.6	9	5	ABP55802	ABG96846 Human leu
52	30	30.6	9	5	ABG96846	ABG96954 Human leu
53	30	30.6	9	5	ABG96954	ABG96698 Human leu
54	30	30.6	9	5	ABG96698	Adl98515 Human leu
55	30	30.6	9	7	ADL98515	Adl98788 Human leu
56	30	30.6	9	7	ADL98788	Adl98679 Human leu
57	30	30.6	9	7	ADL98679	Adl98396 Human leu
58	30	30.6	9	7	ADL98396	ADK03224 Hepatitis
59	30	30.6	9	8	ADK03224	Adk03219 Hepatitis
60	30	30.6	10	8	ADK03219	Adk03227 Hepatitis
61	30	30.6	10	8	ADK03227	Adc35017 Rho-like
62	30	30.6	11	7	ADC35017	ABD97741 Human pro
63	30	30.6	13	5	ABB97741	AEG88540 HER2/NEU
64	30	30.6	13	5	AAG88540	Adg30154 Human can
65	30	30.6	15	6	ABR30154	Adg70385 Human 161
66	30	30.6	15	7	ADG70385	Adg70790 Human 161
67	30	30.6	15	7	ADG70790	AAU01833 Wheat Gli
68	30	30.6	17	4	AAU01833	Adh16208 Gliadin r
69	30	30.6	17	4	AAU01822	Adh16208 Gliadin r
70	30	30.6	17	8	ADH16208	Adh16203 Gliadin r
71	30	30.6	17	8	ADH16203	Adh14604 Gliadin r
72	30	30.6	17	8	ADH14604	Adh14670 Gliadin r
73	30	30.6	17	8	ADH14670	Adh14643 Gliadin r
74	30	30.6	17	8	ADH14643	Adh14661 Gliadin r
75	30	30.6	17	8	ADH14661	Adf14526 Epitope o
76	30	30.6	17	8	ADH14526	Adh14823 Gliadin r
77	29.5	30.1	14	7	ADH14823	Aay79501 Eimeria t
78	29.5	30.1	17	8	ADH14823	Aau82343 Human pap
79	29.5	30.1	18	3	AAU82343	ABG69555 Human CRP
80	29	29.6	9	5	ABG69555	Aar10268 Human ven
81	29	29.6	10	2	AAE96268	Aag96833 Human com
82	29	29.6	10	4	AAE96833	Abu90826 Peptide #
83	29	29.6	10	6	ABU90826	Adg70033 Human 161
84	29	29.6	10	7	ADG70033	Adb21127 Src homol
85	29	29.6	11	3	AAE21127	ABJ01202 Human Sox
86	29	29.6	13	5	ABJ01202	ADG66864 Human ClF
87	29	29.6	13	5	ADG66864	Adg66869 Human ClF
88	29	29.6	13	5	ADG66869	Adp27634 Bythograe
89	29	29.6	13	8	ADR27634	Adp50841 Sequence
90	29	29.6	15	1	AAE82092	ABP82092 HRV2-der1
91	29	29.6	15	1	AAE82092	Aay93323 Antigenic
92	29	29.6	15	3	RAY93323	ABr30262 Human can
93	29	29.6	15	6	ABR30262	ABr30229 Human can
94	29	29.6	15	6	ABR30229	Adb67139 Human rhi
95	29	29.6	15	7	ADB67139	Adc35688 Peptide e
96	29	29.6	15	7	ADB67139	ADG14323 Human thi
97	29	29.6	15	7	ADG14323	
98	29	29.6	15	7	ADG14323	

99 29 29.6 15 8 AD015604 Ad015604 Human rhi  
100 29 29.6 17 6 ABP82697 ABP82697 G protein

## ALIGNMENTS

RESULT 1  
AAB72502  
ID AAB72502 standard; peptide; 18 AA.

XX AC AAB72502;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #3.  
XX KW Dermatological; oxidative stress regulator; colostrinin.  
XX OS Unidentified.

XX FN WO200112650-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US022665.  
XX PR 17-AUG-1999; 99US-0149310P.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the cell  
XX PT with an oxidative stress regulator selected from colostrinin, its  
XX PT constituent peptide, analog or their combinations.

XX PS Claim 6; Page 25; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
XX CC stress level in a cell or a patient, comprising contacting the cell with,  
XX CC or administering to the patient, an oxidative stress regulator selected  
XX CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
XX CC to change the level of an oxidising species in the cell. The method can  
XX CC be used to treat oxidative damage to skin, by decreasing or preventing an  
XX CC increase in the level of damage to a biomolecule of the patient

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18  
|||  
Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2  
AAB59325  
ID AAB59325 standard; peptide; 18 AA.

XX AC AAB59325;  
XX DT 21-MAR-2001 (first entry)  
XX DE Ewe colostrinin peptide fragment B-10.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.  
XX PN WO2000075173-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-GB002128.  
XX PR 02-JUN-1999; 99GB-00012852.  
XX PA (REGE-) REGEN THERAPEUTICS PLC.  
XX PI Georgiades JA;  
XX DR WPI; 2001-071058/08.  
XX PT Peptides having an N-terminal amino acid sequence isolated from  
XX PT colostrinin for treating e.g. disorders of the central nervous system and  
XX PT immune system, viral and bacterial infections, and diseases characterized  
XX PT by amyloid plaques.

XX PS Claim 7; Page 27; 63pp; English.

XX SQ Sequence 18 AA;  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18  
|||  
Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 3  
AAB72248  
ID AAB72248 standard; peptide; 18 AA.

XX AC AAB72248;  
XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 3.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;  
XX KW central nervous system disorder; neurological disorder; mental disorder;  
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
XX KW neurosis; infection.

XX OS Synthetic.

XX PN WO200111937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US022818.

XX PR 17-AUG-1999; 99US-0149311P.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;



DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The peptides

CC have immune response modulatory activity, and are capable of inducing

CC cytokines. Colostrinin and its derived peptides are useful for inducing

CC cytokine production, for modulating an immunological response and for

CC inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 4

AA72534

ID AAB72534 standard; peptide; 18 AA.

AC AAB72534;

XX

XX 09-MAY-2001 (first entry)

XX

XX Colostrinin peptide #3.

XX

XX Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

XX 22-FEB-2001.

XX

XX 17-AUG-2000; 2000WO-US022774.

XX

XX 17-AUG-1999; 99US-0149633P.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

XX

XX Boldogh I;

XX

XX WPI; 2001-226545/23.

XX

XX Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

XX

PS Claim 6; Page 21; 35pp; English.

XX

CC The present invention relates to a method for promoting neural cell

CC differentiation and treating damaged neural cells, using colostrinin and

CC colostrinin constituent peptides (e.g. the present peptide) as a neural

CC cell regulator. Colostrinin is a polypeptide complex found in colostrum

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 5

AA014579

ID AA014579 standard; peptide; 18 AA.

XX

XX AA014579;

XX

XX 27-MAY-2002 (first entry)

XX

XX Neural cell regulatory colostrinin peptide 3.

XX

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

XX

XX Key Location/Qualifiers

PT Modified-site 18

PT /note= "Optional C-terminal amide"

XX

XX WO200213851-A1.

XX

XX 21-FEB-2002.

XX

XX 17-AUG-2000; 2000WO-US022777.

XX

XX 17-AUG-2000; 2000WO-US022777.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

XX

XX Boldogh I, Stanton JG, Hughes TK;

XX

XX WPI; 2002-269152/31.

XX

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog.

XX

XX Claim 7; Page 21; 37pp; English.

XX

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 6

AAM51038

AA51038 standard; peptide; 18 AA.  
AA51038;  
30-MAY-2002 (first entry)  
Colostrinin constituent peptide.  
Colostrinin; colostrum; immunomodulator; cardiovascular;  
blood cell regulator; cytokine inducer; beta-casein; human.  
Homo sapiens.  
Key Location/Qualifiers  
Modified-site 18 /note= "optional C-terminal amidation"  
WO200213849-A1.  
21-FEB-2002.  
17-AUG-2000; 2000WO-US022775.  
17-AUG-2000; 2000WO-US022775.  
(TEXA ) UNIV TEXAS SYSTEM.  
(REGE-) REGEN THERAPEUTICS PLC.  
Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
WPI; 2002-269150/31.  
Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or analog.  
Claim 1; Page 34; 54pp; English.  
The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. It is classified as having a beta-casein homologue precursor. Methods are claimed for: inducing a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell culture, a tissue, an organ or an organism, and the cell is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions effective to induce a cytokine; modulating an immune response in a patient by administering an immunological regulator under conditions effective to induce a cytokine, where the immunological regulator is administered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting blood cells with a blood cell regulator, where the blood cells are present in a cell culture or an organism, are mammalian or human, and where the blood cells are increased in number or differentiated; and a method for modulating blood cell proliferation in a patient. A claimed cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10. It was one of the best overall inducers in almost all cytokine and blood cell proliferation experiments conducted

Sequence 18 AA;  
Query Match 100.0%; Score 98; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DQPPDVEKPDLPQFFQVQS 18  
|||||  
Db 1 DQPPDVEKPDLPQFFQVQS 18  
|||||

RESULT 7  
AAE20230  
ID AAE20230 standard; peptide; 18 AA.  
XX  
AC AAE20230;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Colostrinin constituent peptide #3.  
XX  
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 18 /note= "Optionally C-terminal amide"  
FT  
FN WO200213850-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022776.  
XX  
PR 17-AUG-2000; 2000WO-US022776.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2002-269151/31.  
XX  
PT Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.  
XX  
PS Claim 6; Page 25; 51pp; English.  
XX  
CC The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, organ, or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/ after a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stress regulator is not present. The modulation of oxidative stress results in enhanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide

Sequence 18 AA;  
Query Match 100.0%; Score 98; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DQPPDVEKPDLPQFFQVQS 18  
|||||  
Db 1 DQPPDVEKPDLPQFFQVQS 18  
|||||

RESULT 8

ADN60297  
 ID ADN60297 standard; peptide; 18 AA.  
 XX AC ADN60297;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Constituent peptide of colostrinin SEQ ID NO:3.  
 XX KW modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
 KW DNA damage; beta-amyloid; retinoic acid; cytosstatic; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.  
 XX OS Synthetic.  
 XX PN WO2004037851-A2.  
 XX PD 06-MAY-2004.  
 XX PF 22-OCT-2003; 2003WO-US033423.  
 XX PR 22-OCT-2002; 2002US-0420369P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (BOLD// BOLDGOH I.  
 XX PA (STAN// STANTON J G.  
 XX PA (GEOR// GEORGIADIS J A.  
 XX PA (HUGH// HUGHES T K.  
 XX PA (KRUZ// KRUZEL M.  
 XX PI Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
 XX WPI; 2004-365494/34.  
 XX Use of colostrinin for e.g. modulating an intracellular signaling  
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 PT a cell.  
 XX Claim 6; SEQ ID NO 3; 46pp; English.  
 XX The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 XX SQ Sequence 18 AA;  
 Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DQPPDVEKPDLPQFQVQS 18  
 |||||  
 Db 1 DQPPDVEKPDLPQFQVQS 18  
 |||||  
 RESULT 9  
 ABG67986  
 ID ABG67986 standard; peptide; 15 AA.  
 XX AC ABG67986;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Human ADPI tryptic digest peptide #695.

ADS74401  
 ID ADS74401 standard; peptide; 18 AA.  
 XX AC ADS74401;  
 XX DT 16-DEC-2004 (first entry)  
 XX DE Ovine colostrinin peptide.  
 XX KW Colostrum; colostrinin; sheep; peptide purification.  
 XX OS Ovis aries.  
 XX PN WO2004081038-A1.  
 XX PD 23-SEP-2004.  
 XX PF 10-MAR-2004; 2004WO-GB001014.  
 XX PR 11-MAR-2003; 2003GB-00005552.  
 XX PR 08-MAR-2004; 2004GB-00005190.  
 XX PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
 XX WPI; 2004-677519/66.  
 XX Recovering peptides such as colostrinin from mammalian colostrum, by  
 PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 PT and precipitate, separating alcohol phase from precipitate, and  
 PT recovering alcohol phase.  
 XX Disclosure; SEQ ID NO 18; 41pp; English.  
 XX The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrinin using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.  
 XX SQ Sequence 18 AA;  
 Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DQPPDVEKPDLPQFQVQS 18  
 |||||  
 Db 1 DQPPDVEKPDLPQFQVQS 18  
 |||||  
 RESULT 10  
 ABG67986  
 ID ABG67986 standard; peptide; 15 AA.  
 XX AC ABG67986;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Human ADPI tryptic digest peptide #695.

XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
 KW Alzheimer's disease-associated feature; neuroprotective;  
 KW Alzheimer's disease-associated protein isoform; nootropic;  
 KW ADPI tryptic digest peptide.  
 XX Homo sapiens.  
 XX WO200246767-A2.  
 XX 13-JUN-2002.  
 XX 29-NOV-2001; 2001WO-GB005289.  
 XX 08-DEC-2000; 2000US-0254431P.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2002-508575/54.  
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 PT comprises detecting Alzheimer disease-associated features or Alzheimer  
 PT disease-associated protein isoforms in brain tissue from the subject.  
 XX Claim 7; Page 56; 427pp; English.  
 XX The present invention relates to methods and compositions for the  
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
 CC subject. The method comprises analysing a sample of brain tissue from a  
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
 CC disease-associated features (ADPs), whose relative abundance correlates  
 CC with the presence, absence, stage or severity of AD and comparing the  
 CC abundance of each feature with the abundance of that chosen feature in  
 CC brain tissue from persons free from AD. The invention also describes  
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
 CC brain tissue. The methods and compositions of the invention are useful  
 CC for the screening, diagnosis or prognosis of AD in a subject, for  
 CC determining the stage or severity of AD in a subject, for identifying a  
 CC subject at risk of developing AD, or for monitoring the effect of therapy  
 CC administered to a subject having AD. Antibodies capable of binding to  
 CC ADPIs are useful for treating or preventing AD, and for determining the  
 CC efficacy of a given treatment regime. An agent that modulates the  
 CC activity of ADPI is useful in the manufacture of a medicament for the  
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent  
 CC human ADPI tryptic digest peptides  
 XX Sequence 15 AA;  
 Query Match 41.8%; Score 41; DB 5; Length 15;  
 Best Local Similarity 47.1%; Pred. No. 44;  
 Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;  
 QY 1 DQPPDVEKPDLPQFQVQ 17  
 |||||:|  
 DQPPDIE-----FQIR 15  
 Db 5 DQPPDIE-----FQIR 15  
 RESULT 11  
 ADA24138  
 ID ADA24138 standard; peptide; 15 AA.  
 XX AC ADA24138;  
 XX 20-NOV-2003 (first entry)  
 XX Alzheimer's disease-associated protein isoform tryptic peptide #747.  
 XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
 KW Alzheimer's disease-associated protein isoform; ADPI.  
 XX

OS Homo sapiens.  
 XX US2003064411-A1.  
 XX 03-APR-2003.  
 XX 10-DEC-2001; 2001US-00014340.  
 XX 08-DEC-2000; 2000US-0254431P.  
 XX (HERA/) HERATH H M A C.  
 XX (PARE/) PAREKH R B.  
 XX (ROHL/) ROHLFF C.  
 XX Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2003-540784/51.  
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 PT involves analyzing test sample of brain tissue from subject, and  
 PT comparing feature in test sample with that of person(s) free from  
 PT Alzheimer's disease.  
 XX Disclosure; SEQ ID NO 747; 115pp; English.  
 XX The invention relates to a method of screening or diagnosing Alzheimer's  
 CC disease in a subject. The method is useful for screening, diagnosis or  
 CC prognosis of Alzheimer's disease in a subject for determining the stage  
 CC of severity of Alzheimer's disease in a subject, for identifying a  
 CC subject at risk of developing Alzheimer's disease, or for monitoring the  
 CC effect of therapy administered to a subject having Alzheimer's disease.  
 CC The method is also useful in treating vascular dementia, Lewy body  
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or  
 CC depression. The inventive method identifies sensitive and specific  
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.  
 CC It provides therapeutic agents for Alzheimer's disease that works  
 CC quickly, potentially, specifically with fewer side effects. The present  
 CC sequence represents the amino acid sequence of a Alzheimer's disease-  
 CC associated protein isoform tryptic peptide.  
 XX Sequence 15 AA;  
 Query Match 41.8%; Score 41; DB 6; Length 15;  
 Best Local Similarity 47.1%; Pred. No. 44;  
 Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;  
 QY 1 DQPPDVEKPDLPQFQVQ 17  
 |||||:|  
 DQPPDIE-----FQIR 15  
 Db 5 DQPPDIE-----FQIR 15  
 RESULT 12  
 AAR49858  
 ID AAR49858 standard; peptide; 16 AA.  
 XX AC AAR49858;  
 XX 25-MAR-2003 (revised)  
 DT 12-SEP-1994 (first entry)  
 XX Sequence of tryptic digest peptide of bovine glial growth factor III (GGF  
 DE III).  
 XX Glial growth factor; GGF III; mitogen; Schwann cell.  
 XX Bos taurus.  
 XX WO9404560-A1.  
 XX 03-MAR-1994.  
 XX 13-AUG-1993; 93WO-GB001721.  
 XX

PR 14-AUG-1992; 92GB-00017316.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Goodearl ADJ, Stroobant P, Waterfield MD;  
 PI WPI; 1994-083104/10.  
 XX  
 XX New polypeptide factor and peptide(s) from bovine pituitary - having  
 PT mitogenic activity in stimulating division of Schwann cells, used for  
 PT therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell  
 PT tumours, etc.  
 XX  
 XX Claim 32; Page 31; 44pp; English.  
 XX  
 CC A novel polypeptide was purified from bovine pituitaries. It has  
 CC mitogenic activity stimulating the division of Schwann cells, and  
 CC exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was  
 CC digested with trypsin and lysylendopeptidase to obtain novel peptides  
 CC AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49862-  
 CC R49866 were sequenced to completion it was found that none of these  
 CC sequences is apparently related to GGF-I or GGF-II peptide sequences. A  
 CC polypeptide confg. any of the sequences in AAR49858- AAR49871 is claimed,  
 CC as is DNA encoding each of the peptides. The final lys in the sequence is  
 CC bracketed. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 XX Sequence 16 AA;  
 XX  
 Query Match 39.8%; Score 39; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 91;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 6 VERPDLOPF 14  
 Db : ||||: ||  
 2 ISKPDLKPF 10

RESULT 13  
 ABP83082  
 ID ABP83082 standard; peptide; 16 AA.  
 XX  
 AC ABP83082;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1755.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 XX  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 FI Burmer GC, Roush CL, Brown JP;  
 XX

DR WPI; 2003-046718/04.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 XX Claim 1; Fig 2; 523pp; English.  
 PS  
 XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 XX Sequence 16 AA;  
 XX  
 Query Match 39.8%; Score 39; DB 6; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 91;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 QPDPVEKPDLOP 13  
 Db : ||||: ||  
 5 RPPDIRKSDSSP 16

RESULT 14  
 ADM75689  
 ID ADM75689 standard; peptide; 13 AA.  
 XX  
 AC ADM75689;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Potential human MHC class II binding human Factor VIII peptide #909.  
 XX  
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003087161-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 17-APR-2003; 2003WO-EP004063.  
 XX  
 PR 18-APR-2002; 2002EP-00008712.  
 XX  
 PR 24-MAR-2003; 2003EP-00006554.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 FI Jones T, Baker M, Carr FJ;  
 XX

XX WPI; 2003-845307/78.  
 XX  
 XX New modified human Factor VIII molecule being substantially non-  
 PT immunogenic or less immunogenic than non-modified human Factor VIII,  
 PT useful in preparing a composition for treating e.g., Gaucher's disease.  
 XX  
 XX Disclosure; Fig 1; 68pp; English.  
 XX  
 CC The invention relates to a novel modified human Factor VIII molecule. The  
 CC modified human Factor VIII molecule being substantially non-immunogenic  
 CC or less immunogenic than a non-modified human Factor VIII and having  
 CC essentially the same biological specificity and activity when used in  
 CC vivo. The modified human Factor VIII molecule comprises specifically  
 CC altered amino acid residues compared with the non-modified parental  
 CC molecule, where the altered amino acid residues cause a reduction or an  
 CC elimination of one or more of the T-cell epitopes, which act in the  
 CC parental non-modified molecule as MHC class II binding ligands and  
 CC stimulate T-cells. The potential MHC class II binding activity peptide is  
 CC useful for the manufacture of the modified Factor VIII molecule or a  
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
 CC The modified Factor VIII molecule is useful in preparing a composition  
 CC for treating e.g., Gaucher's disease. This sequence represents a human  
 CC Factor VIII peptide with potential human MHC class II binding activity of  
 CC the invention.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 37.8%; Score 37; DB 7; Length 13;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PPVDEKPD 11  
 ||| : ||:  
 DB 5 PPDAQNPD 13  
 ||| : ||:  
 RESULT 15  
 ADM74895  
 ID ADM74895 standard; peptide; 13 AA.  
 AC  
 AC ADM74895;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 XX Potential human MHC class II binding human Factor VIII peptide #115.  
 DE  
 XX human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2003087161-A1.  
 FN  
 XX 23-OCT-2003.  
 PD  
 XX 17-APR-2003; 2003WO-EP004063.  
 PF  
 XX 18-APR-2002; 2002EP-00008712.  
 PR  
 XX 24-MAR-2003; 2003EP-00006554.  
 PR  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Jones T, Baker M, Carr FJ;  
 FI  
 XX WPI; 2003-845307/78.  
 DR  
 XX New modified human Factor VIII molecule being substantially non-  
 PT immunogenic or less immunogenic than non-modified human Factor VIII,  
 PT useful in preparing a composition for treating e.g., Gaucher's disease.  
 XX  
 XX Disclosure; Fig 1; 68pp; English.  
 XX

CC The invention relates to a novel modified human Factor VIII molecule. The  
 CC modified human Factor VIII molecule being substantially non-immunogenic  
 CC or less immunogenic than a non-modified human Factor VIII and having  
 CC essentially the same biological specificity and activity when used in  
 CC vivo. The modified human Factor VIII molecule comprises specifically  
 CC altered amino acid residues compared with the non-modified parental  
 CC molecule, where the altered amino acid residues cause a reduction or an  
 CC elimination of one or more of the T-cell epitopes, which act in the  
 CC parental non-modified molecule as MHC class II binding ligands and  
 CC stimulate T-cells. The potential MHC class II binding activity peptide is  
 CC useful for the manufacture of the modified Factor VIII molecule or a  
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
 CC The modified Factor VIII molecule is useful in preparing a composition  
 CC for treating e.g., Gaucher's disease. This sequence represents a human  
 CC Factor VIII peptide with potential human MHC class II binding activity of  
 CC the invention.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 37.8%; Score 37; DB 7; Length 13;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PPVDEKPD 11  
 ||| : ||:  
 DB 4 PPDAQNPD 12  
 ||| : ||:  
 RESULT 16  
 AAM47777  
 ID AAM47777 standard; peptide; 15 AA.  
 XX  
 AC AAM47777;  
 XX  
 XX 26-FEB-2002 (first entry)  
 DT  
 XX Short chain dehydrogenase 32 peptide fragment.  
 DE  
 XX Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;  
 KW immunological disease; inflammation; gene therapy; cytostatic;  
 KW haemostatic; virucide; immunomodulatory; antiinflammatory.  
 KW  
 XX Unidentified.  
 OS  
 XX CN1307114-A.  
 PN  
 XX 08-AUG-2001.  
 PD  
 XX 28-JAN-2000; 2000CN-00111584.  
 PF  
 XX 28-JAN-2000; 2000CN-00111584.  
 PR  
 XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.  
 PA  
 XX Mao Y, Xie Y;  
 XX  
 XX WPI; 2002-026893/04.  
 PI  
 XX  
 XX New polypeptide for treating malignant tumors and HIV infection,  
 PT comprises the polypeptide-short chain dehydrogenase 32 and polynucleotide  
 PT for coding said polypeptide.  
 PT  
 XX Example 6; Page 27 (Disclosure); 33pp; Chinese.  
 PS  
 XX The present invention relates to short chain dehydrogenase 32 (AAM47776).  
 CC The protein and its coding sequence are useful for treating various  
 CC diseases, such as malignant tumours, haemopathy, HIV infection,  
 CC immunological diseases and inflammations. The present sequence is an N-  
 CC terminal peptide fragment of the protein, which was used in an example  
 CC from the present invention  
 CC  
 XX Sequence 15 AA;  
 SQ

Query Match 36.7%; Score 36; DB 5; Length 15;  
Best Local Similarity 63.6%; Pred. No. 2.3e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 13  
|||||  
DB 5 PPDVEGDDCLP 15

RESULT 17  
ABG67771  
ID ABG67771 standard; peptide; 12 AA.  
XX AC ABG67771;  
XX DT 07-OCT-2002 (first entry)  
XX DE Human ADPI tryptic digest peptide #480.  
XX KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
XX KW Alzheimer's disease-associated feature; neuroprotective;  
XX KW Alzheimer's disease-associated protein isoform; nootropic;  
XX KW ADPI tryptic digest peptide.  
XX OS Homo sapiens.  
XX PN WO200246767-A2.  
XX PD 13-JUN-2002.  
XX PF 29-NOV-2001; 2001WO-GB005289.  
XX PR 08-DEC-2000; 2000US-0254431P.  
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX PI Herath H MAC, Parekh RB, Rohlf C;  
XX DR WPI; 2002-508575/54.  
XX PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
XX PT comprises detecting Alzheimer disease-associated features or Alzheimer  
XX PT disease-associated protein isoforms in brain tissue from the subject.  
XX PS Claim 7; Page 55; 427pp; English.  
XX CC The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
CC subject. The method comprises analysing a sample of brain tissue from a  
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
CC disease-associated features (ADFs), whose relative abundance correlates  
CC with the presence, absence, stage or severity of AD and comparing the  
CC abundance of each feature with the abundance of that chosen feature in  
CC brain tissue from persons free from AD. The invention also describes  
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
CC brain tissue. The methods and compositions of the invention are useful  
CC for the screening, diagnosis or prognosis of AD in a subject, for  
CC determining the stage or severity of AD in a subject, for  
CC subject at risk of developing AD, or for monitoring the effect of therapy  
CC administered to a subject having AD. Antibodies capable of binding to  
CC ADPIs are useful for treating or preventing AD, and for determining the  
CC efficacy of a given treatment regime. An agent that modulates the  
CC activity of ADPI is useful in the manufacture of a medicament for the  
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent  
CC human ADPI tryptic digest peptides  
XX SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 5; Length 12;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 12  
|||||  
DB 3 PPSAEYDPLR 12

RESULT 19  
AAB26624  
ID AAB26624 standard; peptide; 13 AA.  
XX

Db 3 PPSAEYDPLR 12  
|||||  
Query Match 35.7%; Score 35; DB 6; Length 12;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 12  
|||||  
DB 3 PPSAEYDPLR 12

RESULT 18  
ADA23910  
ID ADA23910 standard; peptide; 12 AA.  
XX AC ADA23910;  
XX DT 20-NOV-2003 (first entry)  
XX DE Alzheimer's disease-associated protein isoform tryptic peptide #519.  
XX KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
XX KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
XX KW Alzheimer's disease-associated protein isoform; ADPI.  
XX OS Homo sapiens.  
XX PN US2003064411-A1.  
XX PD 03-APR-2003.  
XX PF 10-DEC-2001; 2001US-00014340.  
XX PR 08-DEC-2000; 2000US-0254431P.  
XX PA (HERA/) HERATH H M A C.  
XX PA (PARE/) PAREKH R B.  
XX PA (ROHL/) ROHLFF C.  
XX PI Herath H MAC, Parekh RB, Rohlf C;  
XX DR WPI; 2003-540784/51.  
XX PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
XX PT involves analyzing test sample of brain tissue from subject, and  
XX PT comparing feature in test sample with that of person(s) free from  
XX PT Alzheimer's disease.  
XX PS Disclosure; SEQ ID NO 519; 115pp; English.  
XX CC The invention relates to a method of screening or diagnosing Alzheimer's  
CC disease in a subject. The method is useful for screening, diagnosis or  
CC prognosis of Alzheimer's disease in a subject for determining the stage  
CC of severity of Alzheimer's disease in a subject, for identifying a  
CC subject at risk of developing Alzheimer's disease, or for monitoring the  
CC effect of therapy administered to a subject having Alzheimer's disease.  
CC The method is also useful in treating vascular dementia, Lewy body  
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or  
CC depression. The inventive method identifies sensitive and specific  
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.  
CC It provides therapeutic agents for Alzheimer's disease that works  
CC quickly, potentially, specifically with fewer side effects. The present  
CC sequence represents the amino acid sequence of a Alzheimer's disease-  
CC associated protein isoform tryptic peptide.  
XX SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 6; Length 12;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVEKPDLPQ 12  
|||||  
DB 3 PPSAEYDPLR 12

RESULT 19  
AAB26624  
ID AAB26624 standard; peptide; 13 AA.  
XX

AAB26624;  
 XX 22-JAN-2001 (first entry)  
 XX  
 DE Partial sequence #24 of Breast Cancer-Associated Protein Isoform.  
 XX  
 KW BPI; breast cancer-associated protein isoform; gene therapy;  
 KW breast cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200055628-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 13-MAR-2000; 2000WO-GB000908.  
 XX  
 XX 12-MAR-1999; 99GB-00005817.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 XX Amess B, Townsend RR, Parekh RB, Waterfield MD, O'hare MJ;  
 XX  
 XX WPI; 2000-602142/57.  
 XX  
 XX Screening, diagnosis of breast cancer and monitoring the effectiveness of  
 PT breast cancer therapy, involves detecting breast cancer-associated  
 PT features and breast cancer-associated protein isoforms.  
 XX  
 XX Disclosure; Page 14; 86pp; English.  
 XX  
 XX The present invention relates to the screening, diagnosis and prognosis  
 CC of breast cancer, for monitoring the effectiveness of breast cancer  
 CC treatment in a human, comprising identifying the presence or absence of  
 CC breast cancer-associated features (BF) or breast cancer-associated  
 CC protein isoforms (BPIs). Antibodies derived from BF and BPIs may be  
 CC useful for the treatment and screening of breast cancer, in particular  
 CC metastatic breast cancer. The present sequence is the partial sequence of  
 CC a BPI  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 35.7%; Score 35; DB 3; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDQLQ 12  
 ||| |||  
 Db 4 PPSAEVPLRL 13  
 ||| |||  
 RESULT 20  
 ABB97740  
 ID ABB97740 standard; peptide; 13 AA.  
 XX  
 AC ABB97740;  
 XX  
 XX 11-JUL-2002 (first entry)  
 DT  
 XX Human procathepsin W epitope peptide #120.  
 DE  
 XX Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200226831-A1.  
 XX  
 XX 04-APR-2002.  
 PD  
 XX 09-JUL-2001; 2001WO-EP007877.  
 PF  
 XX 29-SEP-2000; 2000DE-01048727.  
 PR  
 XX  
 XX

PA (LABS-) LABSOFT DIAGNOSTICS AG.  
 XX  
 XX Weber E;  
 PI  
 XX WPI; 2002-330095/36.  
 DR  
 XX New hybridoma cell lines that produces antibodies specific for human  
 PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.  
 PT  
 XX Disclosure; Fig 1; 23pp; German.  
 PS  
 XX The present invention relates to hybridoma cell lines that produce  
 CC monoclonal antibodies directed against a defined epitope of human  
 CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen  
 CC cells from an animal that has been immunised with recombinant  
 CC procathepsin W. The antibodies produced are useful for analysis,  
 CC diagnosis (detection of human (pro)cathepsin W), purification of  
 CC (pro)cathepsin W (also for clarifying processing of the precursor and  
 CC functional significance of the mature protein), for drug targeting and  
 CC for therapeutic use. The present sequence is an epitope of human  
 CC procathepsin W  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 34.7%; Score 34; DB 5; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VEKPDQLQ 13  
 ||| |||  
 Db 3 VQKPDMPK 10  
 ||| |||  
 RESULT 21  
 ABB97739  
 ID ABB97739 standard; peptide; 13 AA.  
 XX  
 AC ABB97739;  
 XX  
 XX 11-JUL-2002 (first entry)  
 DT  
 XX Human procathepsin W epitope peptide #119.  
 DE  
 XX Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200226831-A1.  
 PN  
 XX 04-APR-2002.  
 PD  
 XX 09-JUL-2001; 2001WO-EP007877.  
 PF  
 XX 29-SEP-2000; 2000DE-01048727.  
 PR  
 XX  
 XX (LABS-) LABSOFT DIAGNOSTICS AG.  
 PA  
 XX Weber E;  
 PI  
 XX WPI; 2002-330095/36.  
 DR  
 XX New hybridoma cell lines that produces antibodies specific for human  
 PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.  
 PT  
 XX Disclosure; Fig 1; 23pp; German.  
 PS  
 XX The present invention relates to hybridoma cell lines that produce  
 CC monoclonal antibodies directed against a defined epitope of human  
 CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen  
 CC cells from an animal that has been immunised with recombinant  
 CC procathepsin W. The antibodies produced are useful for analysis,  
 CC diagnosis (detection of human (pro)cathepsin W), purification of  
 CC (pro)cathepsin W (also for clarifying processing of the precursor and  
 CC functional significance of the mature protein), for drug targeting and  
 CC for therapeutic use. The present sequence is an epitope of human  
 CC procathepsin W  
 XX  
 XX Sequence 13 AA;  
 SQ





KW proline rich.  
 XX  
 OS Rattus sp.  
 XX  
 PN US955259-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 XX  
 PF 19-DEC-1996; 96US-00769745.  
 XX  
 PR 19-DEC-1996; 96US-00769745.  
 XX  
 PA (UYBR-) UNIV BRANDEIS.  
 XX  
 PI Holmes TC, Levitan IB;  
 XX  
 DR WPI; 1999-560490/47.  
 XX  
 XX Identification of compounds that modulate potassium ion channel binding  
 with protein tyrosine kinase SH3 domains.  
 XX  
 PS Disclosure; Col 8; 18pp; English.  
 XX  
 CC A method has been developed for determining if a compound modulates the  
 binding of a potassium ion channel to the SH3 domain of a protein  
 CC tyrosine kinase by contacting the channel with a polypeptide comprising  
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3  
 CC binding. The method is useful for assessing the ability of a compound to  
 CC modulate the formation of channel-SH3 domain complexes to improve the  
 CC understanding of mechanisms of potassium channel blockage and assess the  
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to  
 CC AAY41644 represent mammalian ion channel peptides with proline-rich  
 CC motifs  
 XX  
 SQ Sequence 18 AA;  
 Query Match 33.7%; Score 33; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 7.4e+02;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 QPDPVEKPDLPQ 13  
 |||: |||  
 Db 6 QPPSSPPPLP 17  
 RESULT 25  
 AAE34138  
 ID AAE34138 standard; peptide; 18 AA.  
 AC AAE34138;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE T-cell stimulatory gluten peptide #17.  
 XX  
 KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;  
 KW food-related immune enteropathy; tropical sprue; gluten sensitivity;  
 KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200283722-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002WO-NL000235.  
 XX  
 PR 12-APR-2001; 2001EP-00201377.  
 PR 16-NOV-2001; 2001EP-00204383.  
 XX  
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
 XX  
 PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;  
 WPI; 2003-093000/08.  
 Novel isolated or recombinant human leukocyte antigen-DQ restricted T-cell receptor for treating food-related immune enteropathy such as celiac sprue, tropical sprue, giardiasis and food allergies of childhood.

XX WPI; 2003-093000/08.  
 DR  
 XX Novel isolated or recombinant human leukocyte antigen-DQ restricted T-cell receptor for treating food-related immune enteropathy such as celiac sprue, tropical sprue, giardiasis and food allergies of childhood.  
 PT  
 PT  
 PT  
 XX  
 PS Disclosure; Fig 2; 64pp; English.  
 XX  
 XX The present invention relates to novel isolated or recombinant human leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional equivalent and/or fragment, capable of recognising a prolamine-derived peptide. The invention relates to recombinant or synthetic prolamine derived peptides involved in food-related immune enteropathy. The pharmaceutical composition is useful to treat food-related immune enteropathies such as celiac sprue, tropical sprue, giardiasis or food allergies of childhood. It is useful to induce tolerance, treat gluten-sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the invention are useful to decrease the amount of toxic prolamine-derived peptides in food or food components and to select and/or breed a cereal. The cereal is useful for inclusion in a diet for a gluten sensitive individual. Blocking substances are useful to decrease the binding of HLA-DQ restricted T-cell receptor to a prolamine-derived peptide involved in food-related immune enteropathy for depletion of T-cells bearing the HLA-DQ restricted T-cell receptor. The present sequence is T-cell stimulatory gluten peptide. This sequence is used in the invention  
 XX  
 SQ Sequence 18 AA;  
 Query Match 33.7%; Score 33; DB 6; Length 18;  
 Best Local Similarity 46.7%; Pred. No. 7.4e+02;  
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDLPQFQVQ 17  
 |||: |||  
 Db 2 PPQQFPQPPFPSPQ 16  
 RESULT 26  
 AAE34142  
 ID AAE34142 standard; peptide; 18 AA.  
 XX  
 AC AAE34142;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE T-cell stimulatory gluten peptide #21.  
 XX  
 KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;  
 KW food-related immune enteropathy; tropical sprue; gluten sensitivity;  
 KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200283722-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002WO-NL000235.  
 XX  
 PR 12-APR-2001; 2001EP-00201377.  
 PR 16-NOV-2001; 2001EP-00204383.  
 XX  
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
 XX  
 XX Drijfhout JW, Koning F, Mcadam SN, Sollid LM;  
 WPI; 2003-093000/08.  
 Novel isolated or recombinant human leukocyte antigen-DQ restricted T-cell receptor for treating food-related immune enteropathy such as celiac sprue, tropical sprue, giardiasis and food allergies of childhood.



```
XX SQ Sequence 9 AA;
Query Match 32.7%; Score 32; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPDVEKPD 10
   ||||:|
Db 2 PPDVORVD 9

RESULT 29
AAB21124
ID AAB21124 standard; peptide; 11 AA.
XX
AC AAB21124;
XX
DT 19-JAN-2001 (first entry)
XX
DE Src homology 3 domain binding peptide #1.
XX
KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
OS Synthetic.
XX
FN WO200047607-A1.
XX
PD 17-AUG-2000.
XX
PF 12-FEB-2000; 2000WO-KR000107.
XX
PR 12-FEB-1999; 99AU-00008643.
XX
PR 02-JUN-1999; 99KR-00020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
PI Yoon JH, Han YT, Lee KY;
XX
DR WPI; 2000-533010/48.
XX
PS Claim 3; Page 32; 40pp; English.
XX
CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases
XX
SQ Sequence 11 AA;
Query Match 32.7%; Score 32; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DQPPDVEKPD 10
   :||| |
Db 2 ERPPVPNPDP 11

RESULT 31
AAU01841
ID AAU01841 standard; peptide; 17 AA.
XX
AC AAU01841;
XX
DT 07-SEP-2001 (first entry)
XX
DE Wheat peptide antagonist for A-gliadin 57-73 Q865 #3.
XX
KW Wheat; A-gliadin; 57-75 Q865; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
FN WO200125793-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
```

```
XX DT 19-JAN-2001 (first entry)
XX
DE Src homology 3 domain binding peptide #10.
XX
KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
OS Synthetic.
XX
FN WO200047607-A1.
XX
PD 17-AUG-2000.
XX
PF 12-FEB-2000; 2000WO-KR000107.
XX
PR 12-FEB-1999; 99AU-00008643.
XX
PR 02-JUN-1999; 99KR-00020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
PI Yoon JH, Han YT, Lee KY;
XX
DR WPI; 2000-533010/48.
XX
PS Claim 3; Page 35; 40pp; English.
XX
CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases
XX
SQ Sequence 11 AA;
Query Match 32.7%; Score 32; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DQPPDVEKPD 10
   :||| |
Db 2 ERPPVPNPDP 11

RESULT 31
AAU01841
ID AAU01841 standard; peptide; 17 AA.
XX
AC AAU01841;
XX
DT 07-SEP-2001 (first entry)
XX
DE Wheat peptide antagonist for A-gliadin 57-73 Q865 #3.
XX
KW Wheat; A-gliadin; 57-75 Q865; coeliac disease; gluten intolerance;
KW T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
OS Triticum aestivum.
XX
FN WO200125793-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
```

XX PA (ISIS-) ISIS INNOVATION LTD.  
 XX PI Anderson RP, Hill AVS, Jewell DP;  
 XX DR WPI; 2001-300179/31.  
 XX DR  
 XX PT Diagnosing coeliac disease or susceptibility to the disease in an  
 PT individual, by detecting in vitro or in vivo T cells which bind  
 PT immunodominant T cell epitope obtained from naturally occurring homolog  
 PT of gliadin.  
 XX PS  
 XX PS Example 11; Page 58; 107pp; English.  
 XX CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-  
 CC 73 which is naturally polymorphic in that region and is antagonistic to A  
 CC -gliadin 57-73 Q65 interferon gamma ELISpot (not defined) response. The  
 CC peptides of the invention are used to test mammalian (preferably human)  
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are  
 CC contacted with a blood sample and T cell recognition measured, a positive  
 CC T-cell recognition indicating a susceptibility to coeliac disease. The  
 CC peptides are useful for inducing tolerance in an individual and  
 CC antagonists to the peptides are useful for treating or preventing coeliac  
 CC disease in an individual and for producing an antibody specific to them  
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15  
 CC amino acids in length) whose wild-type sequence can be modified by  
 CC transglutaminase to a sequence that comprises the epitope, but which has  
 CC been modified in such a way that it does not contain sequence which can  
 CC be modified by transglutaminase to a sequence that comprise the epitope  
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac  
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell  
 CC binding of the epitopes are useful for obtaining a transgenic plant cell  
 CC or seed and for the production of a protein. The resultant crop plant is  
 CC useful for obtaining a product of a wheat plant, especially grain, which  
 CC is optionally processed into flour or another grain product. Food  
 CC comprising the antagonistic protein is useful instead of a wild-type  
 CC gliadin  
 XX SQ Sequence 17 AA;  
 XX  
 XX Query Match 32.7%; Score 32; DB 4; Length 17;  
 XX Best Local Similarity 45.5%; Pred. No. 9.7e+02;  
 XX Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDLPQ 13  
 Db ||:: ||  
 7 PPPLYPQTQP 17  
 RESULT 32  
 AAU01840  
 ID AAU01840 standard; peptide; 17 AA.  
 XX AC AAU01840;  
 XX DT 07-SEP-2001 (first entry)  
 XX DE Wheat peptide antagonist for A-gliadin 57-73 Q65 #2.  
 XX KW Wheat; A-gliadin; 57-75 Q65; coeliac disease; gluten intolerance;  
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.  
 XX OS Triticum aestivum.  
 XX PN WO200125793-A2.  
 XX PD 12-APR-2001.  
 XX PF 02-OCT-2000; 2000WO-GB003760.  
 XX PR 01-OCT-1999; 99GB-00023306.  
 XX PA (ISIS-) ISIS INNOVATION LTD.  
 XX PI Anderson RP, Hill AVS, Jewell DP;

XX PI Anderson RP, Hill AVS, Jewell DP;  
 XX DR WPI; 2001-300179/31.  
 XX DR  
 XX PT Diagnosing coeliac disease or susceptibility to the disease in an  
 PT individual, by detecting in vitro or in vivo T cells which bind  
 PT immunodominant T cell epitope obtained from naturally occurring homolog  
 PT of gliadin.  
 XX PS  
 XX PS Example 11; Page 58; 107pp; English.  
 XX CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-  
 CC 73 which is naturally polymorphic in that region and is antagonistic to A  
 CC -gliadin 57-73 Q65 interferon gamma ELISpot (not defined) response. The  
 CC peptides of the invention are used to test mammalian (preferably human)  
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are  
 CC contacted with a blood sample and T cell recognition measured, a positive  
 CC T-cell recognition indicating a susceptibility to coeliac disease. The  
 CC peptides are useful for inducing tolerance in an individual and  
 CC antagonists to the peptides are useful for treating or preventing coeliac  
 CC disease in an individual and for producing an antibody specific to them  
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15  
 CC amino acids in length) whose wild-type sequence can be modified by  
 CC transglutaminase to a sequence that comprises the epitope, but which has  
 CC been modified in such a way that it does not contain sequence which can  
 CC be modified by transglutaminase to a sequence that comprise the epitope  
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac  
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell  
 CC binding of the epitopes are useful for obtaining a transgenic plant cell  
 CC or seed and for the production of a protein. The resultant crop plant is  
 CC useful for obtaining a product of a wheat plant, especially grain, which  
 CC is optionally processed into flour or another grain product. Food  
 CC comprising the antagonistic protein is useful instead of a wild-type  
 CC gliadin  
 XX SQ Sequence 17 AA;  
 XX  
 XX Query Match 32.7%; Score 32; DB 4; Length 17;  
 XX Best Local Similarity 45.5%; Pred. No. 9.7e+02;  
 XX Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDLPQ 13  
 Db ||:: ||  
 7 PPPLYPQTQP 17  
 RESULT 33  
 ADH14690  
 ID ADH14690 standard; peptide; 17 AA.  
 XX AC ADH14690;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Gliadin related epitope peptide.  
 XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 KW vaccine.  
 XX OS Synthetic.  
 XX PN WO2003104273-A2.  
 XX PD 18-DEC-2003.  
 XX PF 05-JUN-2003; 2003WO-GB002450.  
 XX PR 05-JUN-2002; 2002GB-00012885.  
 XX PA (ISIS-) ISIS INNOVATION LTD.  
 XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.  
 XX Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T  
 PT cell receptor.  
 XX  
 XX Example 11; Page 84; 177pp; English.  
 XX  
 CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 17 AA;  
 CC  
 CC Query Match 32.7%; Score 32; DB 8; Length 17;  
 CC Best Local Similarity 45.5%; Pred. No. 9.7e+02;  
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDLPQ 13  
 DB 7 PPELPYPQTQP 17  
 XX  
 XX RESULT 34  
 ADH14691  
 ID ADH14691 standard; peptide; 17 AA.  
 XX  
 XX AC ADH14691;  
 XX  
 XX 11-MAR-2004 (first entry)  
 XX  
 XX Gliadin related epitope peptide.  
 XX  
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 KW vaccine.  
 KW  
 XX Synthetic.  
 OS  
 XX WO2003104273-A2.  
 PN  
 XX 18-DEC-2003.  
 PD  
 XX  
 XX 05-JUN-2003; 2003WO-GB002450.  
 PF  
 XX  
 XX 05-JUN-2002; 2002GB-00012885.  
 PR  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 PA  
 XX  
 XX Anderson RP, Hill AVS, Jewell DP;  
 PI  
 XX WPI; 2004-043640/04.  
 DR  
 XX Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T  
 PT cell receptor.  
 XX  
 XX Example 11; Page 84; 177pp; English.  
 XX  
 CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has

CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 17 AA;  
 CC  
 CC Query Match 32.7%; Score 32; DB 8; Length 17;  
 CC Best Local Similarity 45.5%; Pred. No. 9.7e+02;  
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 PPDVEKPDLPQ 13  
 DB 7 PPELPYPQTQP 17  
 XX  
 XX RESULT 35  
 AAW38909  
 ID AAW38909 standard; peptide; 18 AA.  
 XX  
 XX AC AAW38909;  
 XX  
 XX 27-MAR-1998 (first entry)  
 DT  
 XX  
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.  
 DE  
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;  
 KW PLCgamma; p53bp2; Crk; Yes; Grb2.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9730074-A1.  
 PN  
 XX 21-AUG-1997.  
 PD  
 XX  
 XX 14-FEB-1997; 97WO-US002298.  
 PF  
 XX  
 XX 16-FEB-1996; 96US-00602999.  
 PR  
 XX (CYTO-) CYTOGEN CORP.  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 PA  
 XX Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;  
 PI Rider JE;  
 PI  
 XX WPI; 1997-424972/39.  
 DR  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src tyrosine  
 PT kinase(s) and to stimulate immune response by increasing production of  
 PT certain lymphokine(s), e.g. interleukin-1.  
 XX  
 XX Claim 22; Page 90; 131pp; English.  
 PS  
 XX  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
 CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
 CC can be used in the method to identify inhibitors of their binding to  
 CC their respective SH3 domains, which could be used to modulate the  
 CC pharmacological activity of proteins or polypeptide containing the SH3  
 CC domain. The peptides can also be used to activate Src or Src-related  
 CC protein tyrosine kinases, to stimulate the immune response by increasing

CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
 CC and interleukin-1, or to deliver a conjugated molecule to certain  
 CC cellular compartments containing Src or Src related proteins

XX Sequence 18 AA;

Query Match 32.7%; Score 32; DB 2; Length 18;  
 Best Local Similarity 43.8%; Pred. NO. 1e+03;  
 Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPQFQVQ 17

Db 3 QPPYPPPPYQPIYVQ 18

RESULT 36

ADH14808

ID ADH14808 standard; peptide; 17 AA.

XX

AC ADH14808;

XX

DT 11-MAR-2004 (first entry)

XX

DE Gliadin related epitope peptide.

XX

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.

XX

OS Synthetic.

XX

PN WO2003104273-A2.

XX

PD 18-DEC-2003.

XX

PF 05-JUN-2003; 2003WO-GB002450.

XX

PR 05-JUN-2002; 2002GB-00012885.

XX

PA (ISIS-) ISIS INNOVATION LTD.

XX

PI Anderson RP, Hill AVS, Jewell DP;

XX

DR WPI; 2004-043640/04.

XX

PT Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

XX

PS Example 13; Page 95; 177pp; English.

XX

CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 32.1%; Score 31.5; DB 8; Length 17;

Best Local Similarity 50.0%; Pred. NO. 1.1e+03;

Matches 8; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 2 QPPDVEKPDLPQFQVQ 17

Db 2 QQPPFPQVQ-QPPFPQ 16

RESULT 37

ADH14809

ID ADH14809 standard; peptide; 17 AA.

XX

AC ADH14809;

XX

DT 11-MAR-2004 (first entry)

XX

DE Gliadin related epitope peptide.

XX

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.

XX

OS Synthetic.

XX

PN WO2003104273-A2.

XX

PD 18-DEC-2003.

XX

PF 05-JUN-2003; 2003WO-GB002450.

XX

PR 05-JUN-2002; 2002GB-00012885.

XX

PA (ISIS-) ISIS INNOVATION LTD.

XX

PI Anderson RP, Hill AVS, Jewell DP;

XX

DR WPI; 2004-043640/04.

XX

PT Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

XX

PS Example 13; Page 95; 177pp; English.

XX

CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 32.1%; Score 31.5; DB 8; Length 17;

Best Local Similarity 50.0%; Pred. NO. 1.1e+03;

Matches 8; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 2 QPPDVEKPDLPQFQVQ 17

Db 2 QQPPFPQVQ-QPPFPQ 16

RESULT 38

ADH14821

ID ADH14821 standard; peptide; 18 AA.

XX

AC ADH14821;

XX

DT 11-MAR-2004 (first entry)

XX

DE Gliadin related epitope peptide.

XX

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003104273-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 XX  
 PF 05-JUN-2003; 2003WO-GB002450.  
 XX  
 PR 05-JUN-2002; 2002GB-00012885.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 PI Anderson RP, Hill AVS, Jewell DP;  
 XX  
 DR WPI; 2004-043640/04.  
 XX  
 XX Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T  
 PT cell receptor.  
 XX  
 PS Example 13; Page 95; 17pp; English.  
 XX  
 CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 32.1%; Score 31.5; DB 8; Length 18;  
 Best Local Similarity 53.8%; Pred. No. 1.2e+03;  
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
 QY 2 QPPDVEKPDLPQF 14  
 ||| :|| |||  
 Db 2 QPPFPQPQ-QPF 13  
 RESULT 39  
 AAG97089  
 ID AAG97089 standard; peptide; 10 AA.  
 XX  
 AC AAG97089;  
 XX  
 DT 18-SEP-2001 (first entry)  
 XX  
 DE Human complementary peptide, SEQ ID NO: 3283.  
 XX  
 KW Human; complementary peptide; ligand; drug discovery; drug design.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200142277-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB004776.  
 XX  
 PR 13-DEC-1999; 99GB-00029464.  
 XX  
 PA (PROT-) PROTEOM LTD.  
 XX

PI Roberts GW, Heal JR;  
 XX  
 DR WPI; 2001-408419/43.  
 XX  
 PT A set of peptide ligands consisting of specific complementary peptides to  
 PT proteins encoded by genes of the human genome, useful in an assay for  
 PT screening and identifying of one or more novel peptides which are drug  
 PT candidates or pro-drugs.  
 XX  
 PS Example 4; Page 515; 646pp; English.  
 XX  
 CC The invention relates to a set of complementary peptide ligands generated  
 CC from the human genome. The complementary peptides interact with their  
 CC relevant target proteins encoded in the human genome. They can be used as  
 CC reagents in drug discovery and as lead ligands to facilitate drug design  
 CC and development. The present sequence is a complementary peptide provided  
 CC in the specification  
 XX  
 SQ Sequence 10 AA;  
 Query Match 31.6%; Score 31; DB 4; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 PPDVEKP 9  
 ||| :||  
 Db 3 PPTVQKP 9  
 RESULT 40  
 AAM17451  
 ID AAM17451 standard; peptide; 11 AA.  
 XX  
 AC AAM17451;  
 XX  
 DT 17-JUN-1997 (first entry)  
 XX  
 DE Consensus antibacterial peptide from Podisus maculiventris.  
 XX  
 KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;  
 KW Gram negative; plant treatment.  
 XX  
 OS Podisus maculiventris.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 11  
 FT /note= "X= a peptide residue comprising at least one  
 FT tripeptide Pro-Arg-Pro motif"  
 XX  
 PN FR2732345-A1.  
 XX  
 PD 04-OCT-1996.  
 XX  
 PF 03-APR-1995; 95FR-00004130.  
 XX  
 PR 03-APR-1995; 95FR-00004130.  
 XX  
 PA (RHON ) RHONE POULENC AGROCHIMIE.  
 XX  
 PI Bulet P, Hoffman J, Hetru C, Tchernych S;  
 XX  
 DR WPI; 1996-457711/46.  
 XX  
 PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.  
 PT useful to protect plants against pathogenic bacteria, also for  
 PT antibacterial therapy of animals.  
 XX  
 PS Claim 1; Page 14; 16pp; English.  
 XX  
 CC AAM17451 is a generic sequence of an antibacterial peptide from the bug  
 CC Podisus maculiventris. The proline-rich peptide has antibacterial  
 CC activity against gram negative bacteria. It is useful for protecting  
 CC plants against pathogenic bacteria, but could also be used for



CC antibacterial therapy of animals, including humans. For specific examples

CC see AAW09375-W09378

XX

SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 8.6e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLPQ 13

|:|:|:|

Db 1 VDKPDYRP 8

Search completed: June 7, 2005, 23:10:45

Job time : 99.8727 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 24.5455 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPDLPQFQVQS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	4	US-09-641-803-3
2	33	33.7	14	2	US-07-963-538B-10
3	33	33.7	18	2	US-08-763-745-20
4	32	32.7	18	3	US-08-602-999A-305
5	32	32.7	18	4	US-09-500-124-305
6	31	31.6	17	1	US-08-318-200-21
7	31	31.6	18	1	US-08-336-618-11
8	30.5	31.1	11	2	US-08-343-443B-74
9	30.5	31.1	11	2	US-08-343-443B-94
10	29	29.6	8	4	US-10-365-908-98
11	29	29.6	15	4	US-09-914-259-70
12	29	29.6	17	1	US-08-144-121-12
13	29	29.6	17	2	US-08-735-893-12
14	29	29.6	18	3	US-09-461-697-200
15	28	28.6	11	4	US-09-906-393A-9
16	28	28.6	12	1	US-08-190-788A-43
17	28	28.6	12	1	US-08-190-788A-52
18	28	28.6	12	1	US-08-190-788A-284
19	28	28.6	12	1	US-08-383-474B-48
20	28	28.6	12	1	US-08-383-474B-57
21	28	28.6	12	1	US-08-383-474B-285
22	28	28.6	12	1	US-08-465-391A-43
23	28	28.6	12	1	US-08-465-391A-52
24	28	28.6	12	1	US-08-465-391A-284
25	28	28.6	12	2	US-08-464-538B-43
26	28	28.6	12	2	US-08-464-538B-52
27	28	28.6	12	2	US-08-464-538B-283

28	28	28.6	12	2	US-08-463-076E-87	Sequence 87, Appl
29	28	28.6	12	2	US-08-463-076E-96	Sequence 96, Appl
30	28	28.6	12	2	US-08-463-076E-357	Sequence 357, Appl
31	28	28.6	12	4	US-09-428-082B-673	Sequence 673, App
32	28	28.6	12	4	US-09-428-082B-683	Sequence 683, App
33	28	28.6	12	4	US-09-428-082B-958	Sequence 958, App
34	28	28.6	13	2	US-08-347-335A-13	Sequence 13, Appl
35	28	28.6	15	1	US-08-467-083-53	Sequence 53, Appl
36	28	28.6	15	1	US-08-414-417B-53	Sequence 53, Appl
37	28	28.6	15	2	US-08-486-348A-53	Sequence 53, Appl
38	28	28.6	15	3	US-08-466-680B-53	Sequence 53, Appl
39	28	28.6	15	3	US-08-466-680B-53	Sequence 53, Appl
40	28	28.6	15	4	US-09-354-533-53	Sequence 53, Appl
41	28	28.6	16	1	US-08-150-788A-170	Sequence 170, App
42	28	28.6	16	1	US-08-383-474B-173	Sequence 173, App
43	28	28.6	16	1	US-08-465-391A-170	Sequence 170, App
44	28	28.6	16	2	US-08-464-538B-170	Sequence 170, App
45	28	28.6	16	2	US-08-463-076E-223	Sequence 223, App
46	28	28.6	16	4	US-09-428-082B-786	Sequence 786, App
47	28	28.6	17	1	US-08-150-788A-169	Sequence 169, App
48	28	28.6	17	1	US-08-190-788A-230	Sequence 230, App
49	28	28.6	17	1	US-08-190-788A-233	Sequence 233, App
50	28	28.6	17	1	US-08-190-788A-234	Sequence 234, App
51	28	28.6	17	1	US-08-383-474B-172	Sequence 172, App
52	28	28.6	17	1	US-08-383-474B-233	Sequence 233, App
53	28	28.6	17	1	US-08-383-474B-236	Sequence 236, App
54	28	28.6	17	1	US-08-383-474B-237	Sequence 237, App
55	28	28.6	17	1	US-08-465-391A-169	Sequence 169, App
56	28	28.6	17	1	US-08-465-391A-230	Sequence 230, App
57	28	28.6	17	1	US-08-465-391A-233	Sequence 233, App
58	28	28.6	17	1	US-08-465-391A-234	Sequence 234, App
59	28	28.6	17	2	US-08-464-538B-169	Sequence 169, App
60	28	28.6	17	2	US-08-464-538B-230	Sequence 230, App
61	28	28.6	17	2	US-08-464-538B-233	Sequence 233, App
62	28	28.6	17	2	US-08-464-538B-234	Sequence 234, App
63	28	28.6	17	2	US-08-463-076E-222	Sequence 222, App
64	28	28.6	17	2	US-08-463-076E-284	Sequence 284, App
65	28	28.6	17	2	US-08-463-076E-287	Sequence 287, App
66	28	28.6	17	2	US-08-463-076E-288	Sequence 288, App
67	28	28.6	17	3	US-08-602-999A-338	Sequence 338, App
68	28	28.6	17	4	US-09-500-124-338	Sequence 338, App
69	28	28.6	17	4	US-09-428-082B-785	Sequence 785, App
70	28	28.6	17	4	US-09-428-082B-844	Sequence 844, App
71	28	28.6	17	4	US-09-428-082B-847	Sequence 847, App
72	28	28.6	17	4	US-09-428-082B-848	Sequence 848, App
73	27	27.6	8	1	US-07-923-724-48	Sequence 48, Appl
74	27	27.6	8	2	US-08-609-426A-48	Sequence 48, Appl
75	27	27.6	8	2	US-08-374-652C-38	Sequence 38, Appl
76	27	27.6	9	2	US-08-146-028-431	Sequence 431, App
77	27	27.6	9	2	US-08-146-028-432	Sequence 432, App
78	27	27.6	9	2	US-08-146-028-433	Sequence 433, App
79	27	27.6	9	3	US-08-723-425A-431	Sequence 431, App
80	27	27.6	9	3	US-08-723-425A-432	Sequence 432, App
81	27	27.6	9	3	US-08-723-425A-433	Sequence 433, App
82	27	27.6	9	3	US-09-112-206-431	Sequence 431, App
83	27	27.6	9	3	US-09-112-206-432	Sequence 432, App
84	27	27.6	9	3	US-09-112-206-433	Sequence 433, App
85	27	27.6	9	3	US-09-518-046-148	Sequence 148, App
86	27	27.6	9	4	US-09-790-497A-379	Sequence 379, App
87	27	27.6	9	4	US-09-790-497A-380	Sequence 380, App
88	27	27.6	9	4	US-09-790-497A-381	Sequence 381, App
89	27	27.6	9	4	US-09-790-497A-564	Sequence 564, App
90	27	27.6	9	4	US-09-790-497A-565	Sequence 565, App
91	27	27.6	9	4	US-09-790-497A-566	Sequence 566, App
92	27	27.6	9	4	US-09-576-824A-379	Sequence 379, App
93	27	27.6	9	4	US-09-576-824A-380	Sequence 380, App
94	27	27.6	9	4	US-09-576-824A-381	Sequence 381, App
95	27	27.6	9	4	US-09-680-497-431	Sequence 431, App
96	27	27.6	9	4	US-09-680-497-432	Sequence 432, App
97	27	27.6	9	4	US-09-680-497-433	Sequence 433, App
98	27	27.6	9	4	US-10-365-908-122	Sequence 122, App
99	27	27.6	10	3	US-08-762-428A-1	Sequence 1, Appli
100	27	27.6	10	4	US-10-365-908-114	Sequence 114, App

## ALIGNMENTS

RESULT 1  
US-09-641-803-3  
; Sequence 3, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-3

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPQFQVQS 18  
| | | | | | | | | | | | | | | | | |  
Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2  
US-07-963-538B-10  
; Sequence 10, Application US/07963538B  
; Patent No. 5851983  
; GENERAL INFORMATION:  
; APPLICANT: SUGIYAMA, TAKASHI  
; APPLICANT: KAWIMURA, TAKASHI  
; APPLICANT: MASUDA, KENICHI  
; APPLICANT: OKADA, MASAHIRO  
; APPLICANT: OHTSUKA, EIKO  
; APPLICANT: IMAIZUMI, ATSUSHI  
; APPLICANT: WATANABE, KUNIHITO  
; APPLICANT: SUGA, TETSUYA  
; APPLICANT: MATSUMOTO, YOHICHI  
; APPLICANT: TAKEUCHI, AKIKO  
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND  
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE  
; TITLE OF INVENTION: TECHNOLOGY  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: COOLEY GODWARD LLP  
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/963,538B

; FILING DATE: 20-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/843,359  
; FILING DATE: 25-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/408,483  
; FILING DATE: 22-AUG-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-212399  
; FILING DATE: 17-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-212398  
; FILING DATE: 17-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-355553  
; FILING DATE: 24-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 62-330219  
; FILING DATE: 28-DEC-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NEELEY PH.D., RICHARD L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: TEJN-005/020US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5070  
; TELEFAX: 415-857-0663  
; TELEX: 380816 COOLEY PA  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-963-538B-10

Query Match 33.7%; Score 33; DB 2; Length 14;  
Best Local Similarity 53.8%; Pred. No. 74;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLP 13  
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Db 1 DDPPTVELQGLVP 13

RESULT 3  
US-08-769-745-20  
; Sequence 20, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Rat  
US-08-769-745-20

Query Match 33.7%; Score 33; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 97;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QPPDVEKPDLP 13  
| | | | | | | | | | | |  
Db 6 QPPSSPPPLP 17

RESULT 4  
US-08-602-999A-305  
; Sequence 305, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 457  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-305  
Query Match 32.7%; Score 32; DB 3; Length 18;  
Best Local Similarity 43.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 2 QPPDVEKPDLPFFQVQ 17  
||| |  
Db 3 QPPYPPPPYQPIYPQ 18  
RESULT 5  
US-08-602-999A-305  
; Sequence 305, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-305  
Query Match 32.7%; Score 32; DB 4; Length 18;  
Best Local Similarity 43.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 2 QPPDVEKPDLPFFQVQ 17  
||| |  
Db 3 QPPYPPPPYQPIYPQ 18  
RESULT 6  
US-08-318-200-21  
; Sequence 21, Application US/08318200  
; Patent No. 5578496  
; GENERAL INFORMATION:  
; APPLICANT: Atassi, M. Z.  
; APPLICANT: Ashizawa, T.  
; TITLE OF INVENTION: N-TERMINAL PVA- OR PEG-CONJUGATED  
; TITLE OF INVENTION: PEPTIDES FOR EPITOPE-SPECIFIC IMMUNOSUPPRESSION  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: PO Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,200  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965,670  
; FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-318-200-21

Query Match 31.6%; Score 31; DB 1; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.8e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 PDVEXPDLQPF 14  
| : : : : :  
Db 3 PDSQPDLSNF 13

## RESULT 7

US-08-336-618-11  
Sequence 11, Application US/08336618  
Patent No. 5763590  
GENERAL INFORMATION:  
APPLICANT: Peattie, Debra A.  
APPLICANT: Harding, Matthew W.  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING  
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN  
TITLE OF INVENTION: CDNA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith and Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/336,618  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/963,325  
FILING DATE: 16-OCT-1992  
APPLICATION NUMBER: US 07/777,752  
FILING DATE: 11-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/  
FILING DATE: 09-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: VP191-06A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-618-11

Query Match 31.6%; Score 31; DB 1; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DOPPDVEKPD 10  
| : : : : :  
Db 7 DQPADAEWRD 16

## RESULT 8

US-08-343-443B-74  
Sequence 74, Application US/08343443B  
Patent No. 5968734  
GENERAL INFORMATION:  
APPLICANT: Aurias, Alain  
APPLICANT: Delattre, Olivier  
APPLICANT: Desmaze, Chantal  
APPLICANT: Melot, Thomas  
APPLICANT: Peter, Martine  
APPLICANT: Ploougastel, Beatrice  
APPLICANT: Thomas, Gilles  
APPLICANT: Zucman, Jessica  
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF  
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL  
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS  
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID  
TITLE OF INVENTION: TRANSLOCATIONS  
NUMBER OF SEQUENCES: 129  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weiser & Associates  
STREET: 230 South Fifteenth Street  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: AEDIT 1.0 DOS text editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/343.443B  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR93/00494  
FILING DATE: 19-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/06123  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 989.6121P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-343-443B-74

Query Match 31.1%; Score 30.5; DB 2; Length 11;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 4 PDVEXPDLQPFQV 16  
| : : : : :  
Db 1 PDL---DLDPYQI 10

RESULT 9  
US-08-343-443B-94  
; Sequence 94, Application US/08343443B  
; Patent No. 5968734  
; GENERAL INFORMATION:  
; APPLICANT: Aurias, Alain  
; APPLICANT: Delattre, Olivier  
; APPLICANT: Desmazo, Chantal  
; APPLICANT: Melot, Thomas  
; APPLICANT: Melot, Thomas  
; APPLICANT: Ploougaestel, Beatrice  
; APPLICANT: Thomas, Gilles  
; APPLICANT: Zucman, Jessica  
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF  
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL  
; TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS  
; TITLE OF INVENTION: TUMORS AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID  
; TITLE OF INVENTION: TRANSLOCATIONS  
; NUMBER OF SEQUENCES: 129  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weiser & Associates  
; STREET: 230 South Fifteenth Street  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: AEDIT 1.0 DOS text editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/343,443B  
; FILING DATE: 18-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR93/00494  
; FILING DATE: 19-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92/06123  
; FILING DATE: 20-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 989.6121P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-343-443B-94

Query Match 31.1%; Score 30.5; DB 2; Length 11;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;  
Qy 4 PDVEKPDLPQFQV 16  
Db 1 FDL---DLDPYQI 10

RESULT 10  
US-10-365-908-98  
; Sequence 98, Application US/10365908  
; Patent No. 6797491  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.

; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-98

Query Match 29.6%; Score 29; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6  
Db 2 QPPDV 6

RESULT 11  
US-09-914-259-70  
; Sequence 70, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914,259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: human rhinovirus 2  
US-09-914-259-70

Query Match 29.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLPQ 13  
Db 9 PDLPQ 13

RESULT 12  
US-08-144-121-12  
; Sequence 12, Application US/08144121  
; Patent No. 5610031  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagman, David W.  
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGP-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-144-121-12

Query Match      29.6%; Score 29; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DQPPDVEKPD 10
      :|:|:|:|
Db      1 DENPDIECAD 10

RESULT 13
US-08-735-893-12
; Sequence 12, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: B1K CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,893
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGP-0780.1) MGP-021DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
```

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-735-893-12

Query Match      29.6%; Score 29; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DQPPDVEKPD 10
      :|:|:|:|
Db      1 DENPDIECAD 10

RESULT 14
US-09-461-697-200
; Sequence 200, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-200

Query Match      29.6%; Score 29; DB 3; Length 18;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      6 VEKPDLPQFQV 16
      :|:|:|:|
Db      1 MEKPKLQRHQL 11

RESULT 15
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Patent No. 6780984
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match      28.6%; Score 28; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
```



Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10  
||:|:  
Db 1 PDAKPE 7

## RESULT 16

US-08-190-788A-43  
; Sequence 43, Application US/08190788A  
; Patent No. 5608035  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David N.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 312  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies N.V.  
; STREET: 4001 Miranda Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/190,788A  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,567  
; FILING DATE: 05-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.1  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-190-788A-43

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18  
||:|:  
Db 6 QPYSVQS 12

## RESULT 17

US-08-190-788A-52  
; Sequence 52, Application US/08190788A  
; Patent No. 5608035  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David N.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 312  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies N.V.  
; STREET: 4001 Miranda Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/190,788A  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,567  
; FILING DATE: 05-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.1  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-190-788A-52

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18  
||:|:  
Db 6 QPYSVQS 12

## RESULT 18

US-08-190-788A-284  
; Sequence 284, Application US/08190788A  
; Patent No. 5608035  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David N.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 312  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies N.V.  
; STREET: 4001 Miranda Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/190,788A  
; FILING DATE: 02-FEB-1994

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,567  
FILING DATE: 05-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1019.1  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 284:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 5  
OTHER INFORMATION: /note= "naphthylalanine."  
US-08-190-788A-284

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 19  
US-08-383-474B-48  
Sequence 48, Application US/08383474B  
Patent No. 5767234  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Stephen D.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Baldwin, David N.  
APPLICANT: Jacobs, Jeff W.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
the IL-1 Receptor  
NUMBER OF SEQUENCES: 314  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend & Townsend & Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 01-FEB-1995  
APPLICATION NUMBER: US/08/383,474B  
CLASSIFICATION: 530  
PRIOR APPLICATION INFORMATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1019.3  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-383-474B-48

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 20  
US-08-383-474B-57  
Sequence 57, Application US/08383474B  
Patent No. 5767234  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Stephen D.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Baldwin, David N.  
APPLICANT: Jacobs, Jeff W.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
the IL-1 Receptor  
NUMBER OF SEQUENCES: 314  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend & Townsend & Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 01-FEB-1995  
APPLICATION NUMBER: US/08/383,474B  
CLASSIFICATION: 530  
PRIOR APPLICATION INFORMATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1019.3  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-383-474B-57

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 21  
US-08-383-474B-285  
; Sequence 285, Application US/08383474B  
; Patent No. 5767234  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David W.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: the IL-1 Receptor  
; NUMBER OF SEQUENCES: 314  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend & Townsend & Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/383.474B  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.3  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 285:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 5  
; OTHER INFORMATION: /note= "naphthylalanine."  
US-08-383-474B-285

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 22  
US-08-465-391A-43  
; Sequence 43, Application US/08465391A  
; Patent No. 5786331  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Phillippe R.  
; APPLICANT: Leahy, Ellen M.

; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 405  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465.391A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5786331viel, Vern  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-391A-43

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 23  
US-08-465-391A-52  
; Sequence 52, Application US/08465391A  
; Patent No. 5786331  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Phillippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 405  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California

;  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,391A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5786331viel, Vern  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-465-391A-52

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 24  
US-08-465-391A-284  
; Sequence 284, Application US/08465391A  
; Patent No. 5786331  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Philippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 405  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,391A

;  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5786331viel, Vern  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 284:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 5  
; OTHER INFORMATION: /note="naphthylalanine."  
; US-08-465-391A-284

Query Match 28.6%; Score 28; DB 1; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPQVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 25  
US-08-464-538B-43  
; Sequence 43, Application US/08464538B  
; Patent No. 5861476  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Philippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 402  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,538B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995

; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 16528A-001810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-464-538B-43

Query Match 28.6%; Score 28; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 26  
US-08-464-538B-52  
; Sequence 52, Application US/08464538B  
; Patent No. 5861476  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Philippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 402  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,538B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 16528A-001810

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-464-538B-52

Query Match 28.6%; Score 28; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

RESULT 27  
US-08-464-538B-283  
; Sequence 283, Application US/08464538B  
; Patent No. 5861476  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Philippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 402  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,538B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 16528A-001810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 283:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
; US-08-464-538B-283

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 28
US-08-463-076E-87
; Sequence 87, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; - APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-076E-87

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 29
US-08-463-076E-96
; Sequence 96, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
```

```
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-076E-96

Query Match      28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      12 QPFOVQS 18
      ||: |||
Db      6 QPYSVQS 12

RESULT 30
US-08-463-076E-357
; Sequence 357, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
```

; REGISTRATION NUMBER: 39,381  
; REFERENCE/DOCKET NUMBER: 16528A-001850US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 357:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: /product="OTHER"  
; OTHER INFORMATION: /note="Xaa = naphthylalanine"  
US-08-463-076E-357

Query Match 28.6%; Score 28; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

## RESULT 31

US-09-428-082B-673  
; Sequence 673, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 673  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE  
US-09-428-082B-673

Query Match 28.6%; Score 28; DB 4; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

## RESULT 32

US-09-428-082B-683  
; Sequence 683, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527

; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 683  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE  
US-09-428-082B-683

Query Match 28.6%; Score 28; DB 4; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

## RESULT 33

US-09-428-082B-958  
; Sequence 958, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 958  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE  
; NAME/KEY: misc feature  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine  
US-09-428-082B-958

Query Match 28.6%; Score 28; DB 4; Length 12;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPFOVQS 18  
||: |||  
Db 6 QPYSVQS 12

## RESULT 34

US-08-347-335A-13  
; Sequence 13, Application US/08347335A  
; Patent No. 5856163  
; GENERAL INFORMATION:  
; APPLICANT: Hashida, Miyoko  
; APPLICANT: Abo, Masanobu  
; APPLICANT: Takamura, Yukiko  
; APPLICANT: Kirk, Ole  
; APPLICANT: Halkier, Torben  
; APPLICANT: Pedersen, Sven  
; APPLICANT: Patkar, Shamkant A.

;; APPLICANT: Hansen, Mogens T.  
;; TITLE OF INVENTION: NOVEL ENZYMES  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: No. 58561630 No. 5856163disk of No. 5856163th America, Inc.  
;; STREET: 405 Lexington Avenue, 64th Floor  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: United States of America  
;; ZIP: 10174-6401  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC Compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/347.335A  
;; FILING DATE: 22-DEC-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lambiris, Elias J.  
;; REGISTRATION NUMBER: 33,728  
;; REFERENCE/DOCKET NUMBER: 3706.204-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-867-0123  
;; TELEFAX: 212-878-9655  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 13 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-347-335A-13

Query Match 28.6%; Score 28; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KPDLOPF 14  
Db 3 EPDLMPY 9

RESULT 35  
US-08-467-083-53  
; Sequence 53, Application US/08467083  
; Patent No. 5726023  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,083  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/414,417  
; FILING DATE: 06-JUN-1995

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sharkey, Richard G.  
;; REGISTRATION NUMBER: 32,629  
;; REFERENCE/DOCKET NUMBER: 920010.448C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; TELEX: 3723836 SEEDANBERRY  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-08-467-083-53

Query Match 28.6%; Score 28; DB 1; Length 15;  
Best Local Similarity 45.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLO 12  
Db 5 QPEYVNPQDVR 15

RESULT 36  
US-08-414-417B-53  
; Sequence 53, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417B  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-414-417B-53

Query Match 28.6%; Score 28; DB 1; Length 15;  
Best Local Similarity 45.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLO 12  
Db 5 QPEYVNPQDVR 15



```
RESULT 37
US-08-486-348A-53
; Sequence 53, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-486-348A-53

Query Match 28.6%; Score 28; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQ 12
Db 5 QPEYVNPQDVR 15

RESULT 38
US-08-486-348A-53
; Sequence 53, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-53

Query Match 28.6%; Score 28; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQ 12
Db 5 QPEYVNPQDVR 15

RESULT 39
US-08-466-680B-53
; Sequence 53, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-53

Query Match 28.6%; Score 28; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQ 12
Db 5 QPEYVNPQDVR 15
```

Qy 2 QPPDVEKPDQLQ 12  
|||:|:  
Db 5 QPEYVNPQDVR 15

## RESULT 40

US-09-354-533-53  
; Sequence 53, Application US/09354533  
; Patent No. 6664370  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/354,533  
; FILING DATE: 15-Jul-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:  
US-09-354-533-53

Query Match 28.6%; Score 28; DB 4; Length 15;  
Best Local Similarity 45.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQLQ 12  
|||:|:  
Db 5 QPEYVNPQDVR 15

Search completed: June 7, 2005, 23:23:12  
Job time : 25.5455 secs





; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 759  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-759

Query Match 41.8%; Score 41; DB 14; Length 15;  
Best Local Similarity 47.1%; Pred. No. 39;  
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

Qy 1 DQPDVEKPDLPQFVQ 17  
|||:|:|  
Db 5 DQPDIE-----FQIR 15

RESULT 5  
US-10-225-567A-1755  
; Sequence 1755, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1755  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1755

Query Match 39.8%; Score 39; DB 14; Length 16;  
Best Local Similarity 50.0%; Pred. No. 80;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPDVEKPDLPQ 13  
|||:|:|  
Db 5 RPDIRKSDSP 16

RESULT 6  
US-10-014-340-526  
; Sequence 526, Application US/10014340  
; Publication No. US20030064411A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 526  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-526

Query Match 35.7%; Score 35; DB 14; Length 12;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQ 12  
|||:|:|  
Db 3 PPSAEYDLP 12

RESULT 7  
US-10-474-955-56  
; Sequence 56, Application US/10474955  
; Publication No. US20040241161A1  
; GENERAL INFORMATION:  
; APPLICANT: Drifhout, Jan W.  
; APPLICANT: Koning, Frits  
; APPLICANT: McAdam, Stephan N.  
; APPLICANT: Ludwig, Solliid Magne  
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS  
; FILE REFERENCE: 2799/71244-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/474,955  
; CURRENT FILING DATE: 2003-10-13  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide sequence in pool 51  
; NAME/KEY: MISC FEATURE  
; LOCATION: (7)..(8)  
; OTHER INFORMATION: "y" on position 7 is P/S  
US-10-474-955-56

Query Match 33.7%; Score 33; DB 16; Length 18;  
Best Local Similarity 46.7%; Pred. No. 6.4e+02;  
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQFVQ 17  
|||:|:|  
Db 2 PPQPYFPQPFPSQ 16

RESULT 8  
US-10-474-955-61  
; Sequence 61, Application US/10474955  
; Publication No. US20040241161A1  
; GENERAL INFORMATION:  
; APPLICANT: Drifhout, Jan W.  
; APPLICANT: Koning, Frits  
; APPLICANT: McAdam, Stephan N.  
; APPLICANT: Ludwig, Solliid Magne  
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS  
; FILE REFERENCE: 2799/71244-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/474,955  
; CURRENT FILING DATE: 2003-10-13  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide sequence in pool 54  
; NAME/KEY: MISC FEATURE  
; LOCATION: (7)..(8)  
; OTHER INFORMATION: "y" on position 7 is P/S  
US-10-474-955-61

Query Match 33.7%; Score 33; DB 16; Length 18;  
Best Local Similarity 46.7%; Pred. No. 6.4e+02;  
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPQVEKPDLPQFQV 17  
|||  
Db 2 PPQPYQPQPPPSQ 16

## RESULT 9

US-10-474-955-65  
; Sequence 65, Application US/10474955  
; Publication No. US20040241161A1  
; GENERAL INFORMATION:  
; APPLICANT: Drifhout, Jan W.  
; APPLICANT: Koning, Frits  
; APPLICANT: McAdam, Stephan N.  
; APPLICANT: Ludwig, Solid Magne  
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS A  
; FILE REFERENCE: DQ BINDING PROLAMINE-DERIVED PEPTIDES  
; CURRENT APPLICATION NUMBER: US/10/474,955  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide sequence in pool 57  
; NAME/KEY: MISC FEATURE  
; LOCATION: (7)-(8)  
; OTHER INFORMATION: "Y" on position 7 is P/S  
US-10-474-955-65

Query Match 33.7%; Score 33; DB 16; Length 18;  
Best Local Similarity 46.7%; Pred. No. 6.4e+02;  
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPQVEKPDLPQFQV 17  
|||  
Db 2 PPQPYQPQPPPSQ 16

## RESULT 10

US-10-350-258-6  
; Sequence 6, Application US/10350258  
; Publication No. US20030139345A1  
; GENERAL INFORMATION:  
; APPLICANT: MATTHIAS RATH  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AND M  
; FILE REFERENCE: 119577/23  
; CURRENT APPLICATION NUMBER: US/10/350,258  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/351,317  
; PRIOR FILING DATE: January 23, 2002  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-350-258-6

Query Match 32.7%; Score 32; DB 14; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPQVEKPD 10  
|||  
Db 2 PPQVQVVD 9

## RESULT 11

US-10-901-601-6  
; Sequence 6, Application US/10901601  
; Publication No. US20050095253A1  
; GENERAL INFORMATION:  
; APPLICANT: Cancer Research Campaign Technology Limited  
; APPLICANT: Durrant, Linda G  
; APPLICANT: Spendlove, Ian  
; TITLE OF INVENTION: Tumour Associated Antigen 791Tgp72  
; FILE REFERENCE: SJK/B95758875  
; CURRENT APPLICATION NUMBER: US/10/901,601  
; CURRENT FILING DATE: 2004-07-28  
; PRIOR APPLICATION NUMBER: PCT/GB99/00582  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: GB 9804065.2  
; PRIOR FILING DATE: 1998-02-26  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-901-601-6

Query Match 32.7%; Score 32; DB 17; Length 16;  
Best Local Similarity 63.6%; Pred. No. 7.8e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 3 PPQVEKPDLPQ 13  
|||  
Db 5 PPQV--PNAQP 13

## RESULT 12

US-10-161-791-305  
; Sequence 305, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-305

Query Match 32.7%; Score 32; DB 14; Length 18;  
Best Local Similarity 43.8%; Pred. No. 8.9e+02;  
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPDVEKDPDLPFFQVQ 17  
Db 3 QPPYPPPPYQPIYPQ 18

RESULT 13  
US-09-572-404B-3283  
; Sequence 3283, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 3283  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact with  
; OTHER INFORMATION: Sequence 3284 in this patent.  
US-09-572-404B-3283

Query Match 31.6%; Score 31; DB 10; Length 10;  
Best Local Similarity 71.4%; Pred. No. 6.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9  
Db 3 PPTVQKP 9

RESULT 14  
US-10-601-837-34  
; Sequence 34, Application US/10601837  
; Publication No. US20040053309A1  
; GENERAL INFORMATION:  
; APPLICANT: Holt, Gordon D  
; APPLICANT: Kelly, Michael D  
; APPLICANT: Kennedy, Sandra J  
; APPLICANT: Moyeses, Christopher  
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidney  
; FILE REFERENCE: Response  
; FILE REFERENCE: 2543-1-030  
; CURRENT APPLICATION NUMBER: US/10/601,837  
; CURRENT FILING DATE: 2003-06-23  
; PRIOR APPLICATION NUMBER: PCT/GB01/05777  
; PRIOR FILING DATE: 2001-12-24  
; PRIOR APPLICATION NUMBER: US 60/260392  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Ratus No. US20040053309A1vegicus  
US-10-601-837-34

Query Match 31.6%; Score 31; DB 15; Length 11;  
Best Local Similarity 55.6%; Pred. No. 7.3e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLOPEQ 15  
Db 2 DNPMLPPFQ 10

RESULT 15  
US-10-022-066-144  
; Sequence 144, Application US/10022066  
; Publication No. US20030166057A1  
; GENERAL INFORMATION:  
; APPLICANT: HILDEBRAND, WILLIAM H.  
; APPLICANT: PRILLIMAN, KILEY RAE  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 6680.034  
; CURRENT APPLICATION NUMBER: US/10/022,066  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 09/465,321  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 09/974,366  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 144  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-  
; OTHER INFORMATION: Unknown amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)-  
; OTHER INFORMATION: Unknown amino acid  
US-10-022-066-144

Query Match 30.6%; Score 30; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7  
Db 4 DPPEDMZ 10

RESULT 16  
US-10-022-066-374  
; Sequence 374, Application US/10022066  
; Publication No. US20030166057A1  
; GENERAL INFORMATION:  
; APPLICANT: HILDEBRAND, WILLIAM H.  
; APPLICANT: PRILLIMAN, KILEY RAE  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 6680.034  
; CURRENT APPLICATION NUMBER: US/10/022,066  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
US-10-022-066-374

;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: 09/465,321  
;; PRIOR FILING DATE: 1999-12-17  
;; PRIOR APPLICATION NUMBER: 09/974,366  
;; PRIOR FILING DATE: 2001-10-10  
;; NUMBER OF SEQ ID NOS: 638  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 374  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
;; FEATURE:  
;; NAME/KEY: MOD\_RES  
;; LOCATION: (1)  
;; OTHER INFORMATION: Unknown amino acid  
;; FEATURE:  
;; NAME/KEY: MOD\_RES  
;; LOCATION: (3)  
;; OTHER INFORMATION: Unknown amino acid  
US-10-022-066-374

Query Match 30.6%; Score 30; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPPDVE 7  
| | | | |  
Db 4 DPPDMZ 10

RESULT 17  
US-10-149-138-3845  
;; Sequence 3845, Application US/10149138  
;; Publication No. US20040018971A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Fikes, John  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Celis, Esteban  
;; APPLICANT: Keogh, Elissa  
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
;; FILE REFERENCE: 2060.0140001  
;; CURRENT APPLICATION NUMBER: US/10/149,138  
;; PRIOR FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/33591  
;; PRIOR FILING DATE: 2000-12-11  
;; PRIOR APPLICATION NUMBER: US 09/458,299  
;; NUMBER OF SEQ ID NOS: 4641  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3845  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 15; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDEVKPDLPQ 13  
| | | | |  
Db 1 PEYVNPDPVRP 11

RESULT 18  
US-10-149-138-3845  
;; Sequence 3845, Application US/10149138  
;; Publication No. US20040121946A9  
;; GENERAL INFORMATION:  
;; APPLICANT: Fikes, John  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Celis, Esteban  
;; APPLICANT: Keogh, Elissa  
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
;; FILE REFERENCE: 2060.0140001  
;; CURRENT APPLICATION NUMBER: US/10/149,138  
;; PRIOR FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/33591  
;; PRIOR FILING DATE: 2000-12-11  
;; PRIOR APPLICATION NUMBER: US 09/458,299  
;; PRIOR FILING DATE: 1999-12-11  
;; NUMBER OF SEQ ID NOS: 4641  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3845  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 16; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDEVKPDLPQ 13  
| | | | |  
Db 1 PEYVNPDPVRP 11

RESULT 19  
US-09-891-823-98  
;; Sequence 98, Application US/09891823  
;; Publication No. US20020110566A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Neefe, John R.  
;; APPLICANT: Boux, Leslie J.  
;; APPLICANT: Winnett, Mark T.  
;; APPLICANT: Goldstone, Stephen E.  
;; APPLICANT: Siegel, Marvin  
;; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
;; FILE REFERENCE: 12071-003001  
;; CURRENT APPLICATION NUMBER: US/09/891,823  
;; PRIOR FILING DATE: 2001-10-19  
;; PRIOR APPLICATION NUMBER: US 60/214,202  
;; PRIOR FILING DATE: 2000-06-26  
;; NUMBER OF SEQ ID NOS: 140  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 98  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Human papilloma virus  
US-09-891-823-98

Query Match 29.6%; Score 29; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6  
| | | | |  
Db 2 QPPDV 6



RESULT 20  
US-10-365-908-98  
; Sequence 98, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-98

Query Match 29.6%; Score 29; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6  
| | | | |  
Db 2 QPPDV 6

RESULT 21  
US-10-871-138-98  
; Sequence 98, Application US/10871138  
; Publication No. US20040235741A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/871,138  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-871-138-98

Query Match 29.6%; Score 29; DB 16; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6  
| | | | |  
Db 2 QPPDV 6

RESULT 22  
US-10-033-662-36  
; Sequence 36, Application US/10033662

; Publication No. US20030092197A1  
; GENERAL INFORMATION:  
; APPLICANT: Herman, et al.  
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Cancer  
; FILE REFERENCE: 9195-081  
; CURRENT APPLICATION NUMBER: US/10/033,662  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-662-36

Query Match 29.6%; Score 29; DB 14; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KPDLQP 13  
| | | | |  
Db 1 KPDLSP 6

RESULT 23  
US-09-572-404B-3027  
; Sequence 3027, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 3027  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4  
; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with sequence 3028 in this pa  
US-09-572-404B-3027

Query Match 29.6%; Score 29; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13  
| | | | |  
Db 2 PDLQP 6

RESULT 24  
US-09-992-665-47  
; Sequence 47, Application US/09992665  
; Publication No. US20030092009A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaia Palm  
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE  
; FILE REFERENCE: CEMINES.002A  
; CURRENT APPLICATION NUMBER: US/09/992,665  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 60/249,508  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 13  
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-47

Query Match      29.6%; Score 29; DB 10; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      2 QPPDVEKPDLPQ 13
      ||| : |||
Db      1 QPPSMSSPPPPP 12

RESULT 25
US-10-468-496-1356
; Sequence 1356, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPE AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1356
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1356

Query Match      29.6%; Score 29; DB 16; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DQPPDV 6
      |||||
Db      7 DPPPDP 12

RESULT 26
US-10-468-496-1361
; Sequence 1361, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPE AND USE FOR PREPARING MOLECULES WITH REDUCED
```

```
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1361
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1361

Query Match      29.6%; Score 29; DB 16; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DQPPDV 6
      |||||
Db      6 DPPPDP 11

RESULT 27
US-10-080-608A-70
; Sequence 70, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-10-080-608A-70

Query Match      29.6%; Score 29; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PDLQP 13
      |||||
Db      9 PDLQP 13

RESULT 28
US-10-370-685-159
; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
```

```
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

Query Match          29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
Db 9 PDLQP 13

RESULT 29
US-10-371-067-1
; Sequence 1, Application US/10371067
; Publication No. US20040018587A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NANF-P-003
; CURRENT APPLICATION NUMBER: US/10/371,067
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: (Antibody 8F5) Complexed With Peptide From Human Rhinovirus
; OTHER INFORMATION: (Serotype 2) Viral Capsid Protein Vp2 (Residues 156 -170)
US-10-371-067-1

Query Match          29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
Db 9 PDLQP 13

RESULT 30
US-10-225-567A-1370
; Sequence 1370, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
```

```
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1370
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1370

Query Match          29.6%; Score 29; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 EKPDLPQFQVOS 18
Db 6 KNPDQAIRIAS 17

RESULT 31
US-10-443-349-12
; Sequence 12, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgesson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-349-12

Query Match          29.6%; Score 29; DB 15; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVREKPD 10
Db 1 DENPDIECAD 10

RESULT 32
US-10-841-139-12
; Sequence 12, Application US/10841139
; Publication No. US20040208881A1
; GENERAL INFORMATION:
; APPLICANT: Burgesson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/841,139
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US/10/443,349
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 12  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-841-139-12

Query Match 29.6%; Score 29; DB 16; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DOPDVEKPD 10  
| : ||| : |  
Db 1 DENPDIECAD 10

RESULT 33  
US-09-922-261-200

; Sequence 200, Application US/09922261  
; Patent No. US20020111471A1

; GENERAL INFORMATION:

; APPLICANT: COGENT NEUROSCIENCE, Inc.

; APPLICANT: Lo, Donald C.

; APPLICANT: Barney, Shawn

; APPLICANT: Thomas, Mary Beth

; APPLICANT: Portbury, Stuart D.

; APPLICANT: Puranam, Kasturi

; APPLICANT: Katz, Lawrence C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

; TITLE OF INVENTION: CELL DEATH

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/922,261

; CURRENT FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: US/09/461,697

; PRIOR FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 200

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-922-261-200

Query Match 29.6%; Score 29; DB 9; Length 18;  
Best Local Similarity 54.5%; Pred. No. 2.4e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQFV 16  
: ||| : ||| :  
Db 1 MEKPKLQRHL 11

RESULT 34

US-10-107-532-25

; Sequence 25, Application US/10107532

; Publication No. US20040003418A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Jakobovits, Aya

; APPLICANT: Paris, Mary

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Morrison, Robert Kendall

; APPLICANT: Hubert, Rene S.

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Ge, Wangmao

; APPLICANT: Raitano, Arthur

; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer

; FILE REFERENCE: 51158-200064.00

; CURRENT APPLICATION NUMBER: US/10/107,532

; CURRENT FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: 60/283,112

; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-25

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9  
| : ||| :  
Db 1 QPEPLEKP 8

RESULT 35

US-10-107-532-652

; Sequence 652, Application US/10107532

; Publication No. US20040003418A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Jakobovits, Aya

; APPLICANT: Paris, Mary

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Morrison, Robert Kendall

; APPLICANT: Hubert, Rene S.

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Ge, Wangmao

; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer

; FILE REFERENCE: 51158-200064.00

; CURRENT APPLICATION NUMBER: US/10/107,532

; CURRENT FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: 60/283,112

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/286,630

; PRIOR FILING DATE: 2001-04-25

; NUMBER OF SEQ ID NOS: 6321

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 652

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-107-532-652

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9  
| : ||| :  
Db 2 QPEPLEKP 9

RESULT 36

US-10-107-532-2214

; Sequence 2214, Application US/10107532

; Publication No. US20040003418A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Jakobovits, Aya

; APPLICANT: Paris, Mary

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Morrison, Robert Kendall

; APPLICANT: Hubert, Rene S.

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Ge, Wangmao  
; APPLICANT: Raitano, Arthur  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer  
; FILE REFERENCE: 51158-200064.00  
; CURRENT APPLICATION NUMBER: US/10/107,532  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: 60/283,112  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2214  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-2214

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9  
||| :|||  
Db 1 QPEPLEKP 8

RESULT 37  
US-10-107-532-2776  
; Sequence 2776, Application US/10107532  
; Publication No. US20040003418A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Paris, Mary  
; APPLICANT: Morrison, Robert Kendall  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel E.H.  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Raitano, Arthur  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer  
; FILE REFERENCE: 51158-200064.00  
; CURRENT APPLICATION NUMBER: US/10/107,532  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: 60/283,112  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2776  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-2776

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9  
||| :|||  
Db 1 QPEPLEKP 8

RESULT 38  
US-10-107-532-3286  
; Sequence 3286, Application US/10107532

; Publication No. US20040003418A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Paris, Mary  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Morrison, Robert Kendall  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel E.H.  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Raitano, Arthur  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer  
; FILE REFERENCE: 51158-200064.00  
; CURRENT APPLICATION NUMBER: US/10/107,532  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: 60/283,112  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3286  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-3286

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QPDPVEKP 9  
||| :|||  
Db 1 QPEPLEKP 8

RESULT 39  
US-10-107-532-3991  
; Sequence 3991, Application US/10107532  
; Publication No. US20040003418A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Paris, Mary  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Morrison, Robert Kendall  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel E.H.  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Raitano, Arthur  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; FILE REFERENCE: Entitled 158P3D2 Useful in Treatment and Detection of Cancer  
; FILE REFERENCE: 51158-200064.00  
; CURRENT APPLICATION NUMBER: US/10/107,532  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: 60/283,112  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3991  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-3991

Query Match 28.6%; Score 28; DB 15; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9  
|| :|||  
Db 1 QPEPLEKP 8

## RESULT 40

US-10-107-532-284  
; Sequence 284, Application US/10107532  
; Publication No. US20040003418A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys, Inc.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Paris, Mary  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Morrison, Robert Kendall  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel E.H.  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Raitano, Arthur  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of Cancer  
; FILE REFERENCE: 51158-200064.00  
; CURRENT APPLICATION NUMBER: US/10/107,532  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: 60/283,112  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/286,630  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 6321  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 284  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-107-532-284

Query Match 28.6%; Score 28; DB 15; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.8e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9  
|| :|||  
Db 1 QPEPLEKP 8

Search completed: June 7, 2005, 23:31:34  
Job time : 83 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 16.6909 Seconds  
(without alignments)

103.763 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98

Sequence: 1 DQPPDVKPLQPFQVQS 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	30.6	10	2	urease (EC 3.5.1.5)
2	29	29.6	15	2	protein kinase (EC
3	29	29.6	15	2	plastoquinol-plast
4	28.5	29.1	17	2	fatty acid ethyl e
5	27	27.6	9	2	tetrameric protein
6	25.5	26.0	17	4	hypothetical EWSR1
7	25	25.5	15	2	apolipoprotein A-I
8	24	24.5	10	2	alpha-gliadin 6Ha
9	24	24.5	14	2	bradykinin-like pe
10	24	24.5	18	2	beta-Gliadin 13 -
11	24	24.5	18	2	Na+/K+-exchanging
12	23	23.5	9	2	cytochrome-c oxida
13	23	23.5	11	2	phyllokinin - Rohd
14	23	23.5	12	2	veepakinin M - hor
15	23	23.5	12	2	veepakinin X - hor
16	23	23.5	13	2	Ig lambda chain V-
17	23	23.5	15	2	protein QF200051 -
18	23	23.5	18	2	enkephalin-degradi
19	22	22.4	12	2	tachykinin - Afric
20	22	22.4	16	2	insulin-like growt
21	21	21.4	11	2	ribosomal protein
22	21	21.4	12	2	tachykinin - Afric
23	21	21.4	15	2	dytrophin-associa
24	21	21.4	16	2	leukocyte elastase
25	21	21.4	17	2	caldesmon - rabbit
26	21	21.4	18	2	microtubule-assoc
27	20	20.4	8	2	gene thnslow prote
28	20	20.4	9	2	bradykinin - horn
29	20	20.4	9	2	ATPase R1 subunit

30	20	20.4	9	2	A43065	hydroxyproline-3-b
31	20	20.4	9	2	A61363	bradykinin - commo
32	20	20.4	10	2	A60476	S-layer protein -
33	20	20.4	11	2	S13279	Ile-Ser-bradykinin
34	20	20.4	11	2	YHHU	morphogenetic neur
35	20	20.4	11	2	YHBO	morphogenetic neur
36	20	20.4	11	2	YHJFY	morphogenetic neur
37	20	20.4	11	2	YHXAE	morphogenetic neur
38	20	20.4	12	2	YHRT	hypothetical prote
39	20	20.4	12	2	C64030	actin 7 - soybean
40	20	20.4	13	2	S15755	bradykinin-like pe
41	20	20.4	13	2	A61361	vasotocin-associa
42	20	20.4	15	2	A49155	placental calcium-
43	20	20.4	15	2	I49407	hypothetical 1.5K
44	20	20.4	15	2	B39109	galbladder stone
45	20	20.4	15	2	F57789	vespulin 1 - e
46	20	20.4	17	1	A61339	trypsin (EC 3.4.21
47	20	20.4	17	2	B61334	actin 6 - soybean
48	20	20.4	17	2	S15754	photosystem II pro
49	20	20.4	17	2	S05033	hydroxyproline-ric
50	20	20.4	17	2	S59481	guinaldine oxidore
51	20	20.4	18	2	S29166	dermatan sulfate p
52	20	20.4	18	2	A56798	bradykinin-potenti
53	19.5	19.9	11	2	C37196	bradykinin-potenti
54	19.5	19.9	11	2	D37196	hypothetical MNI/T
55	19.5	19.9	15	4	I38032	ICL2 protein - Par
56	19	19.4	7	2	S71299	Ig heavy chain CRD
57	19	19.4	7	2	PT0283	apolipoprotein A-I
58	19	19.4	8	2	I48935	kidney and bladder
59	19	19.4	9	2	C58502	bradykinin-like pe
60	19	19.4	9	2	A26744	Thr-6 bradykinin -
61	19	19.4	9	2	A61057	bradykinin-like pe
62	19	19.4	9	2	A60579	bradykinin-like pe
63	19	19.4	9	2	A61358	cardioexcitatory n
64	19	19.4	10	2	A32543	complement C3b rec
65	19	19.4	11	2	D45900	megascollakinin -
66	19	19.4	11	2	B26744	hypothetical prote
67	19	19.4	12	2	T46794	Na+/K+-exchanging
68	19	19.4	12	2	S27024	Na+/K+-exchanging
69	19	19.4	12	2	S27023	kaesin - Senegal
70	19	19.4	12	2	S07206	hypothetical prote
71	19	19.4	13	2	T08533	hypothetical prote
72	19	19.4	13	2	S22995	osteoclast functio
73	19	19.4	13	2	A33660	27K protein A 3.4/
74	19	19.4	13	2	S21152	trypsin-releasing
75	19	19.4	15	2	PS0185	small granule S6 c
76	19	19.4	15	2	PS0221	T-cell-receptor be
77	19	19.4	15	2	PC1313	T-cell receptor be
78	19	19.4	16	2	D49655	chlorophyll a/b-bi
79	19	19.4	16	2	PH0759	ribosomal protein
80	19	19.4	17	2	S50901	DNA topoisomerase
81	19	19.4	17	2	S78421	inulinase (EC 3.2.
82	19	19.4	17	2	S10786	alpha-adaptin - bo
83	18.5	18.9	11	1	XASNEA	locustamytotropin I
84	18.5	18.9	15	2	S29207	hementin (EC 3.4.-
85	18.5	18.9	15	2	PM0004	precorrin methyltr
86	18	18.4	6	2	S78764	31K protein 3208 -
87	18	18.4	7	2	I48086	collagen alpha 1(I)
88	18	18.4	8	2	PT0030	beta-glucosidase (
89	18	18.4	9	2	B46250	ribosomal protein
90	18	18.4	9	2	A61620	T-cell receptor be
91	18	18.4	10	2	A61007	calliMIRamide 1 -
92	18	18.4	11	2	S21127	lebetin 1 isoform
93	18	18.4	11	2	PS0257	Ig heavy chain CRD
94	18	18.4	11	2	D56979	
95	18	18.4	11	2	FQ0231	
96	18	18.4	12	2	S36899	
97	18	18.4	12	2	S51737	
98	18	18.4	12	2	E44787	
99	18	18.4	12	2	S71380	
100	18	18.4	13	2	PT0331	

## ALIGNMENTS

## RESULT 1

C35389 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)  
 C:Species: Morganella morganii  
 C>Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004  
 C:Accession: C35389  
 R:Hu, L.F.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
 J. Bacteriol. 172, 3073-3080, 1990  
 A:Title: Morganella morganii urease: purification, characterization, and isolation of gene  
 A:Reference number: A35389; MUID:90264298; PMID:2345135  
 A:Accession: C35389  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <HUA>  
 A:Cross-references: UNIPROT:P17339  
 C:Keywords: hydrolase

Query Match 30.6%; Score 30; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 87;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDVEK 8  
 |||||  
 Db 5 PPEVK 10

## RESULT 2

S20410 protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
 N:Alternate names: LHCI protein kinase  
 C:Species: chloroplast Spinacia oleracea (spinach)  
 C>Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C:Accession: S20410  
 R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.  
 FEBS Lett. 298, 33-35, 1992  
 A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome  
 A:Reference number: S20410; MUID:92183823; PMID:1544419  
 A:Accession: S20410  
 A:Molecule type: protein  
 A:Residues: 1-15 <GAL>  
 A:Cross-references: UNIPROT:Q9T2K8  
 C:Genetics:  
 A:Genome: chloroplast  
 C:Function:  
 A:Description: is responsible for the regulation of energy distribution between photosyn  
 A>Note: does not exhibit redox-controlled activation  
 C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match 29.6%; Score 29; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDVEKDL 11  
 |||||  
 Db 5 PDVEKSTL 12

## RESULT 3

PA0041 plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: PA0041  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugata, A.  
 submitted to JPIB, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
 A:Reference number: PA0001  
 A:Accession: PA0041  
 A:Molecule type: protein  
 A:Residues: 1-15 <KAM>

A:Cross-references: UNIPROT:Q9ZR03; UNIPROT:Q94BI4; UNIPROT:Q9FYB6  
 A:Experimental source: leaf  
 C:Keywords: oxidoreductase

Query Match 29.6%; Score 29; DB 2; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DQPPDVEK 8  
 |||||  
 Db 7 DRVPDMEK 14

## RESULT 4

A42920 fatty acid ethyl ester synthase-II - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A42920  
 R:Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.  
 J. Biol. Chem. 267, 13217-13221, 1992  
 A:Title: Purification and characterization of fatty acid ethyl ester synthase-II from hu  
 A:Reference number: A42920; MUID:92317032; PMID:1618826  
 A:Accession: A42920  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-17 <BOR>  
 A:Cross-references: UNIPROT:Q9UDD6  
 A:Experimental source: myocardium  
 A>Note: sequence extracted from NCBI backbone (NCBI:P107742)

Query Match 29.1%; Score 28.5; DB 2; Length 17;  
 Best Local Similarity 46.2%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 DQPPDVEKPDLP 13  
 |||||  
 Db 1 EDPPD---PDTP 10

## RESULT 5

S66419 tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)  
 C:Species: Spinacia oleracea (spinach)  
 C>Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
 C:Accession: S66419  
 R:Kuwabara, T.  
 FEBS Lett. 371, 195-198, 1995  
 A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spi  
 A:Reference number: S66419; MUID:95402209; PMID:7672127  
 A:Accession: S66419  
 A:Molecule type: protein  
 A:Residues: 1-9 <KUW>  
 A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388

Query Match 27.6%; Score 27; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8  
 |||||  
 Db 5 PDVEK 9

## RESULT 6

I51887 hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
 C:Accession: I51887  
 R:Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; Mc  
 Am. J. Pathol. 143, 1294-1300, 1993  
 A:Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripher



A:Reference number: 151887; MUID:94056652; PMID:8238248

A:Accession: 151887

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-17 <DOM>

A:Cross-references: GB:S66911; NID:g440935; PIDN:AAB28655.1; PID:g440936

C:Comment: This sequence is the chimeric product of a translocation mutation.

C:Genetics:

A:Gene: EWSR1/FLI1; EWS/FLI-1

A:Map position: 22q12/11q24

C:Keywords: fusion protein

Query Match 26.0%; Score 25.5; DB 4; Length 17;

Best Local Similarity 46.2%; Pred. No. 7.9e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 1 DQPPDVEKPDLPQ 13

| | | |

Db 7 DEGPDL---DLDP 16

#### RESULT 7

A60221

apolipoprotein A-I - common carp (fragment)

C:Species: Cyprinus carpio (common carp)

C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004

C:Accession: A60221

R:Harrel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.

J. Neurochem. 55, 1237-1243, 1990

A:Title: Fish apolipoprotein A-I has heparin binding activity: implication for nerve reg

A:Reference number: A60221; MUID:90376100; PMID:2118944

A:Accession: A60221

A:Molecule type: protein

A:Residues: 1-15 <HAR>

A:Cross-references: UNIPROT:Q7LZ45

A:Note: protein from plasma and from optic nerve yielded the same sequence

C:Keywords: lipid binding; lipoprotein

Query Match 25.5%; Score 25; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPP 4

| | | |

Db 1 DQPP 4

#### RESULT 8

B61218

alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)

C:Species: Haynaldia villosa, Dasypyrum villosum

C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004

C:Accession: B61218

R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.

Biochem. Genet. 29, 207-211, 1991

A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald

A:Reference number: A61218; MUID:91315394; PMID:1859356

A:Accession: B61218

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SHE>

A:Cross-references: UNIPROT:Q7M1F6

C:Keywords: seed; storage protein

Query Match 24.5%; Score 24; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 7.4e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

Query Match 24.5%; Score 24; DB 2; Length 18;

Best Local Similarity 62.5%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

#### RESULT 9

A61362

bradykinin-like peptide III - Japanese pond frog

C:Species: Rana nigromaculata (Japanese pond frog)

C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004

A:Accession: A61362

R:Nakajima, T.

Chem. Pharm. Bull. 16, 2088-2089, 1968

A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata

A:Reference number: A61362; MUID:69117202; PMID:5751736

A:Accession: A61362

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <NAK>

A:Cross-references: UNIPROT:Q7LZ53

C:Superfamily: unassigned animal peptides

C:Keywords: skin

Query Match 24.5%; Score 24; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16

| | | | |

Db 3 PGFSPPRV 10

#### RESULT 10

PN0149

beta-Gliadin 13 - Aegilops longissima (fragment)

C:Species: Aegilops longissima

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C:Accession: PN0149

R:Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A:Reference number: PN0146; MUID:90283493; PMID:2354218

A:Accession: PN0149

A:Molecule type: protein

A:Residues: 1-18 <ODI>

A:Cross-references: UNIPROT:Q7M1Z6

A:Experimental source: strain K-202

C:Superfamily: gliadin

Query Match 24.5%; Score 24; DB 2; Length 18;

Best Local Similarity 62.5%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

#### RESULT 11

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A54195

R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-AT

A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <ESM>

A:Cross-references: UNIPROT:Q9PSP6

A:Experimental source: rectal gland

A:Note: sequence extracted from NCBI backbone (NCBIP:149363)

C:Keywords: hydrolase

Query Match

24.5%; Score 24; DB 2; Length 18;

Best Local Similarity

62.5%; Pred. No. 1.4e+03;

Matches

5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

6 VEKPDLPQ 13

| | | | |

Db 3 VPVPQLQP 10

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespa kinin-M, a novel bradykinin analogue containing hydroxyproline, in the vespa

A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <K1S>

A;Cross-references: UNIPROT:Q7M3T3

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 23.5%; Score 23; DB 2; Length 12;  
Best Local Similarity 37.5%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16  
| | | | |  
Db 4 PGFSPFRI 11

RESULT 15

A61359

vespakinin X - hornet (Vespa xanthoptera)

C;Species: Vespa xanthoptera

C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004

C;Accession: A61359

R;Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 25, 936-941, 1977

A;Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The str

A;Reference number: A61359; MUID:87187853; PMID:264186

A;Accession: A61359

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Cross-references: UNIPROT:Q7M3T2

C;Superfamily: unassigned animal peptides

C;Keywords: venom

Query Match 23.5%; Score 23; DB 2; Length 12;  
Best Local Similarity 37.5%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16  
| | | | |  
Db 4 PGFSPFRI 11

RESULT 16

G61458

Ig lambda chain V-II region (AZI) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996

C;Accession: G61458; PLO159

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass

A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: G61458

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycop

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.5%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPDV 6  
| | | | |  
Db 6 QPPSV 10

```
RESULT 17
PA0098
Protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0098
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0098
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 23.5%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKPD 10
Db 1 QKPDIPXDD 9

RESULT 18
A60915
enkephalin-degrading aminopeptidase (EC 3.4.11.1), puromycin-sensitive - rat (fragment)
N:Alternate names: aminoenkephalinase; aminopeptidase MII
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A60915
R:Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moosaw, C.R.; Hersh, L.B.
J. Neurochem. 54, 547-554, 1990
A:Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enzyme
A:Reference number: A60915; MUID:90132681; PMID:2299352
A:Accession: A60915
A:Molecule type: protein
A:Residues: 1-18 <DYB>
A:Cross-references: UNIPROT:Q7M076
A:Note: this sequence represents the N-terminus of both soluble and membrane-associated
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: hydrolase

Query Match 23.5%; Score 23; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
Db 1 PEKPFPE 7

RESULT 19
S07436
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambatin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S07436
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in
A:Reference number: S07436
A:Accession: S07436
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Cross-references: UNIPROT:P08614
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 22.4%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
```

```
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
Db 2 PPDPDR 7

RESULT 20
JH0517
insulin-like growth factor-binding protein 4 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0517
R:Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
A:Reference number: JH0515; MUID:92109718; PMID:1722398
A:Accession: JH0517
A:Molecule type: protein
A:Residues: 1-16 <COL>
A:Cross-references: UNIPROT:P24854
A:Experimental source: serum
C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h

Query Match 22.4%; Score 22; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
Db 8 PPSEK 13

RESULT 21
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: S78765
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: protein
A:Residues: 1-11 <GRA>
A:Cross-references: UNIPROT:Q7M374
C:Keywords: mitochondrion
F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 21.4%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEK 8
Db 4 DVPKDLTK 11

RESULT 22
S10059
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambates-kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S10059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in
A:Reference number: S07436
A:Accession: S10059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Cross-references: UNIPROT:P08613
```

A;Experimental source: skin  
A;Note: the source is designated as Hylambates maculatus  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 21.4%; Score 21; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DVERPD 10  
| | | |  
Db 1 DEPKPD 6

## RESULT 23

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0665

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the dystrophin-associated glycoprotein complex (A3a-IV) in rabbit skeletal muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0665

A;Molecule type: protein

A;Residues: 1-15 &lt;FOS&gt;

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 21.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.4e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15  
| | | |  
Db 9 PNAPPYQ 15

## RESULT 24

A60551

leukocyte elastase (EC 3.4.21.37) - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: A60551

R;Axelsson, L.; Bergengfeldt, M.; Björk, P.; Olsson, R.; Ohlsson, K.

Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A;Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin a

A;Reference number: A60551; MUID:90193608; PMID:1690443

A;Accession: A60551

A;Molecule type: protein

A;Residues: 1-16 &lt;AXE&gt;

A;Cross-references: UNIPROT:Q8MJD1

A;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 21.4%; Score 21; DB 2; Length 16;  
Best Local Similarity 44.4%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 KPDLOPFQ 16  
| | | |  
Db 8 QPAPFPFW 16

## RESULT 25

B44873

caldesmon - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: B44873

R;Ikebe, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei  
A;Reference number: A44873; MUID:91378498; PMID:1898046  
A;Accession: B44873  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <IKE>  
A;Cross-references: UNIPROT:Q9TRW1  
A;Experimental source: skeletal myosin  
A;Note: sequence extracted from NCBI backbone (NCBIP:63202)  
C;Superfamily: caldesmon

Query Match 21.4%; Score 21; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKP 9  
| | | |  
Db 8 VEKP 11

## RESULT 26

S26664

microtubule-associated protein tau - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 26-May-1995

C;Accession: S26664

R;Andreadis, A.; Brown, W.M.; Kosik, K.S.

Biochemistry 31, 10626-10633, 1992

A;Title: Structure and novel exons of the human tau gene.

A;Reference number: S26662; MUID:93041757; PMID:1420178

A;Accession: S26664

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-18 &lt;AND&gt;

A;Cross-references: EMBL:X61375

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

Query Match 21.4%; Score 21; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 4.1e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DQPDVEKPDQ 12  
| | | |  
Db 8 DHP--LQGPDLR 17

## RESULT 27

I57532

gene Tnfrs1 protein - rat (fragment)

C;Species: Rattus sp. (rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997

C;Accession: I57532

R;Banerjee-Basu, S.; Buonanno, A.

Mol. Cell. Biol. 13, 7019-7028, 1993

A;Title: cis-acting sequences of the rat tropinin I slow gene confer tissue- and develop

A;Reference number: I57532; MUID:94019373; PMID:8413291

A;Accession: I57532

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-8 &lt;RES&gt;

A;Cross-references: GB:S66172; NID:g432603

C;Genetics:

A;Gene: Tnfrs1

Query Match 20.4%; Score 20; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVEK 8  
| | | |  
Db 2 PEVER 6

## RESULT 28

S65433  
bradykinin - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65433  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, E.  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran  
A:Reference number: S65431; MUID:96215437; PMID:8647080  
A:Accession: S65433  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <WIJ>  
A:Note: the source is designated as Haematobia irritans exigua

Query Match 20.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15  
| | | |  
Db 3 PGFSPFR 9

## RESULT 29

D48186  
ATPase R1 subunit - wood tobacco (fragment)  
C:Species: Nicotiana sylvestris (wood tobacco)  
C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: D48186  
R:De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993  
A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase  
A:Reference number: A48186; MUID:93317598; PMID:8327463  
A:Accession: D48186  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <DE1>  
A:Cross-references: UNIPROT:Q9T2T4  
A:Experimental source: pollen  
A:Note: sequence extracted from NCBI backbone (NCBI:P134871)

Query Match 20.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 DLQPFQ 15  
| | | |  
Db 4 DLAPYK 9

## RESULT 30

A43065  
hydroxyproline-3-bradykinin - frog (Helleophryne purcellii)  
C:Species: Helleophryne purcellii  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A43065  
R:Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.  
Experientia 35, 1133, 1979  
A:Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South A  
A:Reference number: A43065; MUID:80024576; PMID:488255  
A:Accession: A43065  
A:Molecule type: protein  
A:Residues: 1-9 <NAK>  
A:Cross-references: UNIPROT:Q7LZ17  
C:Keywords: bradykinin; hydroxyproline; skin  
F:3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15  
| | | |  
Db 3 PGFSPFR 9

## RESULT 31

A61363  
bradykinin - common frog  
C:Species: Rana temporaria (common frog)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: A61363  
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.  
Comp. Biochem. Physiol. A 14, 43-52, 1965  
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.  
A:Reference number: A61363  
A:Accession: A61363  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <ANA>  
A:Cross-references: UNIPROT:Q7LZJ8  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 20.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFQ 15  
| | | |  
Db 3 PGFSPFR 9

## RESULT 32

A60476  
S-layer protein - Bacillus thuringiensis (fragment)  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 09-Jul-2004  
R:Luckevich, M.D.; Beveridge, T.J.  
J. Bacteriol. 171, 6656-6667, 1989  
C:Accession: A60476  
A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.  
A:Reference number: A60476; MUID:90078111; PMID:2592346  
A:Accession: A60476  
A:Molecule type: protein  
A:Residues: 1-10 <LUC>  
A:Cross-references: UNIPROT:P49325  
C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 20.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLOP 13  
| | | |  
Db 6 PDVXP 10

## RESULT 33

S13279  
Ile-Ser-bradykinin - human (fragment)  
N:Alternate names: T-kinin  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S13279  
R:Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.  
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990  
A:Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan  
A:Reference number: S13279; MUID:91166748; PMID:2076202  
A:Accession: S13279  
A:Molecule type: protein  
A:Residues: 1-11 <WUN>  
A:Cross-references: UNIPROT:Q7M4P1  
C:Keywords: bradykinin

Query Match 20.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15  
 Db 5 PGFSFPR 11

RESULT 34  
 YHUU  
 morphogenetic neuropeptide - human  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
 C:Accession: B01427; A01427  
 R: Bodenmuller, H.; Schaller, H.C.  
 Nature 293, 579-580, 1981  
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis  
 A:Reference number: A93266; MUID:82035850; PMID:7290191  
 A:Accession: B01427  
 A:Molecule type: protein  
 A:Residues: 1-11 <BOD>  
 A:Cross-references: UNIPROT:P01163  
 R: Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8  
 Db 1 QPPGSK 7

RESULT 35  
 YHBO  
 morphogenetic neuropeptide - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
 C:Accession: C01427; A01427  
 R: Bodenmuller, H.; Schaller, H.C.  
 Nature 293, 579-580, 1981  
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis  
 A:Reference number: A93266; MUID:82035850; PMID:7290191  
 A:Accession: C01427  
 A:Molecule type: protein  
 A:Residues: 1-11 <BOD>  
 A:Cross-references: UNIPROT:P01163  
 R: Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8  
 Db 1 QPPGSK 7

Qy 2 QPPDVEK 8  
 Db 1 QPPGSK 7

RESULT 36  
 YHJFHY  
 morphogenetic neuropeptide - Hydra attenuata  
 N:Alternate names: head activator  
 C:Species: Hydra attenuata  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
 C:Accession: B93900; A01427  
 R: Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A:Reference number: A93900  
 A:Accession: B93900  
 A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 A:Cross-references: UNIPROT:P01163  
 R: Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8  
 Db 1 QPPGSK 7

RESULT 37  
 YHXA  
 morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)  
 N:Alternate names: head activator  
 C:Species: Anthopleura elegantissima  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
 C:Accession: A93900; A01427  
 R: Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A:Reference number: A93900  
 A:Accession: A93900  
 A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 A:Cross-references: UNIPROT:P01163  
 R: Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8  
 Db 1 QPPGSK 7

## RESULT 38

YHRT

morphogenetic neuropeptide - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004

C/Accession: A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A/Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele

A/Reference number: A93266; MUID:82035850; PMID:7290191

A/Accession: A01427

A/Molecule type: protein

A/Residues: 1-11 &lt;BOD&gt;

A/Cross-references: UNIPROT:P01163

R:Birt, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A/Title: Synthesis of a new neuropeptide, the head activator from hydra.

A/Reference number: A91296; MUID:82050803; PMID:7297679

A/Contents: annotation; synthesis

A/Note: the synthetic peptide was identical with the natural peptide in chemical structu

C/Comment: This peptide was first isolated from nerve cells of hydra and was called head

C/Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic

F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match	20.4%;	Score 20;	DB 2;	Length 11;
Best Local Similarity	57.1%;	Pred. No. 3.4e+03;		
Matches	4;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0;

## RESULT 39

C64030

hypothetical protein H11451 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 10-Oct-1997

C/Accession: C64030

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64030

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-12 &lt;TIGR&gt;

A/Cross-references: GB:U32823; GB:L42023; MUID:91574281; PID:91574296; TIGR:H11451

Query Match	20.4%;	Score 20;	DB 2;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 3.7e+03;		
Matches	3;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

## RESULT 40

S15755

actin 7 - soybean (fragment)

C/Species: Glycine max (soybean)

C/Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C/Accession: S15755

R:Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated

A/Reference number: S15754; MUID:91346640; PMID:2102831

A/Accession: S15755

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 <PEA>

A/Cross-references: UNIPROT:P15987; EMBL:X17120; MUID:918527; PID: CAA34980.1; PID:G18528

C/Superfamily: actin

C/Keywords: cytoskeleton; structural protein

Query Match	20.4%;	Score 20;	DB 2;	Length 13;
Best Local Similarity	75.0%;	Pred. No. 4.1e+03;		
Matches	3;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Search completed: June 7, 2005, 23:20:37

Job time : 17.6909 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 79.2 seconds  
(without alignments)

116,382 Million cell updates/sec

Title: US-10-691-157-3

Perfect score: 98  
Sequence: 1 DQPPVEXKPDLPQVQVS 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	31.6	15	1 MK1_PALPR	P80408 palomena pr
2	31	31.6	15	2 MK2_PALPR	P80410 palomena pr
3	31	31.6	16	1 MK2B_PALPR	P80410 palomena pr
4	31	31.6	16	1 MK3_PALPR	P80411 palomena pr
5	31	31.6	18	2 P82674	P82674 bos taurus
6	30	30.6	10	1 URE3_MORMO	P17339 morganella
7	29	29.6	15	2 Q9T2K8	Q9T2K8 spinacia ol
8	29	29.6	17	2 Q8UT86	Q8UT86 human immun
9	28.5	29.1	17	2 Q9UND6	Q9UND6 homo sapien
10	28	28.6	18	2 Q6ICE7	Q6ICE7 homo sapien
11	28	28.6	18	2 Q9R4E0	Q9R4E0 pseudomonas
12	28	28.6	16	2 O13167	O13167 xiphias gla
13	27	27.6	10	2 Q9PRY8	Q9PRY8 triakis scy
14	27	27.6	12	2 P82325	P82325 pium sativ
15	27	27.6	15	2 Q6WPA4	Q6WPA4 sturnus vul
16	27	27.6	15	2 Q6WPA5	Q6WPA5 anas platyr
17	27	27.6	15	2 Q6WPA6	Q6WPA6 podager nac
18	27	27.6	15	2 Q6WPA7	Q6WPA7 falco pereg
19	27	27.6	15	2 Q6WPA8	Q6WPA8 strix urale
20	27	27.6	15	2 Q6WPA9	Q6WPA9 surina ulul
21	27	27.6	15	2 Q6WPA9	Q6WPA9 surina ulul
22	27	27.6	16	2 Q9UC12	Q9UC12 homo sapien
23	27	27.6	18	2 Q8MNX0	Q8MNX0 bombyx mori
24	27	27.6	18	2 Q9S8G8	Q9S8G8 psophocarpu
25	26	26.5	13	2 Q9UWH3	Q9UWH3 homo sapien
26	26	26.5	15	2 Q9UWH3	Q9UWH3 thermococcu
27	26	26.5	15	2 Q9TR14	Q9TR14 bos taurus
28	26	26.5	17	2 Q9JX08	Q9JX08 mus musculu
29	26	26.5	17	2 P90402	P90402 human immun
30	26	26.5	17	2 Q9Q709	Q9Q709 human immun
31	26	26.5	18	2 Q9TWL5	Q9TWL5 lucilia cup

32	26	26.5	18	2 Q9X3E9	Q9X3E9 prochloroco
33	25.5	26.0	17	2 P83061	P83061 spinacia ol
34	25	25.5	15	2 Q7L245	Q7L245 cyprinus ca
35	25	25.5	18	2 Q9UCT9	Q9UCT9 homo sapien
36	24	24.5	10	2 Q7M1P6	Q7M1P6 haynaldia v
37	24	24.5	11	2 Q9S618	Q9S618 prochloroco
38	24	24.5	12	2 P82328	P82328 pium sativ
39	24	24.5	13	2 Q9R3R6	Q9R3R6 prochloroco
40	24	24.5	14	2 Q9R3R6	Q9R3R6 rana nigrom
41	24	24.5	17	2 Q6Y1B2	Q6Y1B2 branchiost
42	24	24.5	17	2 Q9IB06	Q9IB06 prochloroco
43	24	24.5	18	2 Q7M1Z6	Q7M1Z6 aegilops lo
44	24	24.5	18	2 Q67971	Q67971 synchococc
45	23.5	24.0	9	2 Q9UCS8	Q9UCS8 homo sapien
46	23.5	24.0	14	2 Q6JVP2	Q6JVP2 otomappus e
47	23.5	24.0	14	2 Q6JVP4	Q6JVP4 jefea ping
48	23.5	24.0	14	2 Q6JVP6	Q6JVP6 angeliptyum
49	23	23.5	9	1 COX2_THUOB	P80975 thunnus obo
50	23	23.5	9	2 Q9R735	Q9R735 streptomyce
51	23	23.5	11	1 BRKP_PHYRO	Q71452 phyllomedus
52	23	23.5	12	1 VESP_VESMA	Q7M32 vespa manda
53	23	23.5	12	1 VESP_VESXA	Q7M32 vespa xanth
54	23	23.5	12	2 Q6EPAS	Q6EPAS chlamydomon
55	23	23.5	14	2 Q6JVP7	Q6JVP7 elaphandra
56	23	23.5	14	2 Q6JVP7	Q6JVP7 dimerostemm
57	23	23.5	14	2 Q6JVP1	Q6JVP1 blattvillia
58	23	23.5	14	2 Q6JVP2	Q6JVP2 baltimora r
59	23	23.5	14	2 Q6JVP4	Q6JVP4 angeliptyum
60	23	23.5	15	1 PBI_PROTR	P83764 protocentru
61	23	23.5	15	1 PBI_PROTR	P83766 protocentru
62	23	23.5	15	2 Q6JVP9	Q6JVP9 dimerostemm
63	23	23.5	17	2 P97135	P97135 mycobacteri
64	23	23.5	18	2 Q7S9C7	Q7S9C7 neurospora
65	23	23.5	18	2 Q7YMC5	Q7YMC5 pogonatum s
66	23	23.5	18	2 Q7M076	Q7M076 ractus norv
67	22	22.4	10	2 Q9L5W6	Q9L5W6 liberibacte
68	22	22.4	11	2 Q8HYM4	Q8HYM4 felis silve
69	22	22.4	12	1 PPK4_PERAM	P82619 periplaneta
70	22	22.4	12	1 TKN2_KASMA	P08614 kassina mac
71	22	22.4	13	2 Q6PF13	Q6PF13 mus musculu
72	22	22.4	14	2 Q9RIU3	Q9RIU3 ractus norv
73	22	22.4	15	2 Q08936	Q08936 nicotiana t
74	22	22.4	15	2 Q69142	Q69142 streptococc
75	22	22.4	16	1 IBP4_PIG	P24854 sus scrofa
76	22	22.4	16	2 Q69F17	Q69F17 strephylum
77	22	22.4	16	2 Q9QV12	Q9QV12 mus sp. mep
78	22	22.4	17	2 Q7S179	Q7S179 neurospora
79	22	22.4	17	2 Q46667	Q46667 macropus ro
80	22	22.4	17	2 Q95M99	Q95M99 equus cabal
81	22	22.4	17	2 Q9EUP4	Q9EUP4 thermus the
82	22	22.4	17	2 Q9QVC2	Q9QVC2 ractus sp.
83	22	22.4	17	2 Q9QVC6	Q9QVC6 ractus norv
84	22	22.4	17	2 Q919B0	Q919B0 human papil
85	22	22.4	17	2 Q6PUY7	Q6PUY7 hepatitis c
86	22	22.4	18	2 Q96C65	Q96C65 homo sapien
87	22	22.4	18	2 Q9POM3	Q9POM3 homo sapien
88	22	22.4	18	2 Q56610	Q56610 vibrio chol
89	22	22.4	18	2 Q9WTP8	Q9WTP8 ractus norv
90	22	22.4	18	2 Q919A8	Q919A8 human papil
91	22	22.4	18	2 Q919B3	Q919B3 human papil
92	22	22.4	18	2 Q919B5	Q919B5 human papil
93	22	22.4	18	2 Q919B7	Q919B7 human papil
94	22	22.4	18	2 Q919B9	Q919B9 human papil
95	22	22.4	18	2 Q919C5	Q919C5 human papil
96	22	22.4	18	2 Q919C7	Q919C7 human papil
97	22	22.4	18	2 Q919C9	Q919C9 human papil
98	22	22.4	18	2 Q919D1	Q919D1 human papil
99	22	22.4	18	2 Q919D3	Q919D3 human papil
100	22	22.4	18	2 Q919D5	Q919D5 human papil

ALIGNMENTS

## RESULT 1

MK1\_PALPR STANDARD; PRT; 15 AA.  
ID MK1\_PALPR  
AC P80408;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Metalnikowin I.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
OC Pentatominae; Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin."  
RL J. Insect Physiol. 42:81-89(1996).  
CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
KW Antibiotic: Direct protein sequencing. Insect immunity.  
SQ SEQUENCE 15 AA; 1838 MW; 21407B663CE46299 CRC64;

## Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 15;  
Pred. No. 7.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13  
|:|:|:|:|  
DB 1 VDKPDYRP 8

## RESULT 2

MK2\_PALPR STANDARD; PRT; 15 AA.  
ID MK2\_PALPR  
AC P80409;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Metalnikowin IIA.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
OC Pentatominae; Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin."  
RL J. Insect Physiol. 42:81-89(1996).  
CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
KW Antibiotic: Direct protein sequencing. Insect immunity.  
SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

## Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 15;  
Pred. No. 7.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13  
|:|:|:|:|  
DB 1 VDKPDYRP 8

## RESULT 3

MK2B\_PALPR STANDARD; PRT; 16 AA.  
ID MK2B\_PALPR  
AC P80410;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Metalnikowin IIB.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
OC Pentatominae; Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin."  
RL J. Insect Physiol. 42:81-89(1996).  
CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
KW Antibiotic: Direct protein sequencing. Insect immunity.  
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

## Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 16;  
Pred. No. 7.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13  
|:|:|:|:|  
DB 1 VDKPDYRP 8

## RESULT 4

MK3\_PALPR STANDARD; PRT; 16 AA.  
ID MK3\_PALPR  
AC P80411;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Metalnikowin III.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
OC Pentatominae; Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cocciandich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin."  
RL J. Insect Physiol. 42:81-89(1996).  
CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
KW Antibiotic: Direct protein sequencing. Insect immunity.  
SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

## Query Match

Best Local Similarity 31.6%; Score 31; DB 1; Length 16;  
Pred. No. 7.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDLP 13  
|:|:|:|:|  
DB 1 VDKPDYRP 8

Db 1 VDKPYRP 8

RESULT 5

ID P82674 PRELIMINARY; PRT; 18 AA.

AC P82674;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI\_TaxId=9913;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Liver;

RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H.,

RA Sprenull L.L.;

RT "Identification of four proteins from the small subunit of the

RL mammalian mitochondrial ribosome using a proteomics approach.";

CC Submitted (Jun-2000) to Swiss-Prot.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- MASS SPECTROMETRY: MW=974.58; METHOD=Electrospray; RANGE=1-8.

CC -1- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR InterPro; IPR000851; Ribosomal\_S5.

DR PROSITE; PS00585; RIBOSOMAL\_S5; PARTIAL.

KM PROSITE; PS00585; RIBOSOMAL\_S5; PARTIAL.

FT NON\_TER 1 1

FT NON\_CONS 6 9

FT UNSURE 17 17 OR I.

FT NON\_TER 18 18

SQ SEQUENCE 18 AA; 2127 MW; 199BC913E25FAR CRC64;

Query Match

Best Local Similarity 31.6%; Score 31; DB 2; Length 18;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDKPYDLO 12

Db 10 PDKPYDLO 18

RESULT 6

URE3 MORMO

ID URE3 MORMO STANDARD; PRT; 10 AA.

AC P17339;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)

DE (Urease 6 kDa subunit) (Fragment).

GN Name=urea; (Proteus morganii).

OS Morganella morganii (Proteus morganii).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Morganella.

OX NCBI\_TaxId=582;

RN [1]

RP SEQUENCE.

RP MEDLINE=90264298; PubMed=2345135;

RA Hu L.-T., Nicholson B.B., Jones B.D., Lynch M.J., Mobley H.L.T.;

RA "Morganella morganii urease: purification, characterization, and

RT isolation of gene sequences.";

RT J. Bacteriol. 172:3073-3080(1990).

CC -1- CATALYTIC ACTIVITY: Urea + H(2O) = CO(2) + 2 NH(3).

CC -1- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the urease gamma subunit family.

DR PIR; C35389; C35389.

DR HAMAP; MF\_00739; -; 1.

KM Direct protein sequencing; Hydrolase.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match

Best Local Similarity 30.6%; Score 30; DB 1; Length 10;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDKPYR 8

Db 5 PDKPYR 10

RESULT 7

ID Q972K8 PRELIMINARY; PRT; 15 AA.

AC Q972K8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE LHCII kinase, 64 kDa kinase (Fragment).

OS Spinacia oleracea (Spinach).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI\_TaxId=3562;

RN [1]

RP SEQUENCE.

RP MEDLINE=92183823; PubMed=1544419; DOI=10.1016/0014-5793(92)80016-A;

RA Gal A., Herrmann R.G., Lottepeich F., Ohad I.;

RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with

RL the cytochrome complex.";

RL FEBS Lett. 298:33-35(1992).

DR PIR; S20410; S20410.

DR PIR; S66419; S66419.

FT NON\_TER 1 1

FT NON\_CONS 15 15

SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33B CRC64;

Query Match

Best Local Similarity 29.6%; Score 29; DB 2; Length 15;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PDKPYDLO 11

Db 5 PDKPYDLO 12

RESULT 8

Q8UT86

ID Q8UT86 PRELIMINARY; PRT; 17 AA.

AC Q8UT86;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Vpr protein.

GN Name=vpr;

OS Human immunodeficiency virus 1.

OC Viruses; Retrovirus; Retroviridae; Lentivirus.

OX NCBI\_TaxId=11676;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=21988475; PubMed=11991972;

RA DOI=10.1128/JVI.76.11.5435-5451.2002;

RA Novitsky V., Smith U.R., Gilbert P., Chang S.-Y., Peter T., Thior I.,

RA Williams C., Ndung'u T., Klein I., Gassetlwe S., Vanberg P.,

RA Foley B.T., Gaoletke S., Rybak N., Gassetlwe S., Vanberg P.,

RA Marink R., Lee T.-H., Essex M.;

RT "Human immunodeficiency virus type 1 subtype C molecular phylogeny:

RT consensus sequence for an AIDS vaccine design?";

RT J. Virol. 76:5435-5451(2002).

```

RN [2]
RP SEQUENCE FROM N.A.
RA Novitsky V.A., McInane M.F., Chigwedere P., Ndung'u T., Klein I.,
RA Chang S.-Y., Peter T., Thior I., Rybak N., Gassettswe S., Vannberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBS databases.
DR EMBL; AF443097; ALU34763.1; -
DR HSSP; Q73369; IESX.
DR Pfam; PF00522; VPR; 1.
KM AIDS.
SQ SEQUENCE 17 AA; 2018 MW; 58CA6A463F4457C7 CRC64;

Query Match 29.6%; Score 29; DB 2; Length 17;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DQPPVEXKPDLP 14
DB 2 EQAPEDQGFQREPY 15

RESULT 9
Q9UND6 PRELIMINARY; PRT; 17 AA.

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AC Q9UND6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92317032; PubMed=1618826;
RA Bora P.S., Wu X., Spilburg C.A., Lange L.G.;
RT "Purification and characterization of fatty acid ethyl ester synthase-
RT I from human myocardium."
RL J. Biol. Chem. 267:13217-13221(1992).
DR PIR; A42920; A42920.
DR GO; GO:0005829; C:cytosol; NAS.
DR GO; GO:0003039; F:fatty-acyl-ethyl-ester synthase activity; NAS.
DR GO; GO:0006067; P:ethanol metabolism; NAS.
DR GO; GO:0006331; P:fatty acid metabolism; NAS.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 17 AA; 1755 MW; 3456973BF1B39273 CRC64;

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Query Match 29.1%; Score 28.5; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

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QY 1 DQPPVEXKPDLP 13
DB 1 EDPFPD---PDTPP 10

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RESULT 10

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ID Q6LCE7 PRELIMINARY; PRT; 18 AA.
AC Q6LCE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cycloxygenase-1 (EC 1.14.99.1) (Fragment).
OS Name=PTSG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97056106; PubMed=8900446; DOI=10.1016/0090-6980(95)00158-1;
RA Hla T.;
RT "Molecular characterization of the 5.2 KB isoform of the human
RT cyclooxygenase-1 transcript."
RL Prostaglandin 51:81-85(1996).
DR EMBL; U63946; AAC50632.1; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004666; F:prostaglandin-endoperoxide synthase activity; IEA.
KM Oxidoreductase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1884 MW; AFD1BD7AA764188D CRC64;

Query Match 28.6%; Score 28; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DQPPVEXKPDLP 12
DB 6 DDGPAVERPSTE 17

RESULT 11
Q9RAE0 PRELIMINARY; PRT; 18 AA.

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AC Q9RAE0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dipeptidyl aminopeptidase type I (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=96200096; PubMed=8631703;
RA Ogasawara M., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
RA Morikawa Y.;
RT "A novel dipeptidyl aminopeptidase from Pseudomonas sp. strain WO24."
RL J. Bacteriol. 178:1283-1286(1996).
SQ SEQUENCE 18 AA; 1813 MW; 369B0386C394A737 CRC64;

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```

Query Match 28.6%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3 PDPVEX 8
DB 5 PDPVAK 10

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RESULT 12

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ID O13167 PRELIMINARY; PRT; 18 AA.
AC O13167;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein S7 (Fragment).
OS Xiphias gladius (swordfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Xiphiidae; Xiphias.
OX NCBI_TaxID=8245;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Brazil16D, J26B, Peru9C, Peru9A, Peru5C, Peru5B, Japan26C, and
RC Brazil16B;
RA Chow S., Takeyama H.;
RT "Intron length variation observed in the creatine kinase and ribosomal
RT protein genes of the swordfish Xiphias gladius."
RL Fisheries Sci. 64:397-402(2000).

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DR EMBL; U95521; AAB58281.1; -  
 DR EMBL; U89244; AAB58379.1; -  
 DR EMBL; U95515; AAB58275.1; -  
 DR EMBL; U95516; AAB58276.1; -  
 DR EMBL; U95517; AAB58277.1; -  
 DR EMBL; U95518; AAB58278.1; -  
 DR EMBL; U95519; AAB58279.1; -  
 DR EMBL; U95520; AAB58280.1; -  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR Ribosomal protein.  
 KW NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1978 MW; E716F226CC5BEB15 CRC64;

Query Match 28.6%; Score 28; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 2.5e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PDVERPD 10  
 DB 11 PNGEKPD 17

RESULT 13  
 Q9PRY8 PRELIMINARY; PRT; 10 AA.  
 AC Q9PRY8;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Angiotensin I.  
 OS Triakis scyllium (leopard shark) (Triakis scyllia).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
 OC Triakis.  
 OK NCBI\_TaxID=30494;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=94141412; PubMed=8308464;  
 RA Takai Y., Hasagawa Y., Watanabe T.X., Nakajima K., Hazon N.;  
 RT "A novel angiotensin I isolated from an elasmobranch fish.";  
 RJ J. Endocrinol. 139:281-285(1993).  
 SQ SEQUENCE 10 AA; 1284 MW; 20F02FD761E04B47 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 KPDLOPFQV 16  
 DB 2 RPYIHFPOL 10

RESULT 14  
 P82325 PRELIMINARY; PRT; 12 AA.  
 ID P82325;  
 AC P82325;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 24, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid (SPOT106) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucoside I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OK NCBI\_TaxID=3888;  
 RN (1)  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Pelletier J.-B., Fritso G., Kallme D.E., Roepstorff P., Nilsson F.,  
 RA Adamka I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 targeting analysis of lumenal and peripheral thylakoid proteins.";

RL Plant Cell 12:319-341(2000).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR  
 CC PERIPHERY.  
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.3, ITS MW IS: 18.2 kDa.  
 CC GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0009579; C:thylakoid; IEA.  
 KW Chloroplast; Thylakoid.  
 KW NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1236 MW; CEAC7ADCC02633452 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 2.3e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VEKPDLOP 13  
 DB 5 VNKPELLP 12

RESULT 15  
 Q6WFA4 PRELIMINARY; PRT; 15 AA.  
 ID Q6WFA4;  
 AC Q6WFA4;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE BMAL1 (Fragment).  
 GN Name=Bmal1;  
 OS Sturnus vulgaris (Starling).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Sturnus.  
 OK NCBI\_TaxID=9172;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwiner E.;  
 RT "Comparative analysis of avian BMAL1 and CLOCK protein sequences: a  
 RT search for features associated with owl nocturnal behaviour.";  
 RJ Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 DR EMBL; AY291073; AAQ55074.1; -  
 FT NON\_TER 1 1  
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPDVERP 9  
 DB 5 PPDTRSP 11

RESULT 16  
 Q6WFA5 PRELIMINARY; PRT; 15 AA.  
 ID Q6WFA5;  
 AC Q6WFA5;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE BMAL1 (Fragment).  
 GN Name=Bmal1;  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OK NCBI\_TaxID=8839;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwiner E.;  
 RT "Comparative analysis of avian BMAL1 and CLOCK protein sequences: a

RT search for features associated with owl nocturnal behaviour."  
 DL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 RL EMBL; AY291072; AAQ55073.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1514 MW; 832261D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9  
 |||  
 Db 5 PPDTRSP 11

## RESULT 17

ID Q6WFA6 PRELIMINARY; PRT; 15 AA.  
 AC Q6WFA6;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)  
 DE BMA1 (Fragment).  
 GN Name=Bma1;  
 OS Podager nacunda (nacunda nighthawk).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Caprimulgiformes; Caprimulgidae;  
 OC Chordellinae; Podager.  
 OK NCBI\_TaxID=135181;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwinner E.;  
 RT search for features associated with owl nocturnal behaviour."  
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 DR EMBL; AY291071; AAQ55072.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9  
 |||  
 Db 5 PPDTRSP 11

## RESULT 18

ID Q6WFA7 PRELIMINARY; PRT; 15 AA.  
 AC Q6WFA7;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)  
 DE BMA1 (Fragment).  
 GN Name=Bma1;  
 OS Falco peregrinus (Peregrine falcon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Falconiformes; Falconidae; Falco.  
 OK NCBI\_TaxID=8954;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwinner E.;  
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a  
 search for features associated with owl nocturnal behaviour."  
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 DR EMBL; AY291070; AAQ55071.1; -.  
 FT NON\_TER 1 1

FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;  
 Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9  
 |||  
 Db 5 PPDTRSP 11

## RESULT 19

ID Q6WFA8 PRELIMINARY; PRT; 15 AA.  
 AC Q6WFA8;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)  
 DE BMA1 (Fragment).  
 GN Name=Bma1;  
 OS Strix uralensis (Ural owl).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Strix.  
 OK NCBI\_TaxID=36305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwinner E.;  
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a  
 search for features associated with owl nocturnal behaviour."  
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 DR EMBL; AY291069; AAQ55070.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PPDVEKP 9  
 |||  
 Db 5 PPDTRSP 11

## RESULT 20

ID Q6WFA9 PRELIMINARY; PRT; 15 AA.  
 AC Q6WFA9;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)  
 DE BMA1 (Fragment).  
 GN Name=Bma1;  
 OS Surnia ulula (Northern hawk owl).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Surnia.  
 OK NCBI\_TaxID=69940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14662308; DOI=10.1016/S1096-4959(03)00276-8;  
 RA Fidler A.E., Gwinner E.;  
 RT "Comparative analysis of avian BMA1 and CLOCK protein sequences: a  
 search for features associated with owl nocturnal behaviour."  
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003).  
 DR EMBL; AY291068; AAQ55069.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1457 MW; 83226D2D37373AAS CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;

Matches	4;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	3	PPDYVEKP	9						
Db	5	PPDTTSP	11						

RESULT	21
06WFB0	
ID	06WFB0 PRELIMINARY; PRT; 15 AA.
AC	Q6WFB0;
DT	05-JUL-2004 (TREMBLrel, 27, Created)
DT	05-JUL-2004 (TREMBLrel, 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel, 27, Last annotation update)
DE	BMAL1 (Fragment).
GN	Name=BMAL1;
OS	Tyto alba (Barn owl).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Archosauria; Aves; Neognathae; Strigiformes; Tytonidae; Tyto.
OX	NBI1_TaxID=56313;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=14662308; DOI=10.1016/S1096-4459(03)00276-8;
RA	Ridler A.E., Gwimer E.;
RT	"Comparative analysis of avian BMAL1 and CLOCK protein sequences;
RT	search for features associated with owl nocturnal behaviour."
RL	Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 136:861-874(2003)
DR	EMBL; AY291067; AAO5068.1; -.
FT	NON TER 1 15
FT	NON TER 1 15
SQ	SEQUENCE 15 AA; 1457 MW; 83226DD2037373AA5 CRC64;

Query Match	27.6%	Score 27;	DB 2;	Length 15;
Best Local Similarity	57.1%	Pred. No. 2.9e+03;		
Matches	4;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	3	PPDVEKP	9	
Db	5	PPDTRSP	11	

Q	SEQUENCE	16 AA
Q	16 AA; 1960 MW; 7A26C49A1B0A35E CRC64;	
R		
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gw		
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gy		
gz		
ha		
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hc		
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hh		
hi		
hj		

Query Match	27.6%	Score 27	DB 2	Length 16
Best Local Similarity	38.5%	Pred. No.	3.1e+03	
Matches 5	Conservative	4	Mismatches	4
			Indels	0
			Gaps	0

Qy	5	DVEKPDLOPFQVQ	17
		: : : :	
Db	4	DEEKMEIQEIQLK	16

RESULT 23  
Q8MNX0

ID	Q8MNX0	PRELIMINARY;	PRT;	18 AA.
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AC Q8R8X0; 2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RC MEDLINE=22316879; PubMed=12429116; DOI=10.1016/S0965-1748(02)00104-2;  
 RA Severs U., Eytachylo T., Iatrou K.;  
 RT "The orphan nuclear receptors Bme75A and Bme75C of the silkmoth Bombyx  
 RT mori: hormonal control and ovarian expression.";  
 RL Insect Biochem. Mol. Biol. 32:1643-1652(2002).  
 DR EMBL; AF332552; AAM43817.1; --  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 FT TER 1  
 SQ SEQUENCE 18 AA; 2012 MW; 072CCD18DF0E0D5E CRC64;

	Query Match	27.6%	Score 27;	DB 2;	Length 18;
	Best Local Similarity	50.0%	Pred. No.	3.5e+03;	
	Matches	.4;	Conservative	2;	Mismatches 2; Indels 0;
Gy	2 QPDPVEKP	9			
	: : : :				
db	4 KPDSFEED	11			

RESULT 24			
	09S8G8		
ID	09S8G8	PRELIMINARY;	PRT; 18 AA.
AC	09S8G8;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	Proline-rich protein (Fragment).		
OS	Psophocarpus tetragonolobus (soa bean) (Asparagus bean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids		
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;		
OC	Psophocarpaceae.		
OX	NCBI_TaxId=3891;		
RN	[1]		
RP	SEQUENCE:		
RX	MEDLINE=95277008; PubMed=7757337;		
RA	Esaka M., Hayakawa H.;		
RT	"Specific secretion of proline-rich proteins by salt-adapted winged		
RL	bean cells";		
RL	Plant Cell Physiol. 36:441-446(1995).		
QL	SEQUENCE 18 AA; 2252 MW; 4FPDDIDIA18BS094A CRC64;		

Query Match	27.6%;	Score 27;	DB 2;	Length 18;
Best Local Similarity	83.3%;	Pred. No. 3.5e+03;		
Matches	5;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	4 PDVEKP	9		
Db	9 PVEKRP	14		

RESULT 25	
Q9UEE2	
ID Q9UEE2	PRELIMINARY;
	PRT;
	13 AA

DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)

```

DE ERGB transcription factor (Fragment).
GN Name=FL11;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Obata K., Hiraaga H., Nojima T., Yoshida M.C., Abe S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012625; BAA32806.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1541 MW; 2C67798CB566AB7 CRC64;

Query Match
Best Local Similarity 26.5%; Score 26; DB 2; Length 13;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EKPDLPQOV 16
Db 2 QRPDPYQI 11

RESULT 26
Q9UWH3 PRELIMINARY; PRT; 15 AA.
AC Q9UWH3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Keto-valine-ferredoxin oxidoreductase beta-subunit, VOR beta
DE (Fragment).
OS Thermococcus litoralis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCB1_TaxId=2265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoglutarate ferredoxin oxidoreductase, a
RT new and reversible coenzyme A-dependent enzyme involved in peptide
RT fermentation by hyperthermophilic archaea.";
RL J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 15 AA; 1740 MW; 5C0D6371B91D4C4F CRC64;

Query Match
Best Local Similarity 26.5%; Score 26; DB 2; Length 15;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PPVVEKPDLP 14
Db 4 PADVKKRLTF 15

RESULT 27
Q9TR14 PRELIMINARY; PRT; 15 AA.
AC Q9TR14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCB1_TaxId=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96187584; PubMed=8611748;

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RA Nakai Y., Nishimura T., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C.";
RL Biochim. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79B4777 CRC64;

Query Match
Best Local Similarity 26.5%; Score 26; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVVEKPDLP 11
Db 3 PPVVEVPEV 11

RESULT 28
Q9JK08 PRELIMINARY; PRT; 17 AA.
AC Q9JK08;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN Name=Fbp2; Synonyms=FBPase 2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=20237676; PubMed=10773464; DOI=10.1016/S0378-1119(00)00079-2;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
RT fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Stein S.;
RT "Mouse liver fructose-1,6-bisphosphatase: Gene structure,
RT transcriptional start point, chromosomal localization, cDNA cloning,
RT characterization of the recombinant protein, and analysis of tissue-
RT specific expression.";
RL Arch. Biochem. Biophys. 0:0-0(0).
DR EMBL: AJ243021; CAB90668.1; -.
DR MGD: MGI:95491; Fbp2.
DR GO: GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0042578; F:phosphoric ester hydrolase activity; IEA.
DR GO: GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro: IPR000146; In_Fb_phptase.
DR ProDom: PD001491; In_Fb_phptase; 1.
KW Hydrolase.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1887 MW; E2609FPD33922CB8 CRC64;

Query Match
Best Local Similarity 26.5%; Score 26; DB 2; Length 17;
Matches 7; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DQPPVEKPDLP 13
Db 4 DEPS--EKDALQP 14

RESULT 29
P90402 PRELIMINARY; PRT; 17 AA.
AC P90402;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

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DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Vpr proteain.
GN Name=Vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2321B;
RX MEDLINE=97225063; PubMed=9071436;
RA Choi D.J., Dube S., Spicer T.P., Slade H.B., Jensen F.C., Polesz B.J.;
RT "HIV type 1 isolate 2321, the strain used to make a therapeutic HIV
type 1 immunogen, is intersubtype recombinant."
RL AIDS Res. Hum. Retroviruses 13:357-361(1997).
DR EMBL; U76035; AAB54106.1; -.
DR HSP; Q73369; 1ESX.
DR InterPro; IPR000012; Retrov_vpr/X.
DR Pfam; PF00522; VPR; 1.
KW AIDS.
SQ SEQUENCE 17 AA; 1969 MW; 58CA75563F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 17;
Best Local Similarity 30.8%; Pred. No. 4.7e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DQPPVEKPDLPQ 13
DB 2 EQAPEDQGFQREP 14

RESULT 30
ID Q9Q709 PRELIMINARY; PRT; 17 AA.
AC Q9Q709;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Truncated Vpr.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20436917; PubMed=10983640;
RA Janssens W., Laukkanen T., Salminen M.O., Carr J.K., McCutchan F.E.;
RT "HIV-1 subtype H near-full length genome reference strains and
RT analysis of subtype-H-containing inter-subtype recombinants."
RL AIDS 14:1533-1543(2000).
DR EMBL; AF190128; AAF18410.1; -.
DR HSP; Q73369; 1ESX.
DR InterPro; IPR000012; Retrov_vpr/X.
DR Pfam; PF00522; VPR; 1.
KW AIDS.
SQ SEQUENCE 17 AA; 1992 MW; 58CA70F63F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 17;
Best Local Similarity 30.8%; Pred. No. 4.7e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DQPPVEKPDLPQ 13
DB 2 EQAPEDQGFQREP 14

RESULT 31
ID Q9TWL5 PRELIMINARY; PRT; 18 AA.
AC Q9TWL5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)

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DE 24 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbotle fly) (Australian sheep blowfly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OC NCBI_TaxID=7375;
RN [1]
RP SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA."
RL Insect Mol. Biol. 3:201-211(1994).
SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PDLPFQV 16
DB 9 PGLFPYQV 16

RESULT 32
ID Q9X3B9 PRELIMINARY; PRT; 18 AA.
AC Q9X3B9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN Name=petd;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OC NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070147; AAD20766.1; -.
FT NON_TER
SQ SEQUENCE 18 AA; 2029 MW; BBF8A4E54FDCDE56 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 PDVEKPDLPQ 15
DB 7 PDLSDPKLRATQ 18

RESULT 33
ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Putative FK506-binding protein (FKBP) (peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OC NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.

```

```

RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA Kieselbach T.;
CC Submitted (JUN-2001) to Swiss-Prot.
CC -1- FUNCTION: PPIases accelerate the folding of proteins (By
CC similarity)
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR GO:00009507; C:chloroplast; IEA.
DR GO:0016853; F:isomerase activity; IEA.
DR GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO:0006457; P:protein folding; IEA.
DR InterPro: IPR001179; FKBP_PPIase.
KW Chloroplast; Isomerase; Rotamase.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1771 MW; E2013F998F8F908 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25.5; DB 2; Length 17;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 PDVVKPDL 11
DB 4 PPE-EKPKL 11

RESULT 34
ID 07LZ45 PRELIMINARY; PRT; 15 AA.
AC 07LZ45;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RX MEDLINE=90376100; PubMed=2118944;
RA Harel A., Faltaru M., Rubinstein M., Tal N., Schwartz M.;
RT "Fish apolipoprotein A-I has heparin binding activity: implication for
RT nerve regeneration.";
RL J. Neurochem. 55:1237-1243(1990).
DR PIR: A60221; A60221.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1649 MW; 69B5CE5FE6320BF CRC64;

Query Match
Best Local Similarity 25.5%; Score 25; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPP 4
DB 1 DQPP 4

RESULT 35
ID 09UCT9 PRELIMINARY; PRT; 18 AA.
AC 09UCT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE PRG-PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Loeffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RT J. Biol. Chem. 266:17358-17368(1991).
DR GO:0005576; C:extracellular; NAS.
DR GO:0008368; F:Gram-negative bacterial binding; NAS.
DR GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1780 MW; 961FEF80A83D2E40 CRC64;

Query Match
Best Local Similarity 25.5%; Score 25; DB 2; Length 18;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDVVKPDLQPPQ 15
DB 5 PPRPGKPEGPPQ 17

RESULT 36
ID 07MIF6 PRELIMINARY; PRT; 10 AA.
AC 07MIF6;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Alpha-glucan 6Ha (Fragment).
OS Haynaldia villosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE.
RX MEDLINE=91315394; PubMed=1859356;
RA Shewry P.R., Sabelli P.A., Parmar S., Lafandra D.;
RT "alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha
RT of Haynaldia villosa Schur (syn. Daasytrum villosum L.).";
RL Biochem. Genet. 29:207-211(1991).
DR PIR: B61218; B61218.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1132 MW; DEAE5936C772D772 CRC64;

Query Match
Best Local Similarity 24.5%; Score 24; DB 2; Length 10;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VEKPPLOP 13
DB 3 VPVPLOLP 10

RESULT 37
ID 09S618 PRELIMINARY; PRT; 11 AA.
AC 09S618;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
OS Name=petd;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.

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RA Urbach E., Chisholm S.W.;  
RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
RT sorted from the Sargasso Sea and Gulf Stream.";  
RL Limnol. Oceanogr. 43:1615-1630(1998).  
DR EMBL; AF070132; AAD20740.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B763337 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 5.9e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPD 11  
Db 4 LKPPDL 9

RESULT 38  
ID P82328 PRELIMINARY; PRT; 12 AA.  
AC P82328;  
DT 01-JUN-2000 (TRENBLREL. 14, Created)  
DT 01-JUN-2000 (TRENBLREL. 14, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosil 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN (1)  
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Pelletier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
RT targeting analysis of luminal and peripheral thylakoid proteins.";  
RL Plant Cell 12:319-341(2000).  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 21.3 kDa.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0009579; C:thylakoid; IEA.  
KW Chloroplast; Thylakoid.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1264 MW; 96691CB663B1B01 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 6.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PDVEKPD 11  
Db 4 PTEKPPDL 11

RESULT 39  
ID Q9R3R6 PRELIMINARY; PRT; 13 AA.  
AC Q9R3R6;  
DT 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
DE Cytochrome b6/f complex subunit IV (Fragment).  
GN Name=petD;  
OS Prochlorococcus sp.  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=1220;  
RN (1)  
RP SEQUENCE FROM N.A.

RA Urbach E., Chisholm S.W.;  
RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
RT sorted from the Sargasso Sea and Gulf Stream.";  
RL Limnol. Oceanogr. 43:1615-1630(1998).  
DR EMBL; AF070222; AAD23275.1; -.  
DR EMBL; AF070221; AAD23273.1; -.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1522 MW; 4CDE4C38013B763 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 7.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPD 11  
Db 4 LKPPDL 9

RESULT 40  
ID BRK3\_RANNI STANDARD; PRT; 14 AA.  
AC 07LZ53;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bradykinin-like peptide III.  
OS Rana nigromaculata (Japanese pond frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8409;  
RN (1)  
RP SEQUENCE.  
RC TISSUE=skin;  
RX MEDLINE=69117202; PubMed=5751736;  
RA Nakajima T.;  
RT "On the third active peptide on smooth muscle in the skin of Rana  
RT nigromaculata hallowell.";  
RL Chem. Pharm. Bull. 16:2088-2089(1968).  
CC -1- FUNCTION: Induces smooth muscle contraction.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the bradykinin family.  
DR PIR; A61362; A61362.  
KW Bradykinin; Direct protein sequencing; Vasodilator.  
SQ SEQUENCE 14 AA; 1486 MW; 33344EB3978393D7 CRC64;

Query Match 24.5%; Score 24; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 7.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLOPFOV 16  
Db 3 PGFSPPRV 10

Search completed: June 7, 2005, 23:18:54  
Job time : 82.2 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 64.5818 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-4  
Perfect score: 62  
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20005:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	62	100.0	12	4	AA872503 Colostrien
2	62	100.0	12	4	AA859323 Ewe colos
3	62	100.0	12	4	AA872249 Colostrien
4	62	100.0	12	4	AA872535 Colostrien
5	62	100.0	12	5	AA014580 Neural ce
6	62	100.0	12	5	AA051039 Colostrien
7	62	100.0	12	5	AAE20231 Colostrien
8	62	100.0	12	8	ADN60298 Constrictu
9	62	100.0	12	8	AD874339 Ovine col
10	62	100.0	12	8	AA859353 Ewe colos
11	35	56.5	14	4	AA859386 Human pep
12	33	53.2	9	2	AA872194 Human bcl
13	33	53.2	9	8	ADK84035 Human 191
14	33	53.2	9	8	ADK84519 Human 191
15	33	53.2	9	8	ADK85026 Human 191
16	33	53.2	9	8	ADK85074 Human 191
17	33	53.2	9	8	ADK87550 Human 191
18	33	53.2	9	8	ADK88447 Human 191
19	33	53.2	9	8	ADK84560 Human 191
20	33	53.2	9	8	ADK85620 Human 191
21	33	53.2	9	8	ADK86086 Human 191
22	33	53.2	9	8	ADK86641 Human 191
23	33	53.2	9	8	ADK87058 Human 191
24	33	53.2	9	8	ADK86146 Human 191
25	33	53.2	9	8	ADK86653 Human 191
26	33	53.2	9	8	ADK83459 Human 191
27	33	53.2	9	8	ADK85080 Human 191
28	33	53.2	9	8	ADK86684 Human 191
29	33	53.2	9	8	ADK87195 Human 191
30	33	53.2	9	8	ADK84539 Human 191
31	33	53.2	9	8	ADK88123 Human 191
32	33	53.2	9	8	ADK88312 Human 191
33	33	53.2	9	8	ADK88446 Human 191
34	33	53.2	9	8	ADK83504 Human 191
35	33	53.2	9	8	ADK83957 Human 191
36	33	53.2	9	8	ADK87688 Human 191
37	33	53.2	9	8	ADK87898 Human 191
38	33	53.2	9	8	ADK83493 Human 191
39	33	53.2	9	8	ADK84019 Human 191
40	33	53.2	9	8	ADK83977 Human 191
41	33	53.2	9	8	ADK85541 Human 191
42	33	53.2	9	8	ADK87676 Human 191
43	33	53.2	9	8	ADK88134 Human 191
44	33	53.2	9	8	ADK84504 Human 191
45	33	53.2	9	8	ADK85539 Human 191
46	33	53.2	9	8	ADK85041 Human 191
47	33	53.2	10	8	ADK84805 Human 191
48	33	53.2	10	8	ADK89332 Human 191
49	33	53.2	10	8	ADK84236 Human 191
50	33	53.2	10	8	ADK86947 Human 191
51	33	53.2	10	8	ADK88864 Human 191
52	33	53.2	10	8	ADK86378 Human 191
53	33	53.2	10	8	ADK86940 Human 191
54	33	53.2	10	8	ADK85840 Human 191
55	33	53.2	10	8	ADK84256 Human 191
56	33	53.2	10	8	ADK85286 Human 191
57	33	53.2	10	8	ADK88890 Human 191
58	33	53.2	10	8	ADK89485 Human 191
59	33	53.2	10	8	ADK83714 Human 191
60	33	53.2	10	8	ADK84737 Human 191
61	33	53.2	10	8	ADK89186 Human 191
62	33	53.2	10	8	ADK89336 Human 191
63	33	53.2	10	8	ADK89660 Human 191
64	33	53.2	10	8	ADK85806 Human 191
65	33	53.2	10	8	ADK83774 Human 191
66	33	53.2	10	8	ADK85814 Human 191
67	33	53.2	10	8	ADK86405 Human 191
68	33	53.2	10	8	ADK89640 Human 191
69	33	53.2	10	8	ADK83723 Human 191
70	33	53.2	10	8	ADK84297 Human 191
71	33	53.2	10	8	ADK84802 Human 191
72	33	53.2	10	8	ADK86336 Human 191
73	33	53.2	10	8	ADK86874 Human 191
74	33	53.2	10	8	ADK84273 Human 191
75	33	53.2	10	8	ADK85316 Human 191
76	33	53.2	10	8	ADK89476 Human 191
77	33	53.2	10	8	ADK84214 Human 191
78	33	53.2	10	8	ADK84762 Human 191
79	33	53.2	10	8	ADK85358 Human 191
80	33	53.2	10	8	ADK88719 Human 191
81	33	53.2	10	8	ADK83780 Human 191
82	33	53.2	10	8	ADK85298 Human 191
83	33	53.2	10	8	ADK85881 Human 191
84	33	53.2	10	8	ADK85359 Human 191
85	33	53.2	10	8	ADK86913 Human 191
86	33	53.2	15	8	ADK90296 Human 191
87	33	53.2	15	8	ADK90299 Human 191
88	33	53.2	15	8	ADK90535 Human 191
89	33	53.2	15	8	ADK89679 Human 191
90	33	53.2	15	8	ADK89884 Human 191
91	33	53.2	15	8	ADK90058 Human 191
92	33	53.2	15	8	ADK89878 Human 191
93	33	53.2	15	8	ADK90051 Human 191
94	33	53.2	15	8	ADK89885 Human 191
95	33	53.2	15	8	ADK90278 Human 191
96	33	53.2	15	8	ADK90286 Human 191
97	33	53.2	15	8	ADK90298 Human 191
98	33	53.2	15	8	ADK89858 Human 191

99 33 53.2 15 8 ADK90044  
100 33 53.2 15 8 ADK89868

AdK90044 Human 191  
AdK89868 Human 191

## ALIGNMENTS

## RESULT 1

AAB72503

ID AAB72503 standard; peptide; 12 AA.

XX AAB72503;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #4.

KM Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GU, Hughes TK, Boldogh I,

DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell

PT with an oxidative stress regulator selected from colostriin, its

PS constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostriin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12

1 LFFFLPVVNVLP 12

DB 1 LFFFLPVVNVLP 12

## RESULT 2

AAB59323

ID AAB59323 standard; peptide; 12 AA.

XX AAB59323;

DT 21-MAR-2001 (first entry)

DE Ewe colostriin peptide fragment B-8.

KM Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR WPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostriin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostriin. Colostriin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12

1 LFFFLPVVNVLP 12

DB 1 LFFFLPVVNVLP 12

## RESULT 3

AAB72249

ID AAB72249 standard; peptide; 12 AA.

XX AAB72249;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 4.

KW Colostriin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GU, Hughes TK, Boldogh I, Georgiades J,

DR WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PR treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SO Sequence 12 AA;  
 Query Match 100.0%; Score 62; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFFLPVNVLP 12  
 DB 1 LFFFLPVNVLP 12  
 RESULT 4  
 AAB72535  
 ID AAB72535 standard; peptide; 12 AA.  
 XX  
 XX AAB72535;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #4.  
 XX  
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFFLPVNVLP 12  
 DB 1 LFFFLPVNVLP 12  
 RESULT 5  
 AAO14580  
 ID AAO14580 standard; peptide; 12 AA.  
 XX  
 AC AAO14580;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX  
 DE Neural cell regulatory colostrinin peptide 4.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 12 /note="Optional C-terminal amide"  
 FT  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022777.  
 XX  
 PR 17-AUG-2000; 2000WO-US022777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 12 AA;  
 Query Match 100.0%; Score 62; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFFLPVNVLP 12  
 DB 1 LFFFLPVNVLP 12  
 RESULT 6  
 AAM51039

ID AAM51039 standard; peptide; 12 AA.  
 AC AAM51039;  
 XX  
 XX  
 DT 30-MAY-2002 (first entry)  
 DE Colostriin constituent peptide.  
 XX Colostriin; colostrum; immunomodulator; cardiovascular;  
 KM blood cell regulator; cytokine inducer; beta-casein; human.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 12 /note="optional C-terminal amidation"  
 FT  
 FT  
 XX WO200213849-A1.  
 PN  
 PD 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US022775.  
 PF  
 XX 17-AUG-2000; 2000WO-US022775.  
 PR  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 PI WPI; 2002-269150/31.  
 DR  
 XX  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of blood  
 PT cell regulator selected from colostriin, its constituent peptide and/or  
 PT analog.  
 PS Claim 1; Page 34; 54pp; English.  
 XX  
 XX The present sequence is that of a colostriin constituent peptide that is  
 CC preferred for use as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified as having  
 CC a beta-casein homologue precursor. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator, where the  
 CC cell is present in a cell culture, a tissue, an organ or an organism, and  
 CC the cell is mammalian, including human; modulating an immune response in  
 CC a cell by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator is  
 CC administered topically or as part of a dietary supplement, and where the  
 CC immune response is specific or non specific, an interferon response or an  
 CC antibody response; modulating blood cell proliferation by contacting  
 CC blood cells with a blood cell regulator, where the blood cells are  
 CC present in a cell culture or an organism, are mammalian or human, and  
 CC where the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patient. A claimed  
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
 CC active agent such as the present peptide. Cytokines induced by this  
 CC peptide in human leucocyte cultures include interferon-gamma, tumour  
 CC necrosis factor-alpha, interleukin-6 and interleukin-10  
 CC  
 XX  
 SQ Sequence 12 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 62; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12  
 |||||  
 DB 1 LFFFLPVVNVLP 12

RESULT 7

AAE20231  
 ID AAE20231 standard; peptide; 12 AA.  
 AC AAE20231;  
 XX  
 XX  
 DT 18-JUN-2002 (first entry)  
 DE Colostriin constituent peptide #4.  
 XX  
 XX Blood cell regulator; colostriin; constituent peptide; oxidative stress;  
 KM therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KM tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KM transplantation; implantation; dermatological; vulnary.  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 12 /note="Optionally C-terminal amide"  
 FT  
 FT  
 XX WO200213850-A1.  
 PN  
 PD 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US022776.  
 PF  
 XX 17-AUG-2000; 2000WO-US022776.  
 PR  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI WPI; 2002-269151/31.  
 DR  
 XX  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostriin, its  
 PT constituent peptide and/or analog.  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostriin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress level  
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
 CC organ, or organism; or for treating oxidative damage to the skin of a  
 CC patient e.g. animal or human; to modulate oxidative stress during/ after  
 CC a premature birth or normal birth, preventing/delaying aging in a  
 CC patient; enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostriin constituent peptide  
 CC  
 XX  
 SQ Sequence 12 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 62; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00054;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVVNVLP 12  
 |||||  
 DB 1 LFFFLPVVNVLP 12

RESULT 8  
 ADN60298  
 ID ADN60298 standard; peptide; 12 AA.



```

XX AC ADN60298;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Constituent peptide of colostrinin SEQ ID NO:4.
XX XX
XX KW modulator; colostrinin; intracellular signaling molecule modulator;
XX KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;
XX KW DNA damage; beta-amyloid; retinoic acid; cytoskeletal; 4HNE inhibitor;
XX KW 4HNE-protein adduct formation reduction;
XX KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;
XX KW c-Jun NH2-terminal kinase inhibition.
XX OS
XX OS Synthetic.
XX PN WO2004037851-A2.
XX PD 06-MAY-2004.
XX PF 22-OCT-2003; 2003WO-US033423.
XX PR 22-OCT-2002; 2002US-0420369P.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (BOLD/) BOLDOGH I.
XX PA (STAN/) STANTON J G.
XX PA (GEOR/) GEORGIADDES J A.
XX PA (HUGH/) HUGHES T K.
XX PA (KRUZ/) KRUZEL M.
XX PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruznel M;
XX XX
XX DR WPI; 2004-365494/34.
XX PT Use of colostrinin for e.g. modulating an intracellular signaling
XX PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a
XX PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
XX PT a cell.
XX XX
XX PS Claim 6; SEQ ID NO 4; 46pp; English.
XX XX
XX CC The present invention describes the use of a modulator selected from
XX CC colostrinin, its constituent peptide, its active analogue, and a
XX CC combination of these, for modulating an intracellular signaling molecule
XX CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The modulator has cytoskeletal activity, and can be used as a 4HNE
XX CC inhibitor. The modulator is useful in the manufacture of a medicament for
XX CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated
XX CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,
XX CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.
XX CC Colostrinin, or its constituent peptide or active analogue is useful for
XX CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
XX CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
XX CC The present sequence represents a synthetic constituent peptide of
XX CC colostrinin, which can be used as a modulator in the present invention.
XX SQ
XX
XX Query Match 100.0%; Score 62; DB 8; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00054;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLPVVNVLP 12
XX |||||
XX Db 1 LFFFLPVVNVLP 12
XX
XX RESULT 9
XX ADS74399
XX ID ADS74399 standard; peptide; 12 AA.

```

```

XX AC ADS74399;
XX XX
XX DT 16-DEC-2004 (first entry)
XX DE Ovine colostrinin peptide.
XX XX
XX KW Colostrum; colostrinin; sheep; peptide purification.
XX KW Ovis aries.
XX OS
XX OS WO2004081038-A1.
XX PN
XX PD 23-SEP-2004.
XX PF 10-MAR-2004; 2004WO-GB001014.
XX PR 11-MAR-2003; 2003GB-00005552.
XX PR 08-MAR-2004; 2004GB-00005190.
XX XX
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PA Georgiades JA, Polanowski A, Wilusz T, Kruznel M;
XX PI WPI; 2004-677519/66.
XX DR
XX XX
XX PT Recovering peptides such as colostrinin from mammalian colostrum, by
XX PT mixing colostrum with alcohol to form alcohol phase containing peptides
XX PT and precipitate, separating alcohol phase from precipitate, and
XX PT recovering alcohol phase.
XX XX
XX PS Example; SEQ ID NO 16; 41pp; English.
XX XX
XX CC The present sequence is that of a peptide that can be recovered from
XX CC ovine colostrinin using the method of the invention. The invention
XX CC provides a method for the recovery of peptides (especially colostrinin)
XX CC from colostrum in substantially pure, biologically active form and in
XX CC high yield. The method involves mixing the colostrum with an alcohol to
XX CC form an alcohol phase containing the colostrinin and a precipitate
XX CC containing higher molecular weight caseins and other proteins. Best
XX CC results are obtained using methanol or ethanol of at least 80%, and
XX CC preferably up to 100%, purity. The alcohol phase is then separated from
XX CC the precipitate, and the colostrinin is separated from the alcohol,
XX CC preferably by evaporation, to form a colostrinin-rich phase, which is
XX CC recovered. A precipitation agent, such as ammonium sulfate, may be added
XX CC either to the alcohol phase or, preferably, to the colostrinin-rich phase
XX CC to induce precipitation of the colostrinin peptides. The method is
XX CC generally applicable to the separation of peptides from fluids containing
XX CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic
XX CC acids. In an example from the invention, the antigenic profile of
XX CC peptides recovered from sheep colostrum using the alcohol precipitation
XX CC methods was determined by ELISA using antibodies prepared against 9
XX CC synthetic peptides, including a peptide having the present sequence
XX CC (denoted antigen class B-9).
XX XX
XX SQ
XX
XX Query Match 100.0%; Score 62; DB 8; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00054;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLPVVNVLP 12
XX |||||
XX Db 1 LFFFLPVVNVLP 12
XX
XX RESULT 10
XX AAB59353
XX ID AAB59353 standard; peptide; 14 AA.
XX XX
XX AC AAB59353;
XX XX
XX DT 21-MAR-2001 (first entry)

```

XX DE Ewe colostrinin peptide fragment derived sequence #13.  
XX XX  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX XX  
XX Ovis sp.  
XX XX  
XX WO20075173-A2.  
XX XX  
XX 14-DEC-2000.  
XX XX  
XX 02-JUN-2000; 2000WO-GB002128.  
XX PF  
XX 02-JUN-1999; 99GB-00012852.  
XX PR  
XX (REGG-) REGEN THERAPEUTICS PLC.  
XX PA  
XX Georgiades JA;  
XX PI  
XX WPI; 2001-071058/08.  
XX DR  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.  
XX XX  
XX PS Claim 8; Page 27; 63pp; English.  
XX XX  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
CC CC  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 62; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFFLPVNVLP 12  
| | | | | | | | | | | | | |  
DB 2 LFFFLPVNVLP 13  
RESULT 11  
AAM96786  
ID AAM96786 standard; peptide; 14 AA.  
XX AC  
XX AAM96786;  
XX XX  
DT 24-JAN-2002 (first entry)  
XX XX  
DE Human peptide #61 encoded by a SNP oligonucleotide.  
XX XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX KW  
XX Homo sapiens.  
OS  
XX  
XX WO200147944-A2.  
PN  
XX  
XX 05-JUL-2001.  
PD

XX XX  
XX PF 28-DEC-2000; 2000WO-US035498.  
XX XX  
XX 28-DEC-1999; 99US-0173419P.  
PR  
XX 27-DEC-2000; 2000US-00173419.  
XX PR  
XX (CURA-) CURAGEN CORP.  
XX PA  
XX Shinkets RA, Leach M;  
XX PI  
XX WPI; 2001-465210/50.  
XX DR  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX XX  
XX PS Disclosure; Page 3681; 4143pp; English.  
XX XX  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms  
CC XX  
SQ Sequence 14 AA;  
Query Match 56.5%; Score 35; DB 4; Length 14;  
Best Local Similarity 66.7%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FFFLPVNV 10  
| : | | | | | | | | | | | |  
DB 2 FFFLPVNV 10  
RESULT 12  
AA21194  
ID AA21194 standard; protein; 9 AA.  
XX AC  
XX AA21194;  
XX XX  
DT 22-JUL-1999 (first entry)  
XX XX  
DE Human bcl2 proto-oncogene mutant protein fragment 42.  
XX XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin 1; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; semaphorin II; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.  
XX KW  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX WO9845322-A2.  
PN  
XX  
XX 15-OCT-1998.  
PD

XX 02-APR-1998; 98WO-1B000705.  
 PF 10-APR-1997; 97US-0043163P.  
 XX  
 PR  
 XX  
 PA (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.  
 PA (UYUO-) UNIV ROTTERDAM ERASMUS.  
 PA (UYUT-) RIJKSUNIV UTRECHT.  
 XX  
 PI Van Leeuwen FM, Grosveld FG, Burbach JPH;  
 XX WPI; 1998-609901/51.  
 DR N-PSDB; AAX75766.  
 XX  
 PT Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also for  
 PT treatment and prevention with specific ribozymes or wild-type RNA.  
 XX  
 PS Disclosure; Fig 15; 258pp; English.  
 XX  
 CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-Ap), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, spinophilin B, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HMPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A  
 XX  
 SQ Sequence 9 AA;  
 Query Match 53.2%; Score 33; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LFFFLPV 7  
 DB 4 LFFFLPV 9  
 RESULT 13  
 ID ADR84035 standard; peptide; 9 AA.  
 XX  
 AC ADR84035;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human 191P4D12(b) peptide fragment #736.  
 XX  
 KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
 KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
 KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
 KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
 KW Suppression Subtractive Hybridisation; SSH.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016799-A2.  
 XX  
 PD 26-FEB-2004.  
 XX

PF 23-APR-2003; 2003WO-US013013.  
 XX  
 PR 16-AUG-2002; 2002US-0404306P.  
 PR 01-NOV-2002; 2002US-0423290P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris W, Ge W;  
 XX WPI; 2004-203808/19.  
 XX  
 DR  
 XX  
 PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
 PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
 PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
 PT humoral or cellular immune response.  
 XX  
 PS Claim 1; Page 149; 443pp; English.  
 XX  
 CC The present invention relates to novel compositions comprising peptides  
 CC (ADR83300-ADR90584) from 191P4D12(b) and related proteins. It was found  
 CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
 CC expressed in a number of cancers and so the compositions of the invention  
 CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
 CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
 CC uterus or cervix and in eliciting a humoral or cellular immune response.  
 CC To isolate genes that are overexpressed in prostate cancer, the  
 CC suppression subtractive hybridisation (SSH) method was used, using cDNA  
 CC derived from prostate cancer tissues.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 53.2%; Score 33; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFFLPV 6  
 DB 4 LFFFLPV 9  
 RESULT 14  
 ID ADR84519 standard; peptide; 9 AA.  
 XX  
 AC ADR84519;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human 191P4D12(b) peptide fragment #1220.  
 XX  
 KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
 KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
 KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
 KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
 KW Suppression Subtractive Hybridisation; SSH.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016799-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 23-APR-2003; 2003WO-US013013.  
 XX  
 PR 16-AUG-2002; 2002US-0404306P.  
 PR 01-NOV-2002; 2002US-0423290P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris W, Ge W;  
 XX WPI; 2004-203808/19.  
 XX

PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.

PS Claim 1; Page 155; 443pp; English.

XX The present invention relates to novel compositions comprising peptides  
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEFFFLP 6  
|||  
3 LEFFFLP 8

RESULT 15

ID ADK85026 standard; peptide; 9 AA.

AC ADK85026;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #1727.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;  
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;  
XX Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Eid PM, Jakobovits A, Paris M, Ge W;  
XX WPI; 2004-203808/19.

XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,  
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
XX humoral or cellular immune response.

PS Claim 1; Page 161; 443pp; English.

XX The present invention relates to novel compositions comprising peptides  
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention

CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEFFFLP 6  
|||  
1 LEFFFLP 6

RESULT 16

ID ADK85074 standard; peptide; 9 AA.

AC ADK85074;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #1775.

XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;  
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;  
XX Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Eid PM, Jakobovits A, Paris M, Ge W;  
XX WPI; 2004-203808/19.

XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,  
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
XX humoral or cellular immune response.

PS Claim 1; Page 162; 443pp; English.

XX The present invention relates to novel compositions comprising peptides  
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 4 LFFFLP 9

RESULT 17
ADK87550
ID ADK87550 standard; peptide; 9 AA.
XX
AC ADK87550;
XX
XX 20-MAY-2004 (first entry)
XX
DE Human 191P4D12(b) peptide fragment #4251.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;
XX
XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
XX
XX Claim 1; Page 192; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
XX
XX Query Match 53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 1 LFFFLP 6

RESULT 18
ADK88447
ID ADK88447 standard; peptide; 9 AA.
XX

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AC ADK88447;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human 191P4D12(b) peptide fragment #5148.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;
XX
XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
XX
XX Claim 1; Page 204; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
XX (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
XX
XX Query Match 53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LFFFLP 6
   |||||
Db 1 LFFFLP 6

RESULT 19
ADK84560
ID ADK84560 standard; peptide; 9 AA.
XX
XX ADK84560;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human 191P4D12(b) peptide fragment #1261.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX

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XX OS Homo sapiens.
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX PA (AGEN-) AGENSYS INC.
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX DR WPI; 2004-203808/19.
XX CC New composition comprising 191P4D12(b) proteins and polynucleotides,
XX PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX PR bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX PT humoral or cellular immune response.
XX PS Claim 1; Page 156; 443pp; English.
XX CC The present invention relates to novel compositions comprising peptides
XX CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX CC expressed in a number of cancers and so the compositions of the invention
XX CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX CC uterus or cervix and in eliciting a humoral or cellular immune response.
XX CC To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX CC derived from prostate cancer tissues.
XX SQ Sequence 9 AA;

Query Match          53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
   |||||
Db 4 LFFFLP 9

RESULT 20
ADK85620
ID ADK85620 standard; peptide; 9 AA.
XX ADK85620;
XX AC
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Human 191P4D12(b) peptide fragment #2321.
XX KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX KW Suppression Subtractive Hybridisation; SSH.
XX OS Homo sapiens.
XX OS
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.

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XX PA (AGEN-) AGENSYS INC.
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX DR WPI; 2004-203808/19.
XX CC New composition comprising 191P4D12(b) proteins and polynucleotides,
XX PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX PR bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX PT humoral or cellular immune response.
XX PS Claim 1; Page 168; 443pp; English.
XX CC The present invention relates to novel compositions comprising peptides
XX CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
XX CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX CC expressed in a number of cancers and so the compositions of the invention
XX CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX CC uterus or cervix and in eliciting a humoral or cellular immune response.
XX CC To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX CC derived from prostate cancer tissues.
XX SQ Sequence 9 AA;

Query Match          53.2%; Score 33; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6
   |||||
Db 4 LFFFLP 9

RESULT 21
ADK86086
ID ADK86086 standard; peptide; 9 AA.
XX ADK86086;
XX AC
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Human 191P4D12(b) peptide fragment #2787.
XX KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX KW Suppression Subtractive Hybridisation; SSH.
XX OS Homo sapiens.
XX OS
XX PN WO2004016799-A2.
XX PD 26-FEB-2004.
XX PF 23-APR-2003; 2003WO-US013013.
XX PR 16-AUG-2002; 2002US-0404306P.
XX PR 01-NOV-2002; 2002US-0423290P.
XX PA (AGEN-) AGENSYS INC.
XX PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX DR WPI; 2004-203808/19.
XX CC New composition comprising 191P4D12(b) proteins and polynucleotides,
XX PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX PR bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX PT humoral or cellular immune response.

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Db	3	LEFFFLP	8
RESULT 24			
ID	ADK86146	ADK86146 standard; peptide; 9 AA.	
XX			
AC	ADK86146;		
DT	20-MAY-2004	(first entry)	
XX			
DE	Human 191P4D12(b)	peptide fragment #2847.	
XX			
KW	Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;		
KW	prostate cancer; bladder cancer; kidney cancer; colon cancer;		
KW	lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;		
KW	cervix cancer; immune response; human; chromosome 1q22-q23.2;		
KW	Suppression Subtractive Hybridisation; SSH.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004016799-A2.		
PD			
PD	26-FEB-2004.		
XX			
PF	23-APR-2003; 2003WO-US013013.		
XX			
PR	16-AUG-2002; 2002US-0404306P.		
PR	01-NOV-2002; 2002US-0423290P.		
XX			
PA	(AGEN-) AGENSYS INC.		
XX			
PI	Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;		
XX			
DR	WPI; 2004-203808/19.		
XX			
PT	New composition comprising 191P4D12(b) proteins and polynucleotides,		
PT	useful in diagnosing, preventing and treating cancer, e.g. prostate,		
PT	bladder, kidney, colon, lung, pancreas or ovary and in eliciting a		
PT	humoral or cellular immune response.		
XX			
PS	Claim 1, Page 174; 443pp; English.		
XX			
CC	The present invention relates to novel compositions comprising peptides		
CC	(ADK83300-ADK80584) from 191P4D12(b) and related proteins. It was found		
CC	that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly		
CC	expressed in a number of cancers and so the compositions of the invention		
CC	are useful in diagnosing, preventing and treating cancer, e.g. cancer of		
CC	the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,		
CC	uterus or cervix and in eliciting a humoral or cellular immune response.		
CC	To isolate genes that are overexpressed in prostate cancer, the		
CC	Suppression Subtractive Hybridisation (SSH) method was used, using cDNA		
CC	derived from prostate cancer tissues.		
XX			
SQ	Sequence 9 AA;		
Query Match 53.2%; Score 33; DB 8; Length 9;			
Best Local Similarity 100.0%; Pred. No. 1.8e+06;			
Matches	6; Conservative	0; Mismatches	0; Indels 0
OY	1 LEFFFLP 6		
Db	2 LEFFFLP 7		
RESULT 25			
ID	ADK86653	ADK86653 standard; peptide; 9 AA.	
XX			
AC	ADK86653;		
XX			
DT	20-MAY-2004	(first entry)	
XX			

XX	Human 191P4D12(b) peptide fragment #3354.
DB	Cyrotatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW	prostate cancer; bladder cancer; kidney cancer; colon cancer;
KM	lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KV	cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW	Suppression Subtractive Hybridisation; SSH.
XX	
OS	Homo sapiens.
XX	
PN	WO2004016799-A2.
PD	26-FEB-2004.
XX	
PF	23-APR-2003; 2003WO-US013013.
XX	
PR	16-AUG-2002; 2002US-0404306P.
PR	01-NOV-2002; 2002US-0423290P.
XX	
PA	(AGEN-) AGENSYS INC.
PI	Raitano AB, Chailita-Bid PM, Jakobovits A, Paris M, Ge W;
DR	WPI; 2004-203808/19.
PT	New composition comprising 191P4D12(b) proteins and polynucleotides,
PT	useful in diagnosing, preventing and treating cancer; e.g. prostate,
PT	bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX	humoral or cellular immune response.
PS	Claim 1; Page 180; 443pp; English.
XX	
CC	The present invention relates to novel compositions comprising peptides
CC	(ADK83300-ADG90584) from 191P4D12(b) and related proteins. It was found
CC	that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC	expressed in a number of cancers and so the compositions of the invention
CC	are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC	the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC	uterus or cervix and in eliciting a humoral or cellular immune response.
CC	To isolate genes that are overexpressed in prostate cancer, the
CC	Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC	derived from prostate cancer tissues.
SQ	Sequence 9 AA;
OY	Query Match 53.2%; Score 33; DB 8; Length 9;
	Best Local Similarity 100.0%; Pred. No. 1.8e+06;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 LFFPLP 6       3 LFFPLP 8
RESULT 26	
ID	ADK83459 standard; peptide; 9 AA.
AC	ADK83459;
DT	20-MAY-2004 (first entry)
DE	Human 191P4D12(b) peptide fragment #160.
XX	
KM	Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KM	prostate cancer; bladder cancer; kidney cancer; colon cancer;
KM	lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KV	cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW	Suppression Subtractive Hybridisation; SSH.
OS	Homo sapiens.
XX	
PN	WO2004016799-A2.



XX 26-FEB-2004.  
PD 23-APR-2003; 2003WO-US013013.  
XX  
PF 16-AUG-2002; 2002US-0404306P.  
PR 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
DR WPI; 2004-203808/19.  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
PS Claim 1; Page 142; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
XX |||||  
XX 3 LFFFLP 8  
DB

RESULT 27  
ADK85080  
ID ADK85080 standard; peptide; 9 AA.  
XX  
XX ADR85080;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human 191P4D12(b) peptide fragment #1781.  
DE  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 23-APR-2003; 2003WO-US013013.  
PF  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
PI

XX WPI; 2004-203808/19.  
DR  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX Claim 1; Page 162; 443pp; English.  
XX

CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
XX |||||  
XX 2 LFFFLP 7  
DB

RESULT 28  
ADK86684  
ID ADK86684 standard; peptide; 9 AA.  
XX  
XX ADR86684;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT

DE Human 191P4D12(b) peptide fragment #3385.  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD

PF 23-APR-2003; 2003WO-US013013.  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
PI  
XX  
XX WPI; 2004-203808/19.  
DR  
XX  
XX New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
PS Claim 1; Page 180; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides

CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
Db 2 LFFFLP 7

RESULT 29  
ADK87195  
ID ADK87195 standard; peptide; 9 AA.

AC ADK87195;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #3896.

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

PA (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;

DR MPI; 2004-203808/19.

PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.

PS Claim 1; Page 187; 443pp; English.

CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
Db 2 LFFFLP 7

RESULT 30

ADK84539

ID ADK84539 standard; peptide; 9 AA.

AC ADK84539;

DT 20-MAY-2004 (first entry)

DE Human 191P4D12(b) peptide fragment #1240.

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.

OS Homo sapiens.

PN WO2004016799-A2.

PD 26-FEB-2004.

PF 23-APR-2003; 2003WO-US013013.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

PA (AGEN-) AGENSYS INC.

PI Raitano AB, Challita-Bid PM, Jakobovits A, Paris M, Ge W;

DR MPI; 2004-203808/19.

PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.

PS Claim 1; Page 155; 443pp; English.

CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
Db 1 LFFFLP 6

RESULT 31

ADK88123  
ID ADK88123 standard; peptide; 9 AA.  
XX  
AC ADK88123;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human 191P4D12(b) peptide fragment #4824.  
XX  
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
XX Suppression Subtractive Hybridisation; SSH.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016799-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 23-APR-2003; 2003WO-US013013.  
XX  
PR 16-AUG-2002; 2002US-0404306P.  
PR 01-NOV-2002; 2002US-0423290P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;  
XX  
DR WPI; 2004-203808/19.  
XX  
PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
PS Claim 1; Page 200; 443pp; English.  
XX  
CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
SQ Sequence 9 AA:  
XX  
Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 LFFFLP 6  
XX |||||  
DB 1 LFFFLP 6  
XX  
RESULT 32  
ADK88312  
ID ADK88312 standard; peptide; 9 AA.  
XX  
AC ADK88312;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human 191P4D12(b) peptide fragment #5013.  
XX  
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW

KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016799-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 23-APR-2003; 2003WO-US013013.  
XX  
PR 16-AUG-2002; 2002US-0404306P.  
PR 01-NOV-2002; 2002US-0423290P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Raitano AB, Challita-Bid PM, Jakobovits A, Faris M, Ge W;  
XX  
DR WPI; 2004-203808/19.  
XX  
PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
PS Claim 1; Page 202; 443pp; English.  
XX  
CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
SQ Sequence 9 AA:  
XX  
Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 LFFFLP 6  
XX |||||  
DB 1 LFFFLP 6  
XX  
RESULT 33  
ADK88446  
ID ADK88446 standard; peptide; 9 AA.  
XX  
AC ADK88446;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human 191P4D12(b) peptide fragment #5147.  
XX  
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016799-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 23-APR-2003; 2003WO-US013013.

XX 16-AUG-2002; 2002US-0404306P.  
PR 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
XX WPI; 2004-203808/19.  
XX  
XX New composition comprising 191PAD12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX Claim 1; Page 204; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191PAD12(b) and related proteins. It was found  
CC that 191PAD12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
XX Sequence 9 AA;  
SQ  
XX  
XX Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFFLP 6  
DT |||||  
DB 3 LFFFLP 8  
XX  
XX RESULT 34  
ADK83504  
ID ADK83504 standard; peptide; 9 AA.  
XX  
XX ADRK3504;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human 191PAD12(b) peptide fragment #205.  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191PAD12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 23-APR-2003; 2003WO-US013013.  
PF  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
XX WPI; 2004-203808/19.  
XX  
XX New composition comprising 191PAD12(b) proteins and polynucleotides,  
PT

PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX Claim 1; Page 143; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191PAD12(b) and related proteins. It was found  
CC that 191PAD12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.  
XX  
XX Sequence 9 AA;  
SQ  
XX  
XX Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFFLP 6  
DT |||||  
DB 2 LFFFLP 7  
XX  
XX RESULT 35  
ADK83957  
ID ADK83957 standard; peptide; 9 AA.  
XX  
XX ADRK3957;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human 191PAD12(b) peptide fragment #658.  
XX  
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191PAD12(b); cancer;  
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KW Suppression Subtractive Hybridisation; SSH.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004016799-A2.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 23-APR-2003; 2003WO-US013013.  
PF  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
PR  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;  
XX WPI; 2004-203808/19.  
XX  
XX New composition comprising 191PAD12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.  
XX  
XX Claim 1; Page 148; 443pp; English.  
XX  
XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191PAD12(b) and related proteins. It was found  
CC that 191PAD12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of

CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX  
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
XXXXXX  
ID 2 LFFFLP 7

RESULT 36  
ADK87688  
ID ADK87688 standard; peptide; 9 AA.

XX  
AC ADK87688;

XX  
DT 20-MAY-2004 (first entry)

XX  
DE Human 191P4D12(b) peptide fragment #4389.

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KM prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KM lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KM cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KM Suppression Subtractive Hybridisation; SSH.

XX  
OS Homo sapiens.

XX  
PN WO2004016799-A2.

XX  
PD 26-FEB-2004.

XX  
PF 23-APR-2003; 2003WO-US013013.

XX  
PR 16-AUG-2002; 2002US-0404306P.

XX  
PR 01-NOV-2002; 2002US-0423290P.

XX  
PI (AGEN-) AGENSYS INC.

XX  
PI Raitano AB, Challita-Eld PM, Jakobovits A, Faris M, Ge W;

XX  
DR WPI; 2004-203808/19.

XX  
PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.

XX  
PS Claim 1; Page 194; 443pp; English.

XX  
CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX  
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
XXXXXX  
ID 3 LFFFLP 8

RESULT 37  
ADK87898  
ID ADK87898 standard; peptide; 9 AA.

XX  
AC ADK87898;

XX  
DT 20-MAY-2004 (first entry)

XX  
DE Human 191P4D12(b) peptide fragment #4599.

KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;  
KM prostate cancer; bladder cancer; kidney cancer; colon cancer;  
KM lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;  
KM cervix cancer; immune response; human; chromosome 1q22-q23.2;  
KM Suppression Subtractive Hybridisation; SSH.

XX  
OS Homo sapiens.

XX  
PN WO2004016799-A2.

XX  
PD 26-FEB-2004.

XX  
PF 23-APR-2003; 2003WO-US013013.

XX  
PR 16-AUG-2002; 2002US-0404306P.

XX  
PR 01-NOV-2002; 2002US-0423290P.

XX  
PI (AGEN-) AGENSYS INC.

XX  
PI Raitano AB, Challita-Eld PM, Jakobovits A, Faris M, Ge W;

XX  
DR WPI; 2004-203808/19.

XX  
PT New composition comprising 191P4D12(b) proteins and polynucleotides,  
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,  
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a  
PT humoral or cellular immune response.

XX  
PS Claim 1; Page 197; 443pp; English.

XX  
CC The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX  
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLP 6  
XXXXXX  
ID 1 LFFFLP 6

RESULT 38  
ADK83493  
ID ADK83493 standard; peptide; 9 AA.

XX  
AC ADK83493;

```

XX 20-MAY-2004 (first entry)
DT
XX
XX Homo sapiens.
DE Human 191P4D12(b) peptide fragment #194.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
OS
XX Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX
XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
XX
XX Claim 1; Page 142; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
XX (ADR83300-ADR90584) from 191P4D12(b) and related proteins. It was found
XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
XX
XX Query Match          53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLP 6
XX      |||||
XX      1 LFFFLP 6
XX
XX Db
XX
XX RESULT 39
XX ADR84019
XX ID ADR84019 standard; peptide; 9 AA.
XX
XX ADR84019;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human 191P4D12(b) peptide fragment #720.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX

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OS Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX (AGEN-) AGENSYS INC.
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XX Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
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XX WPI; 2004-203808/19.
XX
XX New composition comprising 191P4D12(b) proteins and polynucleotides,
XX useful in diagnosing, preventing and treating cancer, e.g. prostate,
XX bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
XX humoral or cellular immune response.
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XX Claim 1; Page 149; 443pp; English.
XX
XX The present invention relates to novel compositions comprising peptides
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XX that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
XX expressed in a number of cancers and so the compositions of the invention
XX are useful in diagnosing, preventing and treating cancer, e.g. cancer of
XX the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
XX uterus or cervix and in eliciting a humoral or cellular immune response.
XX To isolate genes that are overexpressed in prostate cancer, the
XX CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
XX derived from prostate cancer tissues.
XX
XX Sequence 9 AA;
XX
XX Query Match          53.2%; Score 33; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LFFFLP 6
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XX      3 LFFFLP 8
XX
XX Db
XX
XX RESULT 40
XX ADR83977
XX ID ADR83977 standard; peptide; 9 AA.
XX
XX ADR83977;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human 191P4D12(b) peptide fragment #678.
XX
XX Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
XX prostate cancer; bladder cancer; kidney cancer; colon cancer;
XX lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
XX cervix cancer; immune response; human; chromosome 1q22-q23.2;
XX Suppression Subtractive Hybridisation; SSH.
XX
XX Homo sapiens.
XX
XX WO2004016799-A2.
XX
XX 26-FEB-2004.
XX
XX 23-APR-2003; 2003WO-US013013.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
XX

```

PA (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eld PM, Jakobovits A, Faris M, Ge W;

PI WPI, 2004-203808/19.

XX New composition comprising 191P4D12(b) proteins and polynucleotides,

PT useful in diagnosing, preventing and treating cancer, e.g. prostate,

PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a

PT humoral or cellular immune response.

XX Claim 1; Page 149; 443pp; English.

XX The present invention relates to novel compositions comprising peptides  
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found  
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly  
CC expressed in a number of cancers and so the compositions of the invention  
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of  
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,  
CC uterus or cervix and in eliciting a humoral or cellular immune response.  
CC To isolate genes that are overexpressed in prostate cancer, the  
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA  
CC derived from prostate cancer tissues.

XX Sequence 9 AA;

Query Match 53.2%; Score 33; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LFFFLP 6

DB 1 LFFFLP 6

Search completed: June 7, 2005, 23:10:47  
Job time : 66.5818 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 16.3636 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-4  
Perfect score: 62  
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:  
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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6CTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	29	46.8	11	2	US-08-464-531-57
3	29	46.8	11	2	US-08-461-598-57
4	29	46.8	11	3	US-08-322-137-57
5	29	46.8	11	3	US-08-582-333A-68
6	28	45.2	8	2	US-08-508-664-20
7	27	43.5	18	6	5185441-4
8	27	43.5	18	6	5185441-4
9	26	41.9	5	2	US-08-920-162A-30
10	26	41.9	5	3	US-09-356-931-30
11	26	41.9	5	4	US-09-895-443A-30
12	26	41.9	10	3	US-09-328-501-7
13	26	41.9	10	4	US-09-777-710A-7
14	26	41.9	16	4	US-09-009-953-15
15	25	40.3	10	3	US-08-159-339A-1023
16	25	40.3	13	2	US-08-194-981B-16
17	25	40.3	17	3	US-09-177-249-88
18	25	40.3	17	4	US-09-812-283-88
19	25	40.3	18	3	US-08-482-918-94
20	25	40.3	18	3	US-08-482-918-95
21	25	40.3	18	3	US-09-224-681-94
22	25	40.3	18	3	US-09-224-681-95
23	25	40.3	18	3	US-08-336-728A-94
24	25	40.3	18	3	US-08-336-728A-95
25	25	40.3	18	4	US-09-635-251-94
26	25	40.3	18	4	US-09-635-251-95
27	25	40.3	18	4	US-09-471-276-1473

28	24	38.7	7	3	US-09-103-478-5	Sequence 5, Appl
29	24	38.7	7	3	US-09-103-478-17	Sequence 17, Appl
30	24	38.7	7	3	US-09-193-931C-5	Sequence 5, Appl
31	24	38.7	7	3	US-09-193-931C-17	Sequence 17, Appl
32	24	38.7	7	4	US-09-026-221-5	Sequence 5, Appl
33	24	38.7	7	4	US-09-026-221-17	Sequence 17, Appl
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35	24	38.7	7	4	US-09-516-052-17	Sequence 17, Appl
36	24	38.7	9	2	US-08-934-222-106	Sequence 106, App
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38	24	38.7	9	2	US-09-207-621-106	Sequence 106, App
39	24	38.7	9	2	US-08-532-818-106	Sequence 106, App
40	24	38.7	9	3	US-09-231-797-106	Sequence 106, App
41	24	38.7	9	3	US-08-934-224-106	Sequence 106, App
42	24	38.7	9	3	US-08-933-843-106	Sequence 106, App
43	24	38.7	9	3	US-08-934-223-106	Sequence 106, App
44	24	38.7	9	3	US-09-413-492-106	Sequence 106, App
45	24	38.7	12	4	US-10-118-575A-7	Sequence 7, Appl
46	24	38.7	13	5	PCT-US94-10257A-16	Sequence 16, Appl
47	24	38.7	16	3	US-08-213-419B-7	Sequence 7, Appl
48	24	38.7	5	3	US-08-812-586-25	Sequence 25, Appl
49	24	38.7	5	3	US-08-812-586-35	Sequence 35, Appl
50	24	38.7	5	4	US-09-535-832A-26	Sequence 26, Appl
51	23	37.1	7	2	US-08-559-492-10	Sequence 10, Appl
52	23	37.1	8	3	US-09-171-337A-17	Sequence 17, Appl
53	23	37.1	8	4	US-09-631-022-17	Sequence 17, Appl
54	23	37.1	8	4	US-08-979-847B-150	Sequence 150, App
55	23	37.1	8	4	US-08-979-847B-151	Sequence 151, App
56	23	37.1	8	4	US-08-979-847B-152	Sequence 152, App
57	23	37.1	9	3	US-08-159-339A-1217	Sequence 1217, App
58	23	37.1	9	3	US-08-159-339A-1218	Sequence 1218, App
59	23	37.1	9	3	US-09-492-543-159	Sequence 149, App
60	23	37.1	9	3	US-09-492-543-159	Sequence 159, App
61	23	37.1	9	4	US-09-527-487-5	Sequence 5, Appl
62	23	37.1	9	4	US-09-239-043D-402	Sequence 402, App
63	23	37.1	9	4	US-09-462-453-20	Sequence 20, Appl
64	23	37.1	10	3	US-08-159-339A-1219	Sequence 1219, App
65	23	37.1	10	4	US-09-239-043D-403	Sequence 403, App
66	23	37.1	11	2	US-08-508-664-13	Sequence 13, Appl
67	23	37.1	11	4	US-09-239-043D-366	Sequence 366, App
68	23	37.1	11	4	US-09-239-043D-404	Sequence 404, App
69	23	37.1	11	4	US-09-239-043D-1657	Sequence 1657, App
70	23	37.1	14	3	US-09-082-420-16	Sequence 16, Appl
71	23	37.1	15	3	US-08-159-339A-1215	Sequence 1215, App
72	23	37.1	15	4	US-09-009-953-176	Sequence 176, App
73	23	37.1	15	4	US-09-148-545-224	Sequence 224, App
74	23	37.1	15	4	US-09-947-372A-28	Sequence 28, Appl
75	23	37.1	15	4	US-09-239-043D-2151	Sequence 2151, App
76	23	37.1	15	4	US-09-563-222C-63	Sequence 63, Appl
77	23	37.1	15	5	PCT-US93-06751-86	Sequence 86, Appl
78	23	37.1	16	4	US-09-009-953-25	Sequence 25, Appl
79	23	37.1	17	4	US-09-148-545-221	Sequence 221, App
80	23	37.1	18	1	US-08-451-472-18	Sequence 18, Appl
81	23	37.1	18	1	US-08-451-472-48	Sequence 48, Appl
82	23	37.1	18	1	US-08-451-472-68	Sequence 68, Appl
83	23	37.1	18	1	US-09-171-337A-16	Sequence 16, Appl
84	23	37.1	18	4	US-09-631-022-16	Sequence 16, Appl
85	23	37.1	18	4	US-09-471-276-863	Sequence 863, App
86	22.5	36.3	18	4	US-09-311-784A-254	Sequence 454, App
87	22.5	36.3	15	4	US-09-009-953-51	Sequence 51, Appl
88	22.5	36.3	15	4	US-09-009-953-54	Sequence 54, Appl
89	22.5	36.3	15	4	US-09-009-953-60	Sequence 60, Appl
90	22.5	36.3	15	4	US-09-009-953-63	Sequence 63, Appl
91	22	35.5	5	2	US-08-920-162A-24	Sequence 24, Appl
92	22	35.5	5	2	US-08-920-162A-25	Sequence 25, Appl
93	22	35.5	5	2	US-09-356-931-24	Sequence 24, Appl
94	22	35.5	5	3	US-09-356-931-25	Sequence 25, Appl
95	22	35.5	5	3	US-09-356-931-26	Sequence 26, Appl
96	22	35.5	5	3	US-08-703-675C-24	Sequence 24, Appl
97	22	35.5	5	3	US-08-703-675C-25	Sequence 25, Appl
98	22	35.5	5	3	US-08-703-675C-26	Sequence 26, Appl
99	22	35.5	5	3	US-09-471-276-1473	Sequence 24, Appl
100	22	35.5	5	4	US-09-895-443A-24	Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-803-4  
Sequence 4, Application US/09641803  
Patent No. 6500798  
GENERAL INFORMATION:  
APPLICANT: STANTON, G. John  
APPLICANT: HUGHES, Thomas K.  
APPLICANT: BOLDOGH, Istvan  
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
FILE REFERENCE: 265.00220101  
CURRENT APPLICATION NUMBER: US/09/641,803  
CURRENT FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: 60/149,310  
PRIOR FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO. 4  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-4

Query Match 100.0%; Score 62; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFPLPVNVLP 12  
DB 1 LFFPLPVNVLP 12

RESULT 2  
US-08-464-531-57  
Sequence 57, Application US/08464531  
Patent No. 5789184  
GENERAL INFORMATION:  
APPLICANT: FOMLICKS, Dana M.  
APPLICANT: BROACH, Jim  
APPLICANT: MANFREDI, John  
APPLICANT: KLEIN, Christine  
APPLICANT: MURPHY, Andrew J.  
APPLICANT: PAUL, Jeremy  
APPLICANT: TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,531  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/322,137

FILING DATE: 13-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/309,313  
FILING DATE: 20-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: FOMLICKS-2G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-464-531-57

Query Match 46.8%; Score 29; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. .94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
DB 6 FFFLP 10

RESULT 3  
US-08-461-598-57  
Sequence 57, Application US/08461598  
Patent No. 5876951  
GENERAL INFORMATION:  
APPLICANT: FOMLICKS, Dana M.  
APPLICANT: BROACH, Jim  
APPLICANT: MANFREDI, John  
APPLICANT: KLEIN, Christine  
APPLICANT: MURPHY, Andrew J.  
APPLICANT: PAUL, Jeremy  
APPLICANT: TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,598  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/322,137  
FILING DATE: 13-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/309,313  
FILING DATE: 20-SEP-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: FOLWKES=2F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-461-598-57

Query Match 46.8%; Score 29; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
Db 6 FFFLP 10

## RESULT 4

US-08-322-137-57

Sequence 57, Application US/08322137  
Patent No. 6100042  
GENERAL INFORMATION:  
APPLICANT: FOLWKES, Dana M.  
APPLICANT: BROACH, Jim  
APPLICANT: MANFREDI, John  
APPLICANT: KLEIN, Christine  
APPLICANT: MURPHY, Andrew J.  
APPLICANT: PAUL, Jeremy  
APPLICANT: TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/322,137  
FILING DATE: 13-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/309,313  
FILING DATE: 20-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: FOLWKES=2C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-322-137-57

Query Match 46.8%; Score 29; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
Db 6 FFFLP 10

## RESULT 5

US-08-582-333A-68

Sequence 68, Application US/08582333A  
Patent No. 6255059

GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
APPLICANT: Murphy, Andrew J. M.  
TITLE OF INVENTION: Methods and Compositions for  
TITLE OF INVENTION: Identifying Receptor Effectors  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/582,333A  
FILING DATE: 17-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Catherine J. Kara  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: CPI-012CP5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-4214  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-582-333A-68

Query Match 46.8%; Score 29; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
Db 6 FFFLP 10

## RESULT 6

US-08-508-664-20  
; Sequence 20, Application US/08508664  
; Patent No. 5840542  
; GENERAL INFORMATION:  
; APPLICANT: KANG, YUP  
; APPLICANT: YOON, Ji-Won  
; TITLE OF INVENTION: METHOD FOR MANUFACTURE OF PROINSULIN  
; TITLE OF INVENTION: WITH HIGH EXPORT YIELD  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Darby & Darby PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/508,664  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, S. Peter  
; REGISTRATION NUMBER: 25,351  
; REFERENCE/DOCKET NUMBER: 0136/0B300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7700  
; TELEFAX: 212-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CONN PEPTIDE  
US-08-508-664-20

Query Match 45.2%; Score 28; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFLPVV 8  
|||:|:  
Db 1 FFYTPIV 7

RESULT 7  
5185441-4  
; Patent No. 5185441  
; APPLICANT: WALINER, BARBARA P.; HESSIONS, CATHERINE  
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA  
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE  
; FUNCTION ASSOCIATED ANTIGEN-3  
; NUMBER OF SEQUENCES: 41  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/237,309  
; FILING DATE: 26-AUG-1988  
; SEQ ID NO: 4:  
; LENGTH: 18  
5185441-4

Query Match 43.5%; Score 27; DB 6; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVNVLP 12  
|||:|:  
Db 1 FFYLVLSLP 10

RESULT 8  
5185441-4  
; Patent No. 5185441  
; APPLICANT: WALINER, BARBARA P.; HESSIONS, CATHERINE  
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA  
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE  
; FUNCTION ASSOCIATED ANTIGEN-3  
; NUMBER OF SEQUENCES: 41  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/237,309  
; FILING DATE: 26-AUG-1988  
; SEQ ID NO: 4:  
; LENGTH: 18  
5185441-4

Query Match 43.5%; Score 27; DB 6; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVNVLP 12  
|||:|:  
Db 1 FFYLVLSLP 10

RESULT 9  
US-08-920-162A-30  
; Sequence 30, Application US/08920162A  
; Patent No. 5985242  
; GENERAL INFORMATION:  
; APPLICANT: Pindels, M. et al.  
; TITLE OF INVENTION: Modulators of [SYMBOL 98 \f "Symbol"]-Amyloid Peptide  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/920,162A  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/703,675  
; FILING DATE: 27-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 21-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KARA, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400

TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
US-09-920-162A-30

Query Match  
Best Local Similarity 41.9%; Score 26; DB 2; Length 5;  
Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
DB 1 LFFFL 5

RESULT 10  
US-09-356-931-30  
Sequence 30, Application US/09356931  
Patent No. 6277826  
GENERAL INFORMATION:  
APPLICANT: FIndeis, M. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide  
TITLE OF INVENTION: Aggregation Comprising D-Amino Acids  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1784  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/356,931  
FILING DATE: 19-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/920,162  
FILING DATE: 27-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/897,342  
FILING DATE: 21-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/703,675  
FILING DATE: 27-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Jr., Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
US-09-356-931-30

Query Match  
Best Local Similarity 41.9%; Score 26; DB 3; Length 5;  
Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
DB 1 LFFFL 5

RESULT 11  
US-09-895-443A-30  
Sequence 30, Application US/09895443A  
Patent No. 6689752  
GENERAL INFORMATION:  
APPLICANT: FIndeis, MARK A.  
APPLICANT: GETTER, MALCOLM L.  
APPLICANT: MUSSO, GARY  
APPLICANT: SIGNER, ETHAN R.  
APPLICANT: WAKERFIELD, JAMES  
APPLICANT: MOLINAUX, SUSAN  
APPLICANT: CHIN, JOSEPH  
APPLICANT: LEE, JUNG-JA  
APPLICANT: KELLEY, MICHAEL  
APPLICANT: KOMAR-PANICUCCI, SONJA  
APPLICANT: ARICO-MUENDEL, CHRISTOPHER C.  
APPLICANT: PHILLIPS, KATHRYN  
APPLICANT: HAYWARD, NEIL J.  
TITLE OF INVENTION: MODULATORS OF BETA-AMYLOID PEPTIDE  
TITLE OF INVENTION: AGGREGATION COMPRISING D-AMINO ACIDS  
FILE REFERENCE: PPI-0016CP4CN2  
CURRENT APPLICATION NUMBER: US/09/895,443A  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/356931  
PRIOR FILING DATE: 1990-07-19  
PRIOR APPLICATION NUMBER: 08/920162  
PRIOR FILING DATE: 1997-08-27  
PRIOR APPLICATION NUMBER: 08/548998  
PRIOR FILING DATE: 1995-10-27  
PRIOR APPLICATION NUMBER: 08/616081  
PRIOR FILING DATE: 1996-03-14  
PRIOR APPLICATION NUMBER: 08/703675  
PRIOR FILING DATE: 1996-08-27  
PRIOR APPLICATION NUMBER: 08/897342  
PRIOR FILING DATE: 1997-07-21  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide  
NAME/KEY: VARIANT  
LOCATION: (1)-(5)  
OTHER INFORMATION: Modified site; D amino acid  
US-09-895-443A-30

Query Match  
Best Local Similarity 41.9%; Score 26; DB 4; Length 5;  
Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
DB 1 LFFFL 5

```
RESULT 12
US-09-328-501-7
; Sequence 7, Application US/09328501A
; Patent No. 6258581
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6258581omu
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: Ceramidase Gene
; FILE REFERENCE: 1422-0377P
; CURRENT APPLICATION NUMBER: US/09/328,501A
; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 10-234769 JAPAN
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-328-501-7

Query Match
Best Local Similarity 41.9%; Score 26; DB 3; Length 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPVNV 10
DB 2 FLEVNI 8

RESULT 13
US-09-777-710A-7
; Sequence 7, Application US/09777710A
; Patent No. 6489117
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6489117omu et al.
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-7

Query Match
Best Local Similarity 41.9%; Score 26; DB 4; Length 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPVNV 10
DB 2 FLEVNI 8

RESULT 14
US-09-009-953-15
; Sequence 15, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
```

```
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-009-953-15

Query Match
Best Local Similarity 41.9%; Score 26; DB 4; Length 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFLPVNV 10
DB 5 FFLPALPV 12

RESULT 15
US-08-159-339A-1023
; Sequence 1023, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Betteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 1023:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-1023

Query Match  
Best Local Similarity 40.3%; Score 25; DB 3; Length 10;  
Best Local Similarity 55.6%; Pred. No. 3.8e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLLPVNV 11  
Db 2 FLLRVVDIL 10

RESULT 16  
US-08-194-981E-16  
Sequence 16, Application US/08194981E  
Patent No. 5886157  
GENERAL INFORMATION:  
APPLICANT: GUENGERICH, F. Peter  
APPLICANT: GUO, Zuyi  
APPLICANT: SANDHU, Punam  
APPLICANT: GILLAM, Elizabeth M. J.  
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF  
TITLE OF INVENTION: HUMAN  
TITLE OF INVENTION: CYTOCHROME P450  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: NEEDLE & ROSENBERG, P.C.  
STREET: Suite 1200, 127 Peachtree Street, NE  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,981E  
FILING DATE: February 10, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Selby  
REGISTRATION NUMBER: 38,298  
REFERENCE/DOCKET NUMBER: 22000.0022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-194-981E-16

Query Match  
Best Local Similarity 40.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 62.5%; Pred. No. 5e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFLLPV 8  
Db 5 LAVFLPVI 12

RESULT 17  
US-09-177-249-88  
Sequence 88, Application US/09177249  
Patent No. 6229064  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Onad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
FILE REFERENCE: 023070-086120US  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: US 09/071,838  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 88  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-09-177-249-88

Query Match  
Best Local Similarity 40.3%; Score 25; DB 3; Length 17;  
Best Local Similarity 66.7%; Pred. No. 6.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFLLPV 7  
Db 9 WFFLLP 14

RESULT 18  
US-09-812-283-88  
Sequence 88, Application US/09812283  
Patent No. 6828477  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
FILE REFERENCE: 023070-086120US  
CURRENT FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: 09/177,249  
PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: US 09/071,838  
PRIOR FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 88  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-09-812-283-88

Query Match 40.3%; Score 25; DB 4; Length 17;  
Best Local Similarity 66.7%; Pred. No. 6.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPLPV 7  
Db 9 FFPLPV 14

RESULT 19  
US-08-482-918-94  
Sequence 94, Application US/08482918  
Patent No. 6207417  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Bosseiman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,918  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/33005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-918-94

Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFPLPV 8  
Db 10 FFMLPV 16

RESULT 20

US-08-482-918-95  
Sequence 95, Application US/08482918  
Patent No. 6207417  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Bosseiman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,918  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/33005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-918-95

Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFPLPV 8  
Db 10 FFMLPV 16

RESULT 21  
US-09-224-681-94  
Sequence 94, Application US/09224681  
Patent No. 6207454  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Bosseiman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene  
Transfer with Stem Cell Factor (SCF) Polypeptide  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/224,681  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,893  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/449,653  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/35199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-224-681-94  
Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FFPLPV 8  
DB 10 FFMLPV 16  
RESULT 22  
US-09-224-681-95  
Sequence 95, Application US/09224681  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Bosseiman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene  
NUMBER OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
CITY: Chicago  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
STATE: Illinois

COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/224,681  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,893  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/449,653  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/35199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-224-681-95  
Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FFPLPV 8  
DB 10 FFMLPV 16  
RESULT 23  
US-08-336-728A-94  
Sequence 94, Application US/08336728A  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Bosseiman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: 07/982,255  
APPLICATION NUMBER: US/08/336,728A  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/32956  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-728A-94

Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 2;

QY 2 PFELPV 8  
Db 10 FPMPLPV 16

RESULT 24  
US-08-336-728A-95  
Sequence 95, Application US/08336728A  
Patent No. 6207802  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Boesselman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: 07/982,255  
APPLICATION NUMBER: US/08/336,728A  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/32956  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-728A-95

Query Match 40.3%; Score 25; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 2;

QY 2 PFELPV 8  
Db 10 FPMPLPV 16

RESULT 25  
US-09-635-251-94  
Sequence 94, Application US/09635251  
Patent No. 6759215  
GENERAL INFORMATION:  
APPLICANT: Zeebo, Kristina M.  
APPLICANT: Boesselman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,251
FILING DATE: 07-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,182
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 04-OCT-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32957A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-635-251-94

Query Match          40.3% Score 25; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 FFFLPV 8
        |||||
        10 FFMPLPV 16

Db

RESULT 26
US-09-635-251-95
Sequence 95, Application US/09635251
Patent No. 6759215
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristalina M.
Bosselman, Robert A.
Sugger, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,251
```

```

FILING DATE: 07-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,182
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 04-OCT-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32957A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-635-251-95

Query Match          40.3% Score 25; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 FFFLPV 8
        |||||
        10 FFMPLPV 16

Db

RESULT 27
US-09-471-276-1473
Sequence 1473, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: GENSER. 025CPI
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent. pm
SEQ ID NO 1473
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
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; LOCATION: -16...-1
US-09-471-276-1473

Query Match      40.3%; Score 25; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LFFVLPVV 8
        |||||
        11 LFFVGLVV 18

RESULT 28
US-09-103-478-5
; Sequence 5, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-103-478-5

Query Match      38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
; Sequence 17, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-103-478-17

Query Match      38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 LPVVNV 10
        |||||
        1 LPIANV 6

RESULT 30
US-09-193-931C-5
; Sequence 5, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
```

;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: US 09/026,221  
;; PRIOR FILING DATE: 1998-02-19  
;; PRIOR APPLICATION NUMBER: US 08/804,534  
;; PRIOR FILING DATE: 1997-02-21  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: DNA binding  
;; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor  
;; OTHER INFORMATION: (CBF) protein B domain homolog with transcription  
;; OTHER INFORMATION: activation function  
US-09-193-931C-5

Query Match 38.7%; Score 24; DB 3; Length 7;  
Best Local Similarity 42.9%; Pred. No. 4.1e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPEVNV 11  
: : :  
Db 1 LPIANVI 7

RESULT 31  
US-09-193-931C-17  
; Sequence 17, Application US/09193931C  
; Patent No. 6320102  
; GENERAL INFORMATION:  
; APPLICANT: Harada, John  
; APPLICANT: Lotan, Tamara  
; APPLICANT: Ohto, Masa-aki  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
; FILE REFERENCE: 023070-077620  
; CURRENT APPLICATION NUMBER: US/09/193,931C  
; CURRENT FILING DATE: 1998-11-17  
; PRIOR APPLICATION NUMBER: US 09/103,478  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: US 09/026,221  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 08/804,534  
; PRIOR FILING DATE: 1997-02-21  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNA binding  
; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor  
; OTHER INFORMATION: (CBF-A) protein yeast homolog  
US-09-193-931C-17

Query Match 38.7%; Score 24; DB 3; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPEVNV 10  
: : :  
Db 1 LPIANVI 6

RESULT 32  
US-09-026-221-5  
; Sequence 5, Application US/09026221  
; Patent No. 6545201

;; GENERAL INFORMATION:  
;; APPLICANT: Harada, John J.  
;; APPLICANT: Lotan, Tamara  
;; APPLICANT: Ohto, Masa-aki  
;; APPLICANT: Goldberg, Robert B.  
;; APPLICANT: Fischer, Robert L.  
;; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
;; NUMBER OF SEQUENCES: 18  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/026,221  
;; FILING DATE: 19-FEB-1998  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/804,534  
;; FILING DATE: 21-FEB-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bastian, Kevin L.  
;; REGISTRATION NUMBER: 34,774  
;; REFERENCE/DOCKET NUMBER: 023070-077610US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-026-221-5

Query Match 38.7%; Score 24; DB 4; Length 7;  
Best Local Similarity 42.9%; Pred. No. 4.1e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPEVNV 11  
: : :  
Db 1 LPIANVI 7

RESULT 33  
US-09-026-221-17  
; Sequence 17, Application US/09026221  
; Patent No. 6545201  
; GENERAL INFORMATION:  
; APPLICANT: Harada, John J.  
; APPLICANT: Lotan, Tamara  
; APPLICANT: Ohto, Masa-aki  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: Fischer, Robert L.  
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,221  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-077610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-026-221-17

Query Match 38.7%; Score 24; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNV 10  
||: ||  
Db 1 LPIANV 6

RESULT 34  
US-09-516-052-5  
Sequence 5, Application US/09516052  
Patent No. 6781035  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-Aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: Bui, Anhthu  
APPLICANT: Khong, Raymond  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077630US  
CURRENT APPLICATION NUMBER: US/09/516,052  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 09/193,931  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA binding  
OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor  
OTHER INFORMATION: (CBF) protein B domain homolog with transcription  
US-09-516-052-5

Query Match 38.7%; Score 24; DB 4; Length 7;  
Best Local Similarity 42.9%; Pred. No. 4.1e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNV 11  
||: ||  
Db 1 LPIANV 7

RESULT 35  
US-09-516-052-17  
Sequence 17, Application US/09516052  
Patent No. 6781035  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-Aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: Bui, Anhthu  
APPLICANT: Khong, Raymond  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077630US  
CURRENT APPLICATION NUMBER: US/09/516,052  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 09/193,931  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 17  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA binding  
OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor  
OTHER INFORMATION: (CBF-A) protein yeast homolog  
US-09-516-052-17

Query Match 38.7%; Score 24; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNV 10  
||: ||  
Db 1 LPIANV 6

RESULT 36  
US-08-934-222-106  
Sequence 106, Application US/08934222  
Patent No. 5928896  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,222  
FILING DATE: 19-SEPT-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ. ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-222-106

Query Match 38.7%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVL 12  
| | | | |  
Db 2 PFGNVL 8

RESULT 37  
US-08-933-402-106  
Sequence 106, Application US/08933402  
Patent No. 594887  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ. ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-106

Query Match 38.7%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVL 12  
| | | | |  
Db 2 PFGNVL 8

RESULT 38  
US-09-207-621-106  
Sequence 106, Application US/09207621  
Patent No. 5952465  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/207,621  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ. ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-207-621-106

Query Match 38.7%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVL 12  
| | | | |  
Db 2 PFGNVL 8

RESULT 39  
US-08-532-818-106  
; Sequence 106, Application US/08532818  
; Patent No. 5965698  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Iacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-532-818-106

Query Match 38.7%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVLIP 12  
| | | | |  
DB 2 PFGNVLIP 8

RESULT 40  
US-09-231-797-106  
; Sequence 106, Application US/09231797  
; Patent No. 6084066  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,797  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Iacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-231-797-106

Query Match 38.7%; Score 24; DB 3; Length 9;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVTNVLIP 12  
| | | | |  
DB 2 PFGNVLIP 8

Search completed: June 7, 2005, 23:23:14  
Job time : 18.3636 secs



GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: June 7, 2005, 23:00:52 ; Search time 54 Seconds  
(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-4  
Perfect score: 62  
Sequence: 1 LEFPLPVNVLP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA.\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	62	100.0	12	16	US-10-691-157-4
3	62	100.0	12	17	US-10-691-330-4
4	31	50.0	16	16	US-10-182-110-2
5	31	50.0	9	14	US-10-119-536A-89
6	29	46.8	9	14	US-10-119-536A-182
7	29	46.8	10	10	US-09-935-430-446
8	29	46.8	10	14	US-10-277-292-446
9	29	46.8	10	15	US-10-280-340-446
10	29	46.8	11	9	US-09-747-774A-68
11	29	46.8	11	10	US-09-309-196-57

12	29	46.8	11	10	US-09-201-396-38	Sequence 38, Appl
13	29	46.8	11	10	US-09-953-354-68	Sequence 68, Appl
14	29	46.8	11	14	US-10-277-607-38	Sequence 38, Appl
15	29	46.8	11	15	US-10-263-341-57	Sequence 57, Appl
16	29	46.8	11	15	US-10-600-003-57	Sequence 57, Appl
17	29	46.8	11	17	US-10-752-478-68	Sequence 68, Appl
18	29	46.8	11	17	US-10-116-252-22	Sequence 22, Appl
19	29	46.8	13	14	US-10-706-391-63	Sequence 63, Appl
20	29	46.8	14	14	US-10-014-340-611	Sequence 611, App
21	29	46.8	14	14	US-10-014-340-612	Sequence 612, App
22	29	46.8	18	14	US-10-084-813-249	Sequence 249, App
23	29	46.8	18	14	US-10-084-813-250	Sequence 250, App
24	28	45.2	9	14	US-10-119-536A-84	Sequence 84, Appl
25	28	45.2	9	14	US-10-119-536A-92	Sequence 92, Appl
26	27	43.5	9	15	US-10-447-161-61	Sequence 61, Appl
27	27	43.5	9	16	US-10-415-841A-38	Sequence 38, Appl
28	27	43.5	9	16	US-10-362-715-20	Sequence 20, Appl
29	27	43.5	10	17	US-10-475-049A-103	Sequence 103, App
30	27	43.5	11	10	US-09-201-396-6	Sequence 6, Appl
31	27	43.5	11	14	US-10-277-607-6	Sequence 6, Appl
32	27	43.5	14	14	US-10-269-171A-6	Sequence 6, Appl
33	27	43.5	15	15	US-10-149-135-1941	Sequence 1941, Ap
34	27	43.5	15	15	US-10-149-135-1950	Sequence 1950, Ap
35	27	43.5	15	15	US-10-149-135-2026	Sequence 2026, Ap
36	27	43.5	15	15	US-10-149-135-2412	Sequence 2412, Ap
37	26	41.9	5	9	US-09-895-443-30	Sequence 30, Appl
38	26	41.9	8	15	US-10-137-867-292	Sequence 292, App
39	26	41.9	9	14	US-10-119-536A-176	Sequence 176, App
40	26	41.9	9	14	US-10-119-536A-190	Sequence 190, App
41	26	41.9	9	15	US-10-057-475B-10903	Sequence 10903, A
42	26	41.9	9	15	US-10-057-475B-10956	Sequence 10956, A
43	26	41.9	9	15	US-10-154-884B-10903	Sequence 10903, A
44	26	41.9	9	15	US-10-154-884B-10956	Sequence 10956, A
45	26	41.9	17	17	US-10-705-459-281	Sequence 281, App
46	26	41.9	10	9	US-09-777-710A-7	Sequence 7, Appl
47	26	41.9	10	10	US-09-935-430-427	Sequence 427, App
48	26	41.9	10	10	US-09-935-430-503	Sequence 503, App
49	26	41.9	10	10	US-09-935-440-613	Sequence 613, App
50	26	41.9	10	10	US-09-572-440B-1109	Sequence 1109, Ap
51	26	41.9	10	14	US-10-277-252-427	Sequence 427, App
52	26	41.9	10	14	US-10-277-252-503	Sequence 503, App
53	26	41.9	10	14	US-10-277-292-613	Sequence 613, App
54	26	41.9	10	15	US-10-280-340-427	Sequence 427, App
55	26	41.9	10	15	US-10-280-340-503	Sequence 503, App
56	26	41.9	10	15	US-10-280-340-613	Sequence 613, App
57	26	41.9	14	14	US-10-206-639-37	Sequence 37, Appl
58	26	41.9	14	17	US-10-700-922-39	Sequence 39, Appl
59	26	41.9	15	14	US-10-294-891-11	Sequence 11, Appl
60	26	41.9	15	17	US-10-920-313-11	Sequence 11, Appl
61	26	41.9	16	13	US-10-103-385-15	Sequence 15, Appl
62	26	41.9	16	16	US-10-771-931-22	Sequence 22, Appl
63	26	41.9	17	11	US-09-833-245-570	Sequence 570, App
64	26	41.9	18	14	US-10-084-813-248	Sequence 248, App
65	25	40.3	10	17	US-10-801-990-86	Sequence 86, Appl
66	25	40.3	11	14	US-10-119-528-31	Sequence 31, Appl
67	25	40.3	12	14	US-10-259-171A-5	Sequence 5, Appl
68	25	40.3	12	16	US-10-685-858-27	Sequence 27, Appl
69	25	40.3	12	17	US-10-801-990-370	Sequence 370, App
70	25	40.3	13	9	US-09-826-290-122	Sequence 122, App
71	25	40.3	13	15	US-10-264-309-305	Sequence 305, App
72	25	40.3	13	17	US-10-801-990-142	Sequence 142, App
73	25	40.3	14	14	US-10-261-798-40	Sequence 40, Appl
74	25	40.3	14	15	US-10-162-134A-6	Sequence 6, Appl
75	25	40.3	14	15	US-10-162-134A-10	Sequence 10, Appl
76	25	40.3	14	17	US-10-240-035-10	Sequence 40, Appl
77	25	40.3	16	10	US-09-880-748-2250	Sequence 2250, Ap
78	25	40.3	16	15	US-10-293-418-2250	Sequence 2250, Ap
79	25	40.3	17	9	US-09-071-838-48	Sequence 88, Appl
80	25	40.3	17	10	US-09-759-130B-354	Sequence 354, App
81	25	40.3	17	14	US-10-189-513-84	Sequence 84, Appl
82	25	40.3	17	14	US-10-213-122-88	Sequence 88, Appl
83	25	40.3	17	14	US-10-188-695-84	Sequence 84, Appl
84	25	40.3	17	16	US-10-741-790-354	Sequence 354, App

85	25	40.3	18	9	US-09-005-243-94	Sequence 94, Appl
86	25	40.3	18	9	US-09-005-243-95	Sequence 95, Appl
87	25	40.3	18	9	US-09-224-683-94	Sequence 94, Appl
88	25	40.3	18	9	US-09-224-683-95	Sequence 95, Appl
89	25	40.3	18	16	US-10-175-608-94	Sequence 94, Appl
90	25	40.3	18	16	US-10-175-608-95	Sequence 95, Appl
91	25	40.3	18	17	US-10-620-642-94	Sequence 94, Appl
92	25	40.3	18	17	US-10-620-642-95	Sequence 95, Appl
93	25	40.3	18	17	US-10-926-683-1473	Sequence 1473, Ap
94	24	38.7	10	16	US-10-432-234A-187	Sequence 187, App
95	24	38.7	10	16	US-10-432-234A-188	Sequence 188, App
96	24	38.7	10	16	US-10-432-234A-189	Sequence 189, App
97	24	38.7	10	16	US-10-432-234A-190	Sequence 190, App
98	24	38.7	10	16	US-10-432-234A-191	Sequence 191, App
99	24	38.7	10	16	US-10-432-234A-192	Sequence 192, App
100	24	38.7	12	14	US-10-075-869-41	Sequence 41, Appl

## ALIGNMENTS

## RESULT 1

US-10-281-652-4  
; Sequence 4, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDG, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265, 00220101  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-4

Query Match 100.0%; Score 62; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00097;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12  
|||||

DB 1 LFFFLPVNVLP 12  
|||||

## RESULT 2

US-10-691-157-4  
; Sequence 4, Application US/10691157  
; Publication No. US2004026681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDG, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265, 00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-4

Query Match 100.0%; Score 62; DB 16; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00097;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12  
|||||

DB 1 LFFFLPVNVLP 12  
|||||

## RESULT 3

US-10-691-330-4  
; Sequence 4, Application US/10691330  
; Publication No. US20050042500A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldog, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265, 00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-4

Query Match 100.0%; Score 62; DB 17; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00097;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12  
|||||

DB 1 LFFFLPVNVLP 12  
|||||

## RESULT 4

US-10-182-110-2  
; Sequence 2, Application US/10182110  
; Publication No. US2004017153A1  
; GENERAL INFORMATION:  
; APPLICANT: Regen Therapeutics plc  
; APPLICANT: Georgiades, Jerzy A  
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use  
; FILE REFERENCE: AAT-14173  
; CURRENT APPLICATION NUMBER: US/10/182,110

```
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: GB0001825.9
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated version of a peptide found in colostrin
US-10-182-110-2
```

```
Query Match          50.0%; Score 31; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 FLPVNV 9
    |||||
Db 1 FLPVNV 6
```

```
RESULT 5
US-10-119-536A-89
; Sequence 89, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandaal, Brian Berg
; TITLE OF INVENTION: Method for identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-89
```

```
Query Match          50.0%; Score 31; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LFFLPV 8
    |||||
Db 2 LFFLPV 9
```

```
RESULT 6
US-10-119-536A-182
; Sequence 182, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandaal, Brian Berg
; TITLE OF INVENTION: Method for identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-182
```

```
Query Match          46.8%; Score 29; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LFFLPV 8
    |||||
Db 2 LFFLPV 9
```

```
RESULT 7
US-09-935-430-446
; Sequence 446, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ETD, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-446
```

```
Query Match          46.8%; Score 29; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 FFFLPVNV 11
    |||||
Db 1 FFFLPVNV 10
```

```
RESULT 8
US-10-277-292-446
; Sequence 446, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ETD, PIA
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-446
```

FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 446  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-446

Query Match 46.8%; Score 29; DB 14; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FFELPVVNL 11  
| | | | | : |  
DB 1 FTHLPVSNIL 10

RESULT 9  
US-10-280-340-446  
Sequence 446, Application US/10280340  
Publication No. US20030207835A1  
GENERAL INFORMATION:  
APPLICANT: PARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALILTA-EID, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/280,340  
CURRENT FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 446  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-446

Query Match 46.8%; Score 29; DB 15; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FFELPVVNL 11  
| | | | | : |  
DB 1 FTHLPVSNIL 10

RESULT 10  
US-09-747-774A-68

Sequence 68, Application US/09747774A  
Publication No. US20010026926A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
APPLICANT: Murphy, Andrew J. M.  
APPLICANT: Broach, James R.  
APPLICANT: Manfredi, John  
APPLICANT: Paul, Jeremy  
APPLICANT: Fowlkes, Dana M.  
APPLICANT: Trueheart, Joshua  
TITLE OF INVENTION: Methods and Compositions for Identifying  
TITLE OF INVENTION: Receptor Effectors  
FILE REFERENCE: CFI-012C95DV  
CURRENT APPLICATION NUMBER: US/09/747,774A  
CURRENT FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: US 08/582,333  
PRIOR FILING DATE: 1996-01-17  
PRIOR APPLICATION NUMBER: US 08/464,531  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/461,598  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/461,383  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/463,181  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/322,137  
PRIOR FILING DATE: 1994-10-13  
PRIOR APPLICATION NUMBER: US 08/309,313  
PRIOR FILING DATE: 1994-09-20  
PRIOR APPLICATION NUMBER: US 08/190,328  
PRIOR FILING DATE: 1994-01-31  
PRIOR APPLICATION NUMBER: US 08/041,431  
PRIOR FILING DATE: 1993-03-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 68  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-09-747-774A-68

Query Match 46.8%; Score 29; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFELP 6  
| | | | |  
DB 6 FFELP 10

RESULT 11  
US-09-309-196-57  
Sequence 57, Application US/09309196  
Publication No. US20030008380A1  
GENERAL INFORMATION:  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: BROACH, Jim  
APPLICANT: MANFREDI, John  
APPLICANT: KLEIN, Christine  
APPLICANT: MURPHY, Andrew J.  
APPLICANT: PAUL, Jeremy  
APPLICANT: TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
TITLE OF INVENTION: PHARMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/309,196  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/322,137  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: FOLMKS=2C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-309-196-57

Query Match 46.8%; Score 29; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6  
Db 6 PFPLP 10

RESULT 12  
US-09-201-396-38  
Sequence 38, Application US/09201396A  
Publication No. US2003009022A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
APPLICANT: Murphy, Andrew J.  
APPLICANT: Paul, Jeremy  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
TITLE OF INVENTION: EFFECTORS  
FILE REFERENCE: CPI-012CP9  
CURRENT APPLICATION NUMBER: US/09/201,396A  
CURRENT FILING DATE: 1998-11-30  
EARLIER APPLICATION NUMBER: 08/582,333  
EARLIER FILING DATE: 1996-01-17  
EARLIER APPLICATION NUMBER: 08/322,137  
EARLIER FILING DATE: 1994-10-13  
EARLIER APPLICATION NUMBER: 08/309,313  
EARLIER FILING DATE: 1994-09-20  
EARLIER APPLICATION NUMBER: 08/190,328  
EARLIER FILING DATE: 1994-01-31  
EARLIER APPLICATION NUMBER: 08/041,431  
EARLIER FILING DATE: 1993-03-31  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: construct  
US-09-201-396-38

Query Match 46.8%; Score 29; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6  
Db 6 PFPLP 10

RESULT 13  
US-09-953-354-68  
Sequence 68, Application US/09953354  
Publication No. US20030054402A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
APPLICANT: Murphy, Andrew J. M.  
TITLE OF INVENTION: Methods and Compositions for  
Identifying Receptor Effectors  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/953,354  
FILING DATE: 13-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/689,172  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPI-012CP7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-953-354-68

Query Match 46.8%; Score 29; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPLP 6  
Db 6 PFPLP 10

RESULT 14  
US-10-277-607-38  
Sequence 38, Application US/10277607  
Publication No. US20030166143A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
APPLICANT: Murphy, Andrew J.

APPLICANT: Paul, Jeremy I.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
FILE REFERENCE: CPI-012C9PCN  
CURRENT FILING DATE: 2003-01-31  
PRIOR APPLICATION NUMBER: US/10/277,607  
PRIOR FILING DATE: 2003-01-31  
PRIOR APPLICATION NUMBER: 09/201,396  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: 60/109,902  
PRIOR FILING DATE: 1998-11-25  
PRIOR APPLICATION NUMBER: PCT/US98/21168  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 08/946,298  
PRIOR FILING DATE: 1997-10-07  
PRIOR APPLICATION NUMBER: 08/689,172  
PRIOR FILING DATE: 1996-08-06  
PRIOR APPLICATION NUMBER: 08/582,333  
PRIOR FILING DATE: 1996-01-17  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 38  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-277-607-38

Query Match 46.8%; Score 29; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
Db 6 FFFLP 10

RESULT 15  
US-10-263-341-57  
Sequence 57, Application US/10263341  
Publication No. US20030203417A1  
GENERAL INFORMATION:  
APPLICANT: FOWLKES, Dana M.  
BROACH, Jim  
MANFREDI, John  
KLEIN, Christine  
MURPHY, Andrew J.  
PAUL, Jeremy  
TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/263,341  
FILING DATE: 01-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/322,137  
FILING DATE: 13-Oct-1994  
APPLICATION NUMBER: US 08/309,313

FILING DATE: 20-SEP-1994  
APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994  
APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: FOLWKES=2C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-10-263-341-57

Query Match 46.8%; Score 29; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
Db 6 FFFLP 10

RESULT 16  
US-10-600-003-57  
Sequence 57, Application US/10600003  
Publication No. US20040197840A1  
GENERAL INFORMATION:  
APPLICANT: FOWLKES, Dana M.  
BROACH, Jim  
MANFREDI, John  
KLEIN, Christine  
MURPHY, Andrew J.  
PAUL, Jeremy  
TRUEHEART, Joshua  
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE AND COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/600,003  
FILING DATE: 18-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/286,166  
FILING DATE: 05-APR-1999  
APPLICATION NUMBER: US 08/461,383  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/322,137  
FILING DATE: 13-Oct-1994  
APPLICATION NUMBER: US 08/309,313  
FILING DATE: 20-SEP-1994  
APPLICATION NUMBER: US 08/190,328  
FILING DATE: 31-JAN-1994

APPLICATION NUMBER: US 08/041,431  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CPI-012CP4B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-227-7400  
TELEFAX: 617-227-5941  
TELEX: 752806  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-10-600-003-57

Query Match 46.8%; Score 29; DB 16; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
| | | | |  
Db 6 FFFLP 10

RESULT 17  
US-10-752-478-68  
Sequence 68, Application US/10752478  
Publication No. US20050059135A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
Murphy, Andrew J. M.  
TITLE OF INVENTION: Methods and Compositions for  
Identifying Receptor Effectors  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHYE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/752,478  
FILING DATE: 05-Jan-2004  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPI-012CP7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-10-752-478-68

Query Match 46.8%; Score 29; DB 17; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
| | | | |  
Db 6 FFFLP 10

RESULT 18  
US-10-116-252-22  
Sequence 22, Application US/10116252  
Publication No. US20030028008A1  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,  
File Reference: PT007P1  
CURRENT APPLICATION NUMBER: US/10/116,252  
CURRENT FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: US/09/711,909  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: PCT/US00/13737  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 60/135,167  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 60/143,616  
PRIOR FILING DATE: 1999-07-13  
PRIOR APPLICATION NUMBER: 60/152,934  
PRIOR FILING DATE: 1999-09-09  
PRIOR APPLICATION NUMBER: 60/189,029  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-252-22

Query Match 46.8%; Score 29; DB 14; Length 13;  
Best Local Similarity 54.5%; Pred. No. 3.6e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFLPVVNVL 11  
| | | | | : |  
Db 2 LFFFLPLALIL 12

RESULT 19  
US-10-706-391-63  
Sequence 63, Application US/10706391  
Publication No. US20040137482A1  
GENERAL INFORMATION:  
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
APPLICANT: WASHINGTON DENTAL SERVICE  
APPLICANT: Eckert, Randal  
APPLICANT: Qi, Fengxia  
APPLICANT: Shi, Wenyan  
APPLICANT: Anderson, Maxwell H.  
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL  
FILE REFERENCE: 2101363-991600  
CURRENT APPLICATION NUMBER: US/10/706,391  
CURRENT FILING DATE: 2003-06-16  
PRIOR APPLICATION NUMBER: US 10/077,624  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 09/910,358  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 09/378,577  
PRIOR FILING DATE: 1999-08-20  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 63  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial sequence

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; FEATURE:
; OTHER INFORMATION: Design peptide
US-10-706-391-63

Query Match
Best Local Similarity 46.8%; Score 29; DB 16; Length 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPVVNVL 12
   |||: |||
Db 4 LPVLEVL 11

RESULT 20
US-10-014-340-611
; Sequence 611, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 611
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-611

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNVL 12
   | : |||
Db 4 PPINVL 10

RESULT 21
US-10-014-340-612
; Sequence 612, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 612
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-612

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNVL 12
   | : |||
Db 4 PPINVL 10

RESULT 22
US-10-084-813-249
; Sequence 249, Application US/10084813
; Publication No. US20030068615A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-249

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 18;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFFLPVNVL 11
   | |||: :
Db 6 LGFPLPLTMI 16

RESULT 23
US-10-084-813-250
; Sequence 250, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-250

Query Match
Best Local Similarity 46.8%; Score 29; DB 14; Length 18;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFFLPVNVL 11
   | |||: :
Db 2 LGFPLPLTMI 12

RESULT 24
US-10-119-536A-84
; Sequence 84, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/10091US1
```



; CURRENT APPLICATION NUMBER: US/10/119,536A  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CPN0998 immunogenic peptide  
US-10-119-536A-84

Query Match 45.2%; Score 28; DB 14; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.5e+06;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PFLPVNVY 10  
Db 1 FFLPIILV 9

RESULT 25  
US-10-119-536A-92  
; Sequence 92, Application US/10119536A  
; Publication No. US20030199438A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Allan Christian  
; APPLICANT: Vandahl, Brian Berg  
; TITLE OF INVENTION: Method for identification of proteins from Intracellular Bacteria  
; FILE REFERENCE: 4305/J09JUS1  
; CURRENT APPLICATION NUMBER: US/10/119,536A  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CPN0998 immunogenic peptide  
US-10-119-536A-92

Query Match 45.2%; Score 28; DB 14; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLFVVNVL 11  
Db 1 FLFPIILV 8

RESULT 26  
US-10-447-161-61  
; Sequence 61, Application US/10447161  
; Publication No. US20040023314A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong-fu  
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
; FILE REFERENCE: HO-P02484US1  
; CURRENT APPLICATION NUMBER: US/10/447,161  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/383,530  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-447-161-61

Query Match 43.5%; Score 27; DB 15; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLP 6  
Db 1 VYFFLP 6

RESULT 27  
US-10-415-841A-38  
; Sequence 38, Application US/10415841A  
; Publication No. US20040131598A1  
; GENERAL INFORMATION:  
; APPLICANT: Tatufo, Sabrina  
; APPLICANT: Meier, Ute-Christiane  
; APPLICANT: McMichael, Andrew James  
; APPLICANT: Bell, John Irving  
; APPLICANT: Layton, Guy  
; APPLICANT: Hunter, Michael  
; TITLE OF INVENTION: Cancer Therapy  
; FILE REFERENCE: 3547.1001-000  
; CURRENT APPLICATION NUMBER: US/10/415,841A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/04844  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-415-841A-38

Query Match 43.5%; Score 27; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLP 6  
Db 1 VYFFLP 6

RESULT 28  
US-10-362-715-20  
; Sequence 20, Application US/10362715  
; Publication No. US20040253574A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; APPLICANT: Schuler-Thurner, Beatrice  
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,  
; FILE REFERENCE: 1430/12  
; CURRENT APPLICATION NUMBER: US/10/362,715  
; CURRENT FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-362-715-20

Query Match 43.5%; Score 27; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LFFFLP 6  
:|||||  
Db 1 VFFFLP 6

RESULT 29  
US-10-475-049A-103  
; Sequence 103, Application US/10475049A  
; Publication No. US20050019854A1  
; GENERAL INFORMATION:  
; APPLICANT: Gross, Rene  
; APPLICANT: Lajoix, Anne-Dominique  
; APPLICANT: Ribes, Gerard  
; TITLE OF INVENTION: Novel Method For Screening Inhibitors of  
; TITLE OF INVENTION: the Linkage Between the Neuronal Nitric Oxide Synthase  
; TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal  
; FILE REFERENCE: 50319/005001  
; CURRENT APPLICATION NUMBER: US/10/475,049A  
; PRIOR FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: PCT/FR02/01327  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: FR 01/05248  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 103  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: nNOS mutated protein fragment  
US-10-475-049A-103

Query Match 43.5%; Score 27; DB 17; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PYYVNLIP 12  
:|||||  
Db 4 PVLSTLP 10

RESULT 30  
US-09-201-396-6  
; Sequence 6, Application US/09201396A  
; Publication No. US20030009022A1  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; APPLICANT: Murphy, Andrew J.  
; APPLICANT: Paul, Jeremy  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
; TITLE OF INVENTION: EFFECTORS  
; FILE REFERENCE: CPI-012CP9  
; CURRENT APPLICATION NUMBER: US/09/201,396A  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: 08/582,333  
; PRIOR FILING DATE: 1996-01-17  
; PRIOR APPLICATION NUMBER: 08/322,137  
; PRIOR FILING DATE: 1994-10-13  
; PRIOR APPLICATION NUMBER: 08/309,313  
; PRIOR FILING DATE: 1994-09-20  
; PRIOR APPLICATION NUMBER: 08/190,328  
; PRIOR FILING DATE: 1994-01-31  
; PRIOR APPLICATION NUMBER: 08/041,431  
; PRIOR FILING DATE: 1993-03-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 6  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-201-396-6

Query Match 43.5%; Score 27; DB 10; Length 11;  
Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFFLPV 7  
:|||||  
Db 3 FFFFLPV 8

RESULT 31  
US-10-277-607-6  
; Sequence 6, Application US/10277607  
; Publication No. US20030166143A1  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; APPLICANT: Murphy, Andrew J.  
; APPLICANT: Paul, Jeremy I.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
; TITLE OF INVENTION: EFFECTORS  
; FILE REFERENCE: CPI-012CP9CN  
; CURRENT APPLICATION NUMBER: US/10/277,607  
; PRIOR FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: 09/201,396  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: 60/109,902  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: PCT/US98/21168  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 08/946,298  
; PRIOR FILING DATE: 1997-10-07  
; PRIOR APPLICATION NUMBER: 08/689,172  
; PRIOR FILING DATE: 1996-08-06  
; PRIOR APPLICATION NUMBER: 08/582,333  
; PRIOR FILING DATE: 1996-01-17  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-10-277-607-6

Query Match 43.5%; Score 27; DB 14; Length 11;  
Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFFLPV 7  
:|||||  
Db 3 FFFFLPV 8

RESULT 32  
US-10-269-171A-6  
; Sequence 6, Application US/10269171A  
; Publication No. US20030095979A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank Mattnier  
; APPLICANT: Wolfgang Zauner  
; APPLICANT: Walter Schmidt  
; APPLICANT: Michael Buschle  
; TITLE OF INVENTION: Pharmaceutical preparations comprising modified  
; TITLE OF INVENTION: peptides  
; FILE REFERENCE: SONN-020US  
; CURRENT APPLICATION NUMBER: US/10/269,171A



```

1 PRIOR FILING DATE: 1994-03-04
2 PRIOR APPLICATION NUMBER: US 08/159,184
3 PRIOR FILING DATE: 1993-11-29
4 PRIOR APPLICATION NUMBER: US 08/073,205
5 PRIOR FILING DATE: 1993-06-04
6 PRIOR APPLICATION NUMBER: US 08/027,146
7 PRIOR FILING DATE: 1993-03-05
8 NUMBER OF SEQ ID NOS: 2479
9 SOFTWARE: PatentIn version 3.1
10 SEQ ID NO 2026
11 LENGTH: 15
12 TYPE: PRT
13 ORGANISM: Artificial Sequence
14 FEATURE:
15 OTHER INFORMATION: Artificial Peptide
US-10-149-135-2026

```

Query Match	43.5%	Score 27	DB 15	Length 15
Best Local Similarity	50.0%	Pred. No. 9e+02		
Matches 6	Conservative 2	Mismatches 4	Indels 0	Gaps 0

QY	1	LFFFLPVNNLP	12
		:     :	
Db	2	LVFGIEVEEVP	13

RESULT 36  
US-10-149-135-2412

```

; Sequence 2412, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:

```

1 APPLICANT: Fikes, John  
 2 APPLICANT: Sette, Alessandro  
 3 APPLICANT: Sidney, John  
 4 APPLICANT: Southwood, Scott  
 5 APPLICANT: Chesnut, Robert  
 6 APPLICANT: Celsi, Eateban  
 7 APPLICANT: Keogh, Elissa  
 8 TITLE OF INVENTION: Inducing Cellular Immune Responses to  
 9 TITLE OF INVENTION: MASH2/3 Using Peptide and Nucleic Acid Compositions

Q7 1 LFFFLPVNVLP 12  
1 : 1 : 1

Db 2 LVFGIEVVEVP 13

RESULT 37  
US-09-895-443-30

; Sequence 30, Application US/09895443  
; Patent No. US20020103134A1

APPLICANT: Findeis, M. et al.  
TITLE OF INVENTION: Modulators of  $\alpha$ -Amyloid Peptide

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:

```
; ZIP: 02109-1784  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk
```

```

;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: USC/09/895 443

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/356,931

1 APPLICATION NUMBER: 08/897,342  
2  
3 FILING DATE: 21-JUL-1997  
4 APPLICATION NUMBER: USSN 08/703,675  
5  
6 FILING DATE: 27-AUG-1996  
7 APPLICATION NUMBER: USSN 08/616,081  
8  
9 FILING DATE: 14-MAR-1996  
10 APPLICATION NUMBER: USSN 08/548,998  
11 FILING DATE: 27-OCT-1995  
12  
13 ATTORNEY/AGENT INFORMATION:  
14  
15 NAME: Decenti, Jr., Giulio A.

```

; INFORMATION FOR SEQ ID NO: 30:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 5 amino acids

```

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; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Query Match	41.9%	Score 26	DB 9	Length 5
Best Local Similarity	100.0%	Pred. NO.	1.5e+06	
Matches	5	Conservative	0	Mismatches 0; Indels 0; Gaps 0

QY	1 LFFFL 5
Db	1 LFFFL 5

RESULT 38

```

; Sequence 292, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; SEQ ID NO 292
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-292
```

```
Query Match          41.9%; Score 26; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LFEPFL 5
Db 1 LFEPFL 5
```

```
RESULT 39
US-10-119-536A-176
; Sequence 176, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9) <223> CT841 immunogenic peptide
US-10-119-536A-176
```

```
Query Match          41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 FPELPVVNV 10
Db 1 FPELPVVNV 9
```

RESULT 40

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US-10-119-536A-190
; Sequence 190, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-190
```

```
Query Match          41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 FLEPVVNV 11
Db 1 FMPVIVLV 8
```

```
Search completed: June 7, 2005, 23:31:36
Job time : 56 secs
```

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## ALIGNMENTS

## RESULT 1

T37075 hypothetical protein SCU30.08 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T37075

R:Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999

A:Reference number: T21621

A:Accession: T37075

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 &lt;S&gt;

A:Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070; SCODEB:SCU30.08

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCODEB:SCU30.08

## Query Match

Best Local Similarity 37.1%; Score 23; DB 2; Length 16;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVNVLP 12

DB 1 MPVIRMP 8

## RESULT 2

S53125 cysteine-rich secretory protein-3 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Mar-1999

C:Accession: S53125; S56161

R:Schwiderky, U.; Haendler, B.; Schlenning, W.D.

submitted to the EMBL Data Library, March 1995

A:Description: Isolation and characterization of the androgen-dependent mouse cysteine-rich

A:Reference number: S53125

A:Accession: S53125

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 &lt;SCH&gt;

A:Cross-references: EMBL:X85321

R:Schwiderky, U.; Haendler, B.; Schlenning, W.D.

Biochem. J. 309, 831-836, 1995

A:Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich se

A:Reference number: S56161; MUID:95366959; PMID:7639699

A:Accession: S56161

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-18 &lt;SC2&gt;

A:Cross-references: EMBL:X85321

## Query Match

Best Local Similarity 100.0%; Score 22; DB 2; Length 18;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5

DB 4 PFPL 7

## RESULT 3

S09019 hemolytic protein B9 - edible frog (fragment)

C:Species: Rana esculenta (edible frog)

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C:Accession: S09019

R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erpamer, G.F.; Barra, D.; Bossa, F.

Biochim. Biophys. Acta 1033, 318-323, 1990

A:Title: Purification and characterization of bioactive peptides from skin extracts of R

A:Reference number: S09018; MUID:90198965; PMID:2317508  
A:Accession: S09019  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>  
A:Cross-references: UNIPROT:P32416

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 13;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8

DB 1 FLPLI 5

## RESULT 4

JZYHPI crabrolin - European hornet

C:Species: Vespa crabro (European hornet)

C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004

C:Accession: A01781

R:Argolas, A.; Pisano, J.J.

J. Biol. Chem. 259, 10106-10111, 1984

A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,

A:Reference number: A92441; MUID:84289390; PMID:6206053

A:Accession: A01781

A:Molecule type: protein

A:Residues: 1-13 &lt;ARG&gt;

A:Cross-references: UNIPROT:P01518

C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.

C:Keywords: amidated carboxyl end; venom

F:13/Modified site: amidated carboxyl end (Leu) #status experimental

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 13;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8

DB 1 FLPLI 5

## RESULT 5

JN0390

histamine-releasing peptide II - oriental hornet

N:Alternate names: venom protein HR-2

C:Species: Vespa orientalis (oriental hornet)

C:Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 09-Jul-2004

C:Accession: JN0390; S10919

R:Miroschnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus

Bicoory, Khim. 7, 1467-1477, 1981

A:Title: Structure and properties of histamine releasing peptides from the venom of Vesp

A:Reference number: JN0389

A:Accession: JN0390

A:Molecule type: protein

A:Residues: 1-14 &lt;MIR&gt;

A:Cross-references: UNIPROT:P17236

R:Rutichbaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1968

A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St

A:Reference number: S06445

A:Accession: S10919

A:Molecule type: protein

A:Residues: 1-14 &lt;TVI&gt;

A:Superfamily: crabrolin

C:Keywords: amidated carboxyl end; venom

F:14/Modified site: amidated carboxyl end (Leu) #status experimental

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 14;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8



Db 1 FLPLI 5

## RESULT 6

S62374  
alpha-1-antichymotrypsin - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S62374  
R:Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;  
Kur, J. Biochem. 235, 821-827, 1996  
A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia  
A:Reference number: S62374; MUID:96184564; PMID:8654434  
A:Accession: S62374  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-14 <TSU>  
A:Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DW8; UNIPROT:Q8N177

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 14;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFLPVN 9  
| | | | |  
Db 2 IFMSKVTN 10

## RESULT 7

S15778  
Insulin chain B - bovine (fragments)  
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
C>Date: 19-Mar-1997 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: S15778; S15779  
R:Berghman, T.; Agerbergh, B.; Joernvall, H.  
FEBS Lett. 283, 100-103, 1991  
A:Title: Direct analysis of peptides and amino acids from capillary electrophoresis.  
A:Reference number: S15778; MUID:91243852; PMID:2037061  
A:Accession: S15778  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <FEH1>  
A:Accession: S15779  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 9-17 <FEH2>  
C:Superfamily: Insulin  
C:Keywords: hormone; pancreas

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 17;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6  
| | | | |  
Db 11 FFYTP 15

## RESULT 8

S09731  
photosystem I protein psai - spinach chloroplast (fragment)  
C:Species: chloroplast Spinacia oleracea (spinach)  
C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 19-Jan-1996  
C:Accession: S09731  
R:Ikenuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.  
FEBS Lett. 263, 274-276, 1990  
A:Title: Polypeptide composition of higher plant photosystem I complex. Identification o  
A:Reference number: S09730; MUID:90242987; PMID:2185553  
A:Accession: S09731  
A:Molecule type: protein  
A:Residues: 1-18 <IKE>  
C:Genetics:

A:Gene: psai  
A:Genome: chloroplast  
A:Superfamily: photosystem I protein psai  
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; chy

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 18;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPLVNL 11  
| | | | |  
Db 7 FVLVLGLV 14

## RESULT 9

I40062  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C:Species: Buchnera aphidicola  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C:Accession: I40062  
R:Roubaksh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A:Title: Characterization of a putative 238-SS rRNA operon of Buchnera aphidicola (endos  
A:Reference number: I40061; MUID:95212314; PMID:7535281  
A:Accession: I40062  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-18 <RBS>  
A:Cross-references: EMBL:U10496; MUID:9854711; PIDN:AAA79125.1; PID:9854712  
C:Genetics:  
A:Gene: aroB  
C:Keywords: oxidoreductase

## Query Match

Best Local Similarity 33.9%; Score 21; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12  
| | | | |  
Db 7 NVLP 10

## RESULT 10

S66636  
alpha-2-macroglobulin isoform 2 - bovine (fragment)  
C:Species: Bos primigenius indicus (zebu cattle)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S66636  
R:Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottu  
FEBS Lett. 372, 93-95, 1995  
A:Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o  
A:Reference number: S66634; MUID:96032553; PMID:7556651  
A:Accession: S66636  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <DOL>  
A:Cross-references: UNIPROT:Q7M2N7

## Query Match

Best Local Similarity 32.3%; Score 20; DB 2; Length 9;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12  
| | | | |  
Db 2 NVLP 5

## RESULT 11

S65715  
aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450 K(Ah) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 29-Oct-1999  
C:Accession: S65715

R.Ohgiya, N.; Yokota, H.; Takahashi, M.; Komoro, S.; Yuasa, A.  
Biochim. Biophys. Acta 1289, 122-130, 1996  
A>Title: Purification and properties of a new beta-naphthoflavone inducible cytochrome P  
A:Reference number: S65715; MUID:96195850; PMID:8605221  
A:Accession: S65715  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <OHG>  
C:Keywords: monooxygenase; oxidoreductase

Query Match 32.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPLVNVLP 12  
|||:  
Db 3 VPLXLLP 10

RESULT 12  
S09018  
hemolytic protein A1 - edible frog (fragment)

C:Species: Rana esculenta (edible frog)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S09018  
R:Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erpamer, G.F.; Barra, D.; Bossa, F.  
Biochim. Biophys. Acta 1033, 318-323, 1990  
A>Title: Purification and characterization of bioactive peptides from skin extracts of R  
A:Reference number: S09018; MUID:90198965; PMID:2317508  
A:Accession: S09018  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>  
A:Cross-references: UNIPROT:P32415

Query Match 32.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPPV 8  
|||:  
Db 1 FLPPAI 5

RESULT 13  
AF0832

phe leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (strai  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A>Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AF0832  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, F.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AF0832  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:gl6503820; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2853a

Query Match 32.3%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPFL 5  
|||:  
Db 10 PPFI 13

RESULT 14  
A39040  
calsequestrin, cardiac muscle - dog (fragments)

C:Species: Canis lupus familiaris (dog)  
C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 09-Jul-2004  
C:Accession: A39040  
R:Calà, S.E.; Jones, L.R.  
J. Biol. Chem. 266, 391-398, 1991  
A>Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein  
A:Reference number: A39040; MUID:91093153; PMID:1985907  
A:Accession: A39040  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <CAL>  
A:Cross-references: UNIPROT:P12637

C:Keywords: cardiac muscle; heart; phosphoprotein

Query Match 32.3%; Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPLVN 9  
|||:  
Db 8 LPTIN 12

RESULT 15  
S04229

N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24k chain - rat (fragment)  
N:Alternate names: glycosylasparaginase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
C:Accession: S04229  
R:Tollersrud, O.K.; Aronson, Jr., N.N.  
Biochem. J. 260, 101-108, 1989  
A>Title: Purification and characterization of rat liver glycosylasparaginase.  
A:Reference number: S04228; MUID:89374025; PMID:2775174  
A:Accession: S04229  
A:Molecule type: protein  
A:Residues: 1-18 <ROL>  
C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase  
C:Keywords: hydrolase

Query Match 31.5%; Score 19.5; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 LP-VNVNLP 12  
|||:  
Db 4 LPLVNVTP 12

RESULT 16  
S01119

photosystem II protein psbK - spinach chloroplast (fragment)  
C:Species: chloroplast Spinacia oleracea (spinach)  
C:Date: 30-Jun-1989 #sequence\_revision 31-Dec-1990 #text\_change 19-Jan-1996  
C:Accession: S01119  
R:Murata, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugiura, M.  
FEBS Lett. 235, 283-288, 1988  
A>Title: Identification of a new gene in the chloroplast genome encoding a low-molecular  
A:Reference number: S01119  
A:Accession: S01119  
A:Molecule type: protein  
A:Residues: 1-13 <MUR>  
C:Genetics:  
A:Gene: psbK  
A:Genome: chloroplast

C:Superfamily: photosystem II protein psbK  
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; th

Query Match 30.6%; Score 19; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFLPVV 8  
| : : |  
Db 8 FLXPV 13

## RESULT 17

170076

glycophorin B/glycophorin A mutant fusion protein St-a (mistranslated) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence\_revision 14-Aug-1997 #text\_change 09-Jul-2004

C:Accession: I70076

R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990

A:Title: Identification of the crossing-over point of a hybrid gene encoding human glyco

A:Reference number: I55334; MUID:90264417; PMID:1971625

A:Accession: I70076

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-13 <REA>

A:Cross-references: UNIPROT:Q14462; GB:M33507; GB:J05465; NID:9183743; PIDN:AAA35942.1;

A>Note: the translation is from an incorrect reading frame

C:Genetics:

A:Gene: GYPB/GYPB

C:Keywords: fusion protein

Query Match 30.6%; Score 19; DB 4; Length 13;  
Best Local Similarity 33.3%; Pred. No. 3.4e+03;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPLVNV 10  
| : : : : |  
Db 6 LPIISL 11

## RESULT 18

PA0029

protein QAL00012 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C:Accession: PA0029

R:Kam, M.; Kawakami, T.; Miyake, N.; Tsugita, A.

submitted to JRPD July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A:Reference number: PA0001

A:Accession: PA0029

A:Molecule type: protein

A:Residues: 1-15 <KAM>

A:Experimental source: callus

Query Match 30.6%; Score 19; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 3.9e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 FLPVNV 12  
| : : : |  
Db 7 FTLVNV 15

## RESULT 19

S13973

chlorophyll a/b-binding protein type II - garden pea (fragment)

C:Species: Pisum sativum (garden pea)

C:Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

C:Accession: S13973

R:Jahn, P.; Junge, W.

Bur. J. Biochem. 193, 731-736, 1990

A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the P

A:Reference number: S13973; MUID:91065379; PMID:2174565

A:Accession: S13973

A:Molecule type: protein

A:Residues: 1-15 <JAH>

C:Genetics:

A:Genome: nuclear

C:Keywords: chlorophyll; chloroplast; light-harvesting complex; thylakoid; transmembrane

Query Match 30.6%; Score 19; DB 2; Length 15;  
Best Local Similarity 30.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFFPLPVNV 10  
| : : : : |  
Db 5 VFTSIGITNV 14

## RESULT 20

S54712

zein Zp22/6 protein - maize

C:Species: Zea mays (maize)

C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: S54712

R:Chaudhuri, S.; Messing, J.

Mol. Gen. Genet. 246, 707-715, 1995

A:Title: RFLP mapping of the maize dzrl locus, which regulates methionine-rich 10 kDa ze

A:Reference number: S54712; MUID:95206245; PMID:7898438

A:Accession: S54712

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <CHA>

A:Cross-references: UNIPROT:Q7M1P8

Query Match 30.6%; Score 19; DB 2; Length 15;  
Best Local Similarity 30.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FFLPVNV 12  
| : : : : |  
Db 1 FIPQGSILAP 10

## RESULT 21

T09741

photosystem I chain psal - upland cotton chloroplast (fragment)

C:Species: chloroplast Gossypium hirsutum (upland cotton)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T09741

R:Small, R.L.; Ryburn, J.A.; Cronm, R.C.; Seelanan, T.; Wendel, J.F.

Am. J. Bot. 85, 1301-1315, 1998

A:Title: The tortoise and the hare: choosing between noncoding plastome and nuclear Adh

A:Reference number: Z16323

A:Accession: T09741

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <SMA>

A:Cross-references: UNIPROT:O19971; EMBL:AF031581; NID:92623684; PID:G3723945

C:Genetics:

A:Gene: psal

A:Genome: chloroplast

C:Keywords: chloroplast; photosynthesis; photosystem I

Query Match 30.6%; Score 19; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8  
| : : : |  
Db 11 FVLV 15

## RESULT 22

T44936

calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T44936  
 R:Alamy, V.; Alique, R.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z22873  
 C:Accession: T44936  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <ALE>  
 A:Cross-references: UNIPROT:Q94554; EMBL:U57982; PIDN:AAD09466.1

Query Match  
 Best Local Similarity 30.6%; Score 19; DB 2; Length 16;  
 Pred. No. 4.1e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 FFLPVVN 9  
 |||||  
 DB 10 FFLVVTN 16

RESULT 23  
 C37520  
 glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 30-Sep-1993  
 C:Accession: C37520; N24735  
 R:Mannerlyk, B.; Alin, P.; Guttenberg, C.; Jensen, H.; Tahir, M.K.; Warholm, M.; Jorner  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985  
 A:Title: Identification of three classes of cytosolic glutathione transferase common to  
 A:Reference number: A24735; MUID:86042634; PMID:3864155  
 A:Accession: C37520  
 A:Molecule type: protein  
 A:Residues: 1-17 <MAN>  
 C:Superfamily: glutathione transferase  
 C:Keywords: transferase

Query Match  
 Best Local Similarity 30.6%; Score 19; DB 2; Length 17;  
 Pred. No. 4.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLPVNV 9  
 :|||:  
 DB 7 YFPVVD 12

## RESULT 24

S70612  
 alpha-macroglobulin proteinase inhibitor, tetrameric - bloodfluke planorb (fragment)

C:Species: Biomphalaria glabrata (bloodfluke planorb)  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
 C:Accession: S70612  
 R:Bender, R.C.; Bayne, C.J.  
 Biochem. J. 316, 893-900, 1996  
 A:Title: Purification and characterization of a tetrameric alpha-macroglobulin proteinase  
 A:Reference number: S70612; MUID:96265058; PMID:8670168  
 A:Accession: S70612  
 A:Molecule type: protein  
 A:Residues: 1-18 <BEN>  
 A:Cross-references: UNIPROT:Q9TWEO  
 C:Complex: homotetramer  
 C:Function:

A:Description: inhibits proteinases possessing different catalytic mechanisms by steric

Query Match  
 Best Local Similarity 30.6%; Score 19; DB 2; Length 18;  
 Pred. No. 4.6e+03;  
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 FFLPVNVLP 12  
 :|||:  
 DB 3 YFISAPRVVP 13

RESULT 25  
 JQ2030

hypothetical 1.9k protein - Oryzia pseudotsugata multicapsid nuclear polyhedrosis virus

N:Alternate names: ORF2 mini gene protein  
 C:Species: Oryzia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNPV  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
 C:Accession: JQ2030  
 R:Russell, R.L.Q.; Rohmann, G.F.  
 J. Gen. Virol. 74, 1191-1195, 1993  
 A:Title: Nucleotide sequence of the ubiquitin-39k gene region from the Oryzia pseudotsug  
 A:Reference number: PQ0633; MUID:93286576; PMID:8389803  
 A:Accession: JQ2030  
 A:Molecule type: DNA  
 A:Residues: 1-17 <RUS>  
 A:Cross-references: DBJ:DJ3375; MUID:g222217; PIDN:BA02640.1; PID:dl003144; PID:g222222

Query Match  
 Best Local Similarity 29.8%; Score 18.5; DB 2; Length 17;  
 Pred. No. 5.3e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5 LPVNVVL 11  
 |||||  
 DB 3 LP-VNVVL 8

## RESULT 26

LEECFS

phes2 operon leader peptide - Escherichia coli (strain K-12)

N:Alternate names: phenylalanyl-tRNA synthetase operon leader peptide  
 C:Species: Escherichia coli  
 C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
 C:Accession: S11551; I53984; G64930; S06908  
 R:Payat, G.; Mayaux, J.F.; Secerdot, C.; Fromant, M.; Springer, M.; Grunberg-Manago, M.;  
 J. Mol. Biol. 171, 239-261, 1983  
 A:Title: Escherichia coli phenylalanyl-tRNA synthetase operon region. Evidence for an at  
 A:Reference number: A30391; MUID:84090239; PMID:6317865  
 A:Accession: S11551

A:Molecule type: DNA

A:Residues: 1-14 <RAY>

A:Cross-references: UNIPROT:P06985; EMBL:V00291; MUID:g43065; PIDN:CAA23563.1; PID:g43069

R:Mayaux, J.

Gene 30, 137-146, 1984

A:Title: IS4 transposition in the attenuator region of the Escherichia coli phes2 opero

A:Reference number: I53984; MUID:85077605; PMID:6096210

A:Accession: I53984

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-14 <RES>

A:Cross-references: GB:M13251; MUID:g147182; PIDN:AA24333.1; PID:g147185

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G64930

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-14 <BLAT>

A:Cross-references: GB:AE000266; GB:U00096; MUID:g1787997; PIDN:AACT4785.1; PID:g1788008;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: phem

A:Map position: 37 min

C:Function:

A:Description: probably involved in attenuation regulation of phenylalanyl-tRNA synthetase

Query Match  
 Best Local Similarity 29.0%; Score 18; DB 1; Length 14;  
 Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
 ||||  
 DB 8 FFF 10

## RESULT 27

pheST operon leader peptide - Escherichia coli (strain O157:H7, substrain RIMD 0509952)  
F90931  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: F90931  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasekawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F90931  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <HAV>  
A:Cross-references: UNIPROT:P06985; GB:BA000007; PIDD:BA035845.1; PID:g13361889; GSPDB:G  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs2422  
C:Superfamily: pheST leader peptide

Query Match 29.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PFF 4  
DB 8 PFF 10

## RESULT 28

pheST operon leader peptide - Escherichia coli (strain O157:H7, substrain EDL933)  
B85780  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: B85780  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Linn, A.; Dimmlanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: AB5480; MUID:21074935; PMID:11206551  
A:Accession: B85780  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <STO>  
A:Cross-references: UNIPROT:P06985; GB:AE005174; NID:g12515726; PIDD:AA056702.1; GSPDB:G  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: pheM  
C:Superfamily: pheST leader peptide

Query Match 29.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PFF 4  
DB 8 PFF 10

## RESULT 29

pollen allergen Lol p IV - perennial ryegrass (fragments)  
A60737  
C:Species: Lolium perenne (perennial ryegrass)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 17-Mar-1999  
C:Accession: A60737  
R:Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kiehl, F.T.  
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1999  
A:Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.  
A:Reference number: A60737; MUID:90007726; PMID:2793222  
A:Accession: A60737  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-14 <JAG>  
C:Keywords: pollen

Query Match 29.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 5.4e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 3 PFLPVNVNVL 11  
DB 1 FLSLPVNGLT 9

## RESULT 30

phenylalanyl-tRNA synthetase operon leader peptide [imported] - Salmonella enterica subsp.  
AG0705  
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium  
A:Note: this species has also been called Salmonella typhimurium  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AG0705  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AG0705  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <PAR>  
A:Cross-references: GB:AL513382; PIDD:CA020216.1; PID:g16502854; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY1774

Query Match 29.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PFF 4  
DB 8 PFF 10

## RESULT 31

phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain  
AF0296  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AF0296  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0296  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <KUR>  
A:Cross-references: UNIPROT:Q8ZDM9; GB:AL590842; PIDD:CA021234.1; PID:g15980423; GSPDB:G  
C:Genetics:  
A:Gene: pheM

Query Match 29.0%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PFF 4  
DB 8 PFF 10

## RESULT 32

LFRCF

phe operon leader peptide - Escherichia coli (strain K-12)  
N.Alternate names: attenuator peptide

C.Species: Escherichia coli  
C.Date: 18-Aug-1982 #sequence\_revision 18-Aug-1992 #text\_change 09-Jul-2004  
C.Accession: A03593; B36494; A65038

R.Zunawati, G.; Brown, K.; Killingly, D.; Yanofsky, C.  
Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A.Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli  
A.Reference number: A03593; MUID:79033820; PMID:360214

A.Accession: A03593  
A.Molecule type: DNA

A.Residues: 1-15 <2UR>  
A.Cross-references: UNIPROT:P03057; GB:V00314; GB:J01658; NID:942378; PIDN:CAA23600.1; F

R.Gavin, N.; Davidson, B.E.  
J. Biol. Chem. 265, 21532-21535, 1990

A.Title: PheA mutants of Escherichia coli have a defective pheA attenuator.  
A.Reference number: A36494; MUID:91072346; PMID:2254312

A.Accession: B36494  
A.Molecule type: DNA

A.Residues: 1-15 <GAV>  
A.Cross-references: GB:M58024; GB:J05694; NID:9147178; PIDN:AAA62783.1; PID:9147180

R.Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997

A.Title: The complete genome sequence of Escherichia coli K-12.  
A.Reference number: A64720; MUID:97426617; PMID:9278503

A.Accession: A65038  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA  
A.Residues: 1-15 <BLAT>

A.Cross-references: GB:A6000346; GB:U00096; NID:92367141; PIDN:AC75647.1; PID:91788950;  
A.Experimental source: strain K-12, substrain MG1655

C.Genetics:  
A.Gene: pheU, pheA

A.Map position: 56 min  
C.Superfamily: pheA leader peptide

Query Match 29.0%; Score 18; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
|||

DB 6 FFF 8

## RESULT 33

PS0185

27K protein A 3.4/5 - rice (fragment)

C.Species: Oryza sativa (rice)  
C.Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Feb-1995

C.Accession: PS0185  
R.Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991  
A.Reference number: PS0184

A.Accession: PS0185  
A.Molecule type: protein

A.Residues: 1-15 <KAM>

Query Match 29.0%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.8e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VVNVLP 12  
:|:|

DB 5 IVDVAP 10

## RESULT 34

S71306

heat shock protein 90 - rat (fragment)

C.Species: Rattus norvegicus (Norway rat)

C.Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C.Accession: S71306

R.Conconi, M.; Szweda, L.I.; Levine, R.L.; Stadman, E.R.; Friguet, B.  
Arch. Biochem. Biophys. 331, 232-240, 1996

A.Title: Age-related decline of rat liver multicatalytic proteinase activity and protect  
A.Reference number: S71306; MUID:9629287; PMID:8660703

A.Accession: S71306  
A.Molecule type: protein

A.Residues: 1-15 <CON>  
A.Experimental source: liver

A.Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 29.0%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.8e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PVNVLP 11  
:|:|

DB 9 PIVETL 14

## RESULT 35

E91061

hypothetical protein EC53461 [imported] - Escherichia coli (strain O157:H7, substrain RI

C.Species: Escherichia coli  
C.Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C.Accession: E91061  
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gatawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001

A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A.Reference number: A96229; MUID:21156231; PMID:11258796

A.Accession: E91061  
A.Status: preliminary

A.Molecule type: DNA  
A.Residues: 1-15 <HAY>

A.Cross-references: UNIPROT:Q8X2E0; UNIPROT:Q8FEZ7; GB:BA000007; PIDN:BAB36884.1; PID:91  
A.Experimental source: strain O157:H7, substrain RIMD 050952

C.Genetics:  
A.Gene: EC53461

Query Match 29.0%; Score 18; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
|||

DB 6 FFF 8

## RESULT 36

A36279

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C.Species: Lumbricus terrestris (common earthworm)  
C.Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004

C.Accession: A36279  
R.Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990  
A.Title: Purification and characterization of a chemoattractant from electric shock-ind

snakes.  
A.Reference number: A36279; MUID:90256800; PMID:2160465

A.Accession: A36279  
A.Status: preliminary

A.Molecule type: protein  
A.Residues: 1-15 <JIA>

A.Cross-references: UNIPROT:O44335

Query Match 29.0%; Score 18; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.8e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FFFLP 6

Db 8 FTYLTP 12

## RESULT 37

S11290  
matrix protein M1 - influenza A virus (strain A/FPV/Rosstock/34 [H7N1]) (fragment)  
C:Species: Influenza A virus  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: S11290  
R:Robertson, J.S.  
Nucleic Acids Res. 6, 3745-3757, 1979  
A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A:Reference number: S11286; MUID:80034428; PMID:493121  
A:Accession: S11290  
A:Molecule type: genomic RNA  
A:Residues: 1-16 <ROB>  
A:Cross-references: UNIPROT:Q84098; EMBL:J02112  
C:Genetics:  
A:Map position: segment 7  
C:Superfamily: influenza virus matrix protein M1

Query Match 29.0%; Score 18; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVLP 12  
Db 11 VLSVVP 16

## RESULT 38

S68730  
bleomycin-binding protein - Streptomyces verticillius (fragment)  
C:Species: Streptomyces verticillius  
C:Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: S68730  
R: Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuian, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakam  
PEBS Lett. 362, 80-84, 1995  
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Strept  
al characterisation.  
A:Reference number: S68730; MUID:95212588; PMID:7535252  
A:Accession: S68730  
A:Molecule type: protein  
A:Residues: 1-16 <SUG>  
A:Cross-references: UNIPROT:Q7M0J7  
A:Experimental source: ATCC 15003  
C:Keywords: antibiotic resistance

Query Match 29.0%; Score 18; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 6.1e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FLPPVNVLP 11  
Db 4 FLGAVPVL 11

## RESULT 39

E23734  
insulin-like growth factor-binding protein 3 - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C:Accession: E23734  
R:Shimada, S.; Gao, L.; Shimomura, M.; Ling, N.  
Mol. Endocrinol. 5, 938-948, 1991  
A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6  
A:Reference number: A23734; MUID:92049376; PMID:1719383  
A:Accession: E23734  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <SHI>

Query Match 29.0%; Score 18; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 6.5e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PVPVNVLP 12  
Db 9 PVRXEP 15

## RESULT 40

A32220  
T-cell receptor delta chain precursor V region (DN7.3-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1989 #sequence\_revision 20-Oct-1989 #text\_change 30-May-1997  
C:Accession: A32220  
R:Korman, A.J.; Maruyama, J.; Rauler, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 86, 267-271, 1989  
A:Title: Rearrangement by inversion of a T-cell receptor delta variable region gene loc  
A:Reference number: A32220; MUID:89098895; PMID:2789518  
A:Accession: A32220  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-18 <KOR>  
A:Cross-references: GB:M23095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 29.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPF 4  
Db 9 PPF 11

Search completed: June 7, 2005, 23:20:39  
Job time : 13.1273 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 52.8 seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-4  
Perfect score: 62  
Sequence: 1 LFFFLPVNVLP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	48.4	14	2 Q7SBM9	Q7SBM9 neurospora
2	27	43.5	13	2 Q7R8X6	Q7R8X6 plasmodium
3	26	41.9	12	1 RAN5_RANCA	P82820 rana catesb
4	26	41.9	13	1 TEM1_RANPI	P82848 rana pipien
5	26	41.9	15	2 Q7RPE9	Q7RPE9 plasmodium
6	26	41.9	17	2 Q8HKE6	Q8HKE6 rhidipcephal
7	26	41.9	17	2 Q9ERZ2	Q9ERZ2 mus musculi
8	25	40.3	13	1 CRBL_VESMA	P17232 vespa manda
9	25	40.3	15	2 Q9TNO1	Q9TNO1 mus sp. bet
10	24	38.7	17	2 Q7IUQ2	Q7IUQ2 homo sapien
11	24	38.7	18	2 Q7IQB5	Q7IQB5 mus musculi
12	24	38.7	18	2 Q91BM7	Q91BM7 autographa
13	23	37.1	12	1 GRAR_RANRU	P40754 rana rugosa
14	23	37.1	13	1 CRBL_VESLE	P17235 vespa lew
15	23	37.1	13	1 CRBL_VESXA	P17234 vespa xanth
16	23	37.1	13	1 TE1A_RANBO	P84116 rana boylii
17	23	37.1	17	2 Q8HKE6	Q8HKE6 rhidipcephal
18	23	37.1	18	2 Q8NED1	Q8NED1 homo sapien
19	23	37.1	19	2 Q7RAU4	Q7RAU4 plasmodium
20	22	35.5	13	1 BLAC_STRGR	P81173 streptomyce
21	22	35.5	15	2 Q367Z7	Q367Z7 homo sapien
22	22	35.5	15	2 Q46436	Q46436 clostridium
23	22	35.5	15	2 Q71IMS	Q71IMS lactobacill
24	22	35.5	16	2 Q6QVE1	Q6QVE1 phaseolus v
25	22	35.5	17	2 UP36_UPEMJ	P82043 uperoleia v
26	22	35.5	17	2 Q95XQ7	Q95XQ7 sus scrofa
27	22	35.5	17	2 Q8OT36	Q8OT36 mus musculi
28	21.5	34.7	14	1 TEMC_RANLU	P82832 rana luteiv
29	21	33.9	9	2 Q9PBE5	Q9PBE5 kluyveromyc
30	21	33.9	11	2 Q9TQSO	Q9TQSO bos taurus
31	21	33.9	13	1 CRBL_VESAN	P17233 vespa anali

32	21	33.9	13	1 CRBL_VESCR	P01518 vespa crabr
33	21	33.9	13	1 CRBL_VESTR	P17231 vespa tropi
34	21	33.9	13	1 HPB9_RANES	P32416 rana esculi
35	21	33.9	13	1 TEM1_RANTE	P56917 rana tempor
36	21	33.9	13	1 TEMF_RANTE	P56921 rana tempor
37	21	33.9	14	1 CRBL_VESOR	P17336 vespa orien
38	21	33.9	15	2 Q9QVD7	Q9QVD7 raticus sp.
39	21	33.9	17	2 Q9URC6	Q9URC6 saccharomyc
40	21	33.9	17	2 Q95795	Q95795 homo sapien
41	21	33.9	17	2 Q95F78	Q95F78 hizaikia fus
42	21	33.9	18	2 Q19969	Q19969 gossypium a
43	21	33.9	18	2 Q19979	Q19979 gossypium t
44	20	32.3	8	2 Q40530	Q40530 nicotiana t
45	20	32.3	9	2 Q7M2N7	Q7M2N7 bos indicus
46	20	32.3	10	2 Q7ZET2	Q7ZET2 salvelinus
47	20	32.3	12	2 Q7RW16	Q7RW16 neurospora
48	20	32.3	13	2 HPAL_RANES	P32415 rana esculi
49	20	32.3	13	2 Q6LBE3	Q6LBE3 vibrio harv
50	20	32.3	14	2 Q8M099	Q8M099 tockus nauu
51	20	32.3	14	2 P82340	P82340 pisum sativ
52	20	32.3	15	1 THBI_BOTUA	P84026 bochrops ja
53	20	32.3	15	2 Q63CR8	Q63CR8 bemisia arg
54	20	32.3	15	2 Q68425	Q68425 buchmera ap
55	20	32.3	15	2 Q8XPE4	Q8XPE4 salmoneila
56	20	32.3	15	2 Q7CPZ9	Q7CPZ9 salmoneila
57	20	32.3	16	2 Q9UMK4	Q9UMK4 methanobact
58	20	32.3	17	2 Q06800	Q06800 saccharomyc
59	20	32.3	17	2 Q712V6	Q712V6 homo sapien
60	20	32.3	17	2 Q6URW9	Q6URW9 spiranthes
61	20	32.3	18	1 ALA2_CYPDO	P82153 cydia pomon
62	20	32.3	18	2 Q7R809	Q7R809 plasmodium
63	20	32.3	18	2 Q7R9Y4	Q7R9Y4 plasmodium
64	20	32.3	18	2 Q8M0A0	Q8M0A0 tockus leuc
65	20	32.3	18	2 Q700A1	Q700A1 ciccer ariet
66	19	30.6	5	1 PAP2_PAPMA	P81864 padachirus
67	19	30.6	8	2 P83532	P83532 lactobacill
68	19	30.6	9	2 Q9GD36	Q9GD36 junco effu
69	19	30.6	10	2 Q7RS14	Q7RS14 plasmodium
70	19	30.6	10	2 Q67B09	Q67B09 bacterioph
71	19	30.6	11	2 Q9A1Z7	Q9A1Z7 carsonella
72	19	30.6	12	2 Q9G196	Q9G196 petunia hyb
73	19	30.6	12	2 Q37071	Q37071 petunia hyb
74	19	30.6	13	1 TE1E_RANCL	Q94196 sargassum p
75	19	30.6	13	1 TEMD_RANTE	P82884 rana clamit
76	19	30.6	13	2 Q14462	P56919 rana tempor
77	19	30.6	13	2 Q16007	Q16007 homo sapien
78	19	30.6	13	2 Q6TKD3	Q6TKD3 praecitrull
79	19	30.6	13	2 Q6TKD4	Q6TKD4 sechium edu
80	19	30.6	13	2 Q6TKD5	Q6TKD5 sticyos angu
81	19	30.6	13	2 Q6TKD6	Q6TKD6 trichosanthe
82	19	30.6	13	2 Q6TKD7	Q6TKD7 luffa grave
83	19	30.6	13	2 Q6TKD8	Q6TKD8 luffa echin
84	19	30.6	13	2 Q6TKD9	Q6TKD9 cucurbita p
85	19	30.6	13	2 Q6TKD0	Q6TKD0 benincasa h
86	19	30.6	13	2 Q6TKD1	Q6TKD1 marah orege
87	19	30.6	13	2 Q6TKD2	Q6TKD2 cyclanthera
88	19	30.6	13	2 Q6TKD3	Q6TKD3 echinocysti
89	19	30.6	13	2 Q6TKD4	Q6TKD4 luffa quing
90	19	30.6	13	2 Q6TKD5	Q6TKD5 lagenaria l
91	19	30.6	13	2 Q6TKD6	Q6TKD6 citrullus l
92	19	30.6	13	2 Q6TKD7	Q6TKD7 citrullus c
93	19	30.6	13	2 Q6TKD8	Q6TKD8 acanthosicy
94	19	30.6	13	2 Q6TKD9	Q6TKD9 bryonia dio
95	19	30.6	13	2 Q6TKD0	Q6TKD0 coccolina pa
96	19	30.6	13	2 Q6TKF1	Q6TKF1 diploycyclos
97	19	30.6	13	2 Q6TKF2	Q6TKF2 ecballium e
98	19	30.6	13	2 Q9QVX6	Q9QVX6 ractus sp.
99	19	30.6	13	2 Q9PXB5	Q9PXB5 duck hepatic
100	19	30.6	14	1 UC15_MAIZE	P80621 zea mays (m

## ALIGNMENTS

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RESULT 1
Q7SBM9 PRELIMINARY; PRT; 14 AA.
ID 07SBM9
AC 07SBM9
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DE Predicted protein.
GN Name=NC005740.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Mashburne M.,
RA Seltrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kotze G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,
RA Kamel M., Kamysseis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Kiyotova S., Raasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nariyig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander B.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100165; EAA33802.1; -
SQ SEQUENCE 14 AA; 1563 MW; 4B270FF67ACB7CB7 CRC64;

Query Match
Best Local Similarity 48.4%; Score 30; DB 2; Length 14;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFLPVNV 11
Db 3 LFLFLSYVAL 13

RESULT 2
Q7RBX6 PRELIMINARY; PRT; 13 AA.
ID 07RBX6
AC 07RBX6;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY07094;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RA Published=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooji T.W., Petrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

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RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002528; EAA19451.1; -
KW Hypothetical protein.
SQ SEQUENCE 13 AA; 1611 MW; DFB71AF6048E29C9 CRC64;

Query Match
Best Local Similarity 43.5%; Score 27; DB 2; Length 13;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PFFLPVNV 10
Db 5 PFFLSMISL 13

RESULT 3
RAN5_RANCA STANDARD; PRT; 12 AA.
ID RAN5_RANCA
AC P82820;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ranatuerin 5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=skin secretion;
RX PubMed=9784389;
RA Goraya U., Knopp F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Antibiotic; Direct protein sequencing.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;

Query Match
Best Local Similarity 41.9%; Score 26; DB 1; Length 12;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPPVNV 11
Db 1 FLPIASL 8

RESULT 4
TEML_RANPI STANDARD; PRT; 13 AA.
ID TEML_RANPI
AC P82848;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Temporin-1P.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCB1_TaxID=8404;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya U., Wang Y., Li Z., O'Flaherty M., Knopp F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families

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RT isolated from the skins of the North American frogs Rana luteiventris,
RL Rana berlandieri and Rana pipiens."
CC Bur. J. Biochem. 267:894-900(2000).
CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
CC S. aureus.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=1368; METHOD=Electrospray; RANGE=1-13;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC Anticaction; Amphibian defense peptide; Antibiotic;
CC Direct protein sequencing.
CC MOD RES 13 13 Leucine amide.
SQ SEQUENCE 13 AA; 1370 MW; 3EP3402B9DF92338 CRC64;

Query Match 41.9%; Score 26; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FFPLPVNVL 11
DB 1 FFPIVGL 8

RESULT 5
O7RPE9 PRELIMINARY; PRT; 15 AA.
AC O7RPE9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY01510;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Kool J.T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Sengen J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallon S.J., van Aken S.E., Riedmuller S.B., Feldlynn T.V.,
RA Cho J.K., Quackenbush J., Sedeghan M., Shoib A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABL0100400; EAA20851.1; -.
CC KW Hypothetical protein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1927 MW; DE1B84632CB57860 CRC64;

Query Match 41.9%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFPLPVNV 9
DB 5 LFFFYNNKIN 13

RESULT 6
O8HK6 PRELIMINARY; PRT; 17 AA.
AC O8HK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=ND1;
OS Rhinipcephalus pulchellus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhinipcephalus.
OX NCBI_TaxID=72859;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22660786; PubMed=12775521; DOI=10.1080/106351503093325;
RA Murrell A., Campbell N.J.H., Barker S.C.;
RT "The value of idiosyncratic markers and changes to conserved tRNA
RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:
RT Ixodidae) for phylogenetic inference."
RL Syst. Biol. 52:296-310(2003).
DR EMBL: AY059228; AAL79425.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 17
SQ SEQUENCE 17 AA; 2121 MW; 15A93BBBC1743136 CRC64;

Query Match 41.9%; Score 26; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FFPLPVNVL 11
DB 2 FMEFLSMINPI 11

RESULT 7
O9ER22 PRELIMINARY; PRT; 17 AA.
AC O9ER22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Protein tyrosine phosphatase RPTP-GW1 (Fragment).
GN Name=RPTPg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Wright M.B., Foerzler D., Pech M.;
RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF265561; AAG22700.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;

Query Match 41.9%; Score 26; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFPL 5
DB 4 LFFPL 8

RESULT 8
CRBL_VESMA STRAND; PRT; 13 AA.
ID CRBL_VESMA
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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O8HK6

```
RT isolated from the skins of the North American frogs Rana luteiventris,
RL Rana berlandieri and Rana pipiens."
CC Bur. J. Biochem. 267:894-900(2000).
CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
CC S. aureus.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=1368; METHOD=Electrospray; RANGE=1-13;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC Anticaction; Amphibian defense peptide; Antibiotic;
CC Direct protein sequencing.
CC MOD RES 13 13 Leucine amide.
SQ SEQUENCE 13 AA; 1370 MW; 3EP3402B9DF92338 CRC64;

Query Match 41.9%; Score 26; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FFPLPVNVL 11
DB 1 FFPIVGL 8

RESULT 5
O7RPE9 PRELIMINARY; PRT; 15 AA.
AC O7RPE9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY01510;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Kool J.T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Sengen J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallon S.J., van Aken S.E., Riedmuller S.B., Feldlynn T.V.,
RA Cho J.K., Quackenbush J., Sedeghan M., Shoib A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., White O.R.,
RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABL0100400; EAA20851.1; -.
CC KW Hypothetical protein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1927 MW; DE1B84632CB57860 CRC64;

Query Match 41.9%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFPLPVNV 9
DB 5 LFFFYNNKIN 13

RESULT 6
O8HK6 PRELIMINARY; PRT; 17 AA.
AC O8HK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=ND1;
OS Rhinipcephalus pulchellus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhinipcephalus.
OX NCBI_TaxID=72859;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22660786; PubMed=12775521; DOI=10.1080/106351503093325;
RA Murrell A., Campbell N.J.H., Barker S.C.;
RT "The value of idiosyncratic markers and changes to conserved tRNA
RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:
RT Ixodidae) for phylogenetic inference."
RL Syst. Biol. 52:296-310(2003).
DR EMBL: AY059228; AAL79425.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 17
SQ SEQUENCE 17 AA; 2121 MW; 15A93BBBC1743136 CRC64;

Query Match 41.9%; Score 26; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FFPLPVNVL 11
DB 2 FMEFLSMINPI 11

RESULT 7
O9ER22 PRELIMINARY; PRT; 17 AA.
AC O9ER22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Protein tyrosine phosphatase RPTP-GW1 (Fragment).
GN Name=RPTPg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Wright M.B., Foerzler D., Pech M.;
RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF265561; AAG22700.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;

Query Match 41.9%; Score 26; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFPL 5
DB 4 LFFPL 8

RESULT 8
CRBL_VESMA STRAND; PRT; 13 AA.
ID CRBL_VESMA
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
```

DE Vespid chemotactic peptide M (VESP-M).  
 OS Vespa mandarina (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 NCBI\_TaxID=7446;

-RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,  
 RA Fujino M.;  
 RL (in) Munekata E. (eds.);  
 RL Peptide chemistry 1983, pp.185-190. Protein Research Foundation, Osaka  
 (1984).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 of neutrophils.  
 KM Amidation; Chemotaxis; Direct protein sequencing;  
 KM Mast cell degranulation.  
 FT MOD\_RES 13  
 FT MOD\_RES 13  
 SQ SEQUENCE 13 AA; 1384 MW; 265040289DF92338 CRC64;

Query Match 40.3%; Score 25; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLPPVVNV 11  
 ID 1 FLPIIGKL 8

RESULT 9  
 Q9TN01 PRELIMINARY; PRT; 15 AA.

DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-OCT-2002 (TREMblrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
 DE Beta 2m- class I-binding PEPTIDE=MAJOR histocompatibility complex H-  
 DE 2KB-specific molecule POORLY associated with beta 2-microglobulin  
 DE (Fragment).

OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;  
 RP SEQUENCE.  
 RX MEDLINE=94240094; PubMed=8183884;  
 RT Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathanson S.G.;  
 RT "Characterization of an incompletely assembled major  
 RT histocompatibility class I molecule (H-2B) associated with unusually  
 RT long peptides: implications for antigen processing and presentation.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).

FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F180DC7 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 2.7e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPPVVNV 11  
 ID 7 LPPVVKVM 13

RESULT 10  
 Q71U02 PRELIMINARY; PRT; 17 AA.

AC 071U02;  
 DT 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Advanced glycosylation end product-specific receptor (Fragment).

GN Name=RAGE;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;

RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Blazkova M., Kankova K.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065212; AAD15889.1;  
 DR GO; GO:0004872; F:receptor activity; IEA.

KM Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1906 MW; 5E9B9ED01E183530 CRC64;

Query Match 38.7%; Score 24; DB 2; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 4.5e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLPPVVNV 10  
 ID 2 FLPPVGI 8

RESULT 11  
 Q7TOB5 PRELIMINARY; PRT; 18 AA.

DT 01-OCT-2003 (TREMblrel. 25, Created)  
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Programmed cell death 1 ligand 2 (Fragment).

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.

RX MEDLINE=22791977; PubMed=12909129; DOI=10.1016/S0161-5890(03)00085-3;  
 RA Goraki K.S., Shin T., Crafoon E., Otsuji M., Rattis F.M., Huang X.,  
 RA Kelleher E., Francisco U., Pardoll D., Iuchiya H.;  
 RT "A set of genes selectively expressed in mature dendritic cells:  
 RT utility of related cis-acting sequences for lentiviral gene  
 RT transfer.";  
 RT MOL. Immunol. 40:35-47(2003).

DR EMBL; AY225192; AA034707.1; --  
 FT NON\_TER 18  
 FT NON\_TER 18  
 SQ SEQUENCE 18 AA; 1999 MW; A9B68E78F78F517 CRC64;

Query Match 38.7%; Score 24; DB 2; Length 18;  
 Best Local Similarity 30.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFFFLPPVVNV 10  
 ID 1 MLLLPINTL 10

RESULT 12  
 Q91BM7 PRELIMINARY; PRT; 18 AA.

AC 091BM7;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
 DE P10 peptide (Fragment).  
 OS Autographa californica nuclear polyhedrosis virus (AcNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 NCBI\_TaxID=46015;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RX MEDLINE=90085829; PubMed=2688302;  
 RA Kuzio J., Jacques R., Faulkner P.;  
 RT "Identification of p74, a gene essential for virulence of baculovirus  
 RT occlusion bodies.";   
 RL Virology 173:759-763(1989).  
 DR EMBL; M31301; AAA46728.2; -.  
 FT NON TER  
 SQ SEQUENCE 18 AA; 1923 MW; FFA5B12C2CBFD17A CRC64;

Query Match 38.7%; Score 24; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 4.7e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPPVNTLP 12  
 | | | | |  
 Db 9 LVVNVNVP 16

RESULT 13  
 GRAR\_RANRU STANDARD; PRT; 12 AA.

AC P40754;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Granuliberin-R.  
 OS Rana rugosa (wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=78062810; PubMed=589733;  
 RA Nakajima T., Yasuhara T.;  
 RT "A new mast cell degranulating peptide, granuliberin-R, in the frog  
 RT (Rana rugosa) skin.";   
 RL Chem. Pharm. Bull. 25:2464-2465(1977).  
 RN [2]

RP SYNTHESIS.  
 RX MEDLINE=78189201; PubMed=657408;  
 RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,  
 RA Koyama K., Yajima H.;  
 RT "Synthesis of the dodecapeptide amide corresponding to the entire  
 RT amino acid sequence of granuliberin-R, a new frog skin peptide from  
 RT Rana rugosa.";   
 RL Chem. Pharm. Bull. 26:1222-1230(1978).  
 CC -1- FUNCTION: Mast cell degranulating peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
 KW Mast cell degranulation.  
 FT MOD RES 12 Serine amide.  
 FT MOD RES 12  
 SQ SEQUENCE 12 AA; 1424 MW; 2B974BB9CA1B5047 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 4.8e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PFFLPV 7  
 | | | | |  
 Db 1 PFFLPV 6

RESULT 14  
 CRBL\_VESLE STANDARD; PRT; 13 AA.

AC P17235;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vespid chemotactic peptide L (VESCP-L).

OS Vesputia lewisii (yellow jacket) (wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vesputia.  
 OX NCBI\_TaxID=7452;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
 RL Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
 RL (in) Izumiya N. (eds.);  
 RL Peptide Chemistry 1984, pp.177-182. Protein Research Foundation, Osaka  
 RL (1985).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 KW Amidation; Chemotaxis; Direct protein sequencing;  
 KW Mast cell degranulation.  
 FT MOD RES 13 Leucine amide.  
 FT MOD RES 13  
 SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PFPVV 8  
 | | | | |  
 Db 1 PFPVV 5

RESULT 15  
 CRBL\_VESXA STANDARD; PRT; 13 AA.

AC P17234;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vespid chemotactic peptide X (VESCP-X).  
 OS Vespa xanthoptera (Japanese hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7448;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
 RA (in) Izumiya N. (eds.);  
 RL Peptide Chemistry 1984, pp.177-182. Protein Research Foundation, Osaka  
 RL (1985).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 KW Amidation; Chemotaxis; Direct protein sequencing;  
 KW Mast cell degranulation.  
 FT MOD RES 13 Leucine amide.  
 FT MOD RES 13  
 SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PFPVV 8  
 | | | | |  
 Db 1 PFPVV 5

RESULT 16  
 TEIA\_RANBO STANDARD; PRT; 13 AA.

AC P84116;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Temporalin-18Ya.  
 OS Rana boylii (foothill yellow-legged frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=160499;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX PubMed=14531844;  
RA Conlon J.M., Somervend A., Patel M., Davidson C., Nielsen P.F.,  
RA Pal T., Rollins-Smith L.A.;  
RT "Isolation of peptides of the brevinn-1 family with potent  
RT candidicidal activity from the skin secretions of the frog Rana  
RT boylii.";  
RL J. Pept. Res. 62:207-213(2003).  
CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium  
CC S.aureus.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- MASS SPECTROMETRY: MW=1381.9; METHOD=MALDI; RANGE=1-13;  
CC NOTE=Ref.1.  
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Brevinn subfamily.  
KW Amidation; Amphibian defense peptide; Antibiotic;  
KW Direct protein sequencing.  
FT MOD\_RES 13 13 Leucine amide.  
FT UNSURE 13 13 L or I.  
FT SEQUENCE 13 AA; 1384 MW; C850402B9DECC3D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;  
Best Local Similarity 60.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLPV 8  
DB 1 FLPV 5

RESULT 17  
ID 08HKF6 PRELIMINARY; PRT; 17 AA.  
AC 08HKF6;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE NADH dehydrogenase subunit 1 (Fragment).  
OS Name=ND1;  
OS Rhinipcephalus evertsi.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Parasitiformes; Ixodida; Ixodidae; Rhinipcephalus.  
OX NCBI\_TaxID=60190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;  
RA Murrell A., Campbell N.J.H., Barker S.C.;  
RT "The value of idiosyncratic markers and changes to conserved tRNA  
RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:  
RT Ixodidae) for phylogenetic inference.";  
RL Syst. Biol. 52:296-310(2003).  
DR EMBL; AY059219; AAL79415.1; -;  
DR GO; GO:0005739; C:mitochondrion; IRA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 2071 MW; 15AFD0CC1743422 CRC64;

Query Match 37.1%; Score 23; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 6.6e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 FFLPVV 11  
DB 2 FFLPVV 11

RESULT 18  
ID 08NED1 PRELIMINARY; PRT; 18 AA.  
AC 08NED1;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC032027; AA032027.1; -;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2050 MW; B71A655B65FD253F CRC64;

Query Match 37.1%; Score 23; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 7e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FFLP 6  
DB 1 FFLP 5

RESULT 19  
ID 07RAU4 PRELIMINARY; PRT; 18 AA.  
AC 07RAU4;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN Name=PY06405;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=1236865; DOI=10.1038/nature01099;  
RA Carlton J.M., Anguilo S.V., Suh B.B., Koo J.T.W., Pertea M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shalibi A., Cummings L.M.,  
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
RA Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria  
RT parasite Plasmodium yoelii yoelii.";  
RL Nature 419:512-519(2002).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AABL01002164; EAA18620.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 18 AA; 2023 MW; FABC67565CD73D1E CRC64;

Query Match 37.1%; Score 23; DB 2; Length 18;  
Best Local Similarity 36.4%; Pred. No. 7e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FFLPVV 11  
DB 1 FFLPVV 11

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Db          6  IFFPFPVITIL 16

RESULT 20
BLAC_STRGR
ID _BLAC_STRGR      STANDARD;      PRT;      13 AA.
AC P81173;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DE 05-JUL-2004 (rel. 44, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6) (Fragment).
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OC NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL B-2682;
RX MEDLINE=98386507; PubMed=9720038;
RA Deak E., Szabo I., Kalmanczelyi A., Gal Z., Barabas G., Panyige A.;
RT "Membrane-bound and extracellular beta-lactamase production with
RL Microbiology 144:2169-2177(1998).
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
amino acid.
CC -1- SUBCELLULAR LOCATION: Secreted and membrane-bound.
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PROSITE; PS00146; BETA_LACTAMASE_A; PARTIAL.
KM Antibiotic resistance; Direct protein sequencing; Hydrolase; Membrane.
FT NON_TER      13
SQ SEQUENCE      13 AA; 1236 MW; 14C5129118D54760 CRC64;

Query Match      35.5%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      5  LPVVNV 10
      ||:|
Db      6  IPIANV 11

RESULT 21
Q36727
ID Q36727      PRELIMINARY;      PRT;      15 AA.
AC Q36727;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ND2 protein (Fragment).
CN Name=ND2;
OS Homo sapiens (Human).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94380052; PubMed=8093052;
RA Koeel S., Egensperger R., Mehraein P., Graeber M.B.;
RT "No association of mutations at nucleotide 5460 of mitochondrial NADH
RL dehydrogenase with Alzheimer's disease."
RL Biochem. Biophys. Res. Commun. 203:745-749(1994).
DR EMBL; S73804; AAD14133.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER      1
SQ SEQUENCE      15 AA; 1923 MW; D58870F163B6060 CRC64;

Query Match      35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 8.8e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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OY      1  LFFFLPVV 8
      ||:|
Db      6  LYFYLRLI 13

RESULT 22
Q46456
ID Q46456      PRELIMINARY;      PRT;      15 AA.
AC Q46456;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Tetanus toxin (Fragment).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053814; PubMed=3536478;
RA Eisel U., Jarusch W., Goretzki K., Henechen A., Engels J., Weller U.,
RA Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and homology
RL with botulinum toxins."
RL EMBL; X04436; CAA28032.1; -.
DR EMBL; X04436; CAA28032.1; -.
FT NON_TER      1
SQ SEQUENCE      15 AA; 1706 MW; 08110F73DCCD7BC5 CRC64;

Query Match      35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      6  PIVNVN 11
      ||:|
Db      7  PIVNKL 12

RESULT 23
Q711M5
ID Q711M5      PRELIMINARY;      PRT;      15 AA.
AC Q711M5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Glycosyltransferase family 2 protein (Fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 4797;
RA Langenhelm J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF496244; AAQ06912.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KM Transferase.
FT NON_TER      15
SQ SEQUENCE      15 AA; 1701 MW; CB7895B8DFAEC9B CRC64;

Query Match      35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 8.8e+03;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      5  LPVVNV 11
      ||:|
Db      5  LPVIVSII 11

RESULT 24
Q6QVE1
ID Q6QVE1      PRELIMINARY;      PRT;      16 AA.

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AC Q6QVE1;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Ribonuclease H (Fragment).  
 GN Name=RNase H;  
 OS Phaseolus vulgaris (Kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eusteroideae; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OC NCBI\_TaxID=3885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15060605; DOI=10.1139/g03-102;  
 RA Gallardo L.M., Galtan E., Baccam P., Tohme J.;  
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia  
 retrotransposons in common bean (Phaseolus vulgaris L.)."  
 RL Genome 47:84-95(2004)  
 DR EMBL; AY524258; AAS18555.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 16 AA; 1935 MW; 3E60812E8E2D6A23 CRC64;  
 SQ

Query Match 35.5%; Score 22; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5  
 |||  
 Db 13 PFPL 16

RESULT 25  
 UP36 UPEMJ STANDARD; PRT; 17 AA.  
 AC P82043;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Uperin 3.6.  
 OS Uperoleia mjobergii (Australian toadlet).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OC NCBI\_TaxID=104954;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "New antibiotic uperin peptides from the dorsal glands of the  
 Australian toadlet Uperoleia mjobergii.";  
 RL Aust. J. Chem. 49:1325-1331(1996).  
 CC -1- FUNCTION: Shows antibacterial activity against B.cereus, L.lactis,  
 CC L.limonu, M.luteus, S.aureus, S.epidermis and S.uberis.  
 CC -1- SUBCELLULAR LOCATION: secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=1826; METHOD=FA; RANGE=1-17; NOTE=Ref.1.  
 KW Amination; Amphibian defense peptide; Antibiotic;  
 KW Direct protein sequencing.  
 FT MOD\_RES 17  
 FT SEQUENCE 17 AA; 1778 MW; 784DB8B46263CA3D CRC64;  
 SQ

Query Match 35.5%; Score 22; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVL 11  
 |||||  
 Db 9 VVNVL 13

RESULT 26  
 Q95KQ7 PRELIMINARY; PRT; 17 AA.

AC Q95KQ7;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE B-cell CLL/Lymphoma 9 (Fragment).  
 GN Name=BCL9;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22042654; PubMed=12047235;  
 RA Knoll A., Dvorak J., Konner G.A., Cepica S.;  
 RT "Linkage and cytogenetic mapping of the BCL9 gene to porcine  
 chromosome 4.";  
 RL Anim. Genet. 33:162-163(2002).  
 DR EMBL; AJ16470; CAC94923.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 17 AA; 1825 MW; 90F402DC8C5CF231 CRC64;  
 SQ

Query Match 35.5%; Score 22; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 9.9e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVVNVLP 12  
 |||:|:  
 Db 10 LPVVNVLP 17

RESULT 27  
 Q80T36 PRELIMINARY; PRT; 17 AA.  
 AC Q80T36;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE G protein-coupled receptor brain-specific angiogenesis inhibitor 1  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;  
 RA Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,  
 RA Morfitt M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,  
 RA Bergmann J.E., Galtan E.;  
 RT "The G protein-coupled receptor repertoires of human and mouse.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).  
 DR EMBL; AY255613; AAO85125.1; -.  
 DR GO; GO:0004872; P:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT SEQUENCE 17 AA; 2133 MW; A20F02808DBA5BFB CRC64;  
 SQ

Query Match 35.5%; Score 22; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5  
 |||||  
 Db 3 PFPL 6

RESULT 28  
 TEMC\_RANLU STANDARD; PRT; 14 AA.  
 AC P82832;  
 DT 29-MAR-2004 (Rel. 43, Created)



DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DB Tempurin-11c.  
 OS Rana luteiventris (Spotted frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 RN NCBI\_TaxID=58176;  
 [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20117700; PubMed=10651828;  
 RA Gozaya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,  
 RA Conlon J.M.;  
 RT "Peptides with antimicrobial activity from four different families  
 isolated from the skins of the North American frogs Rana luteiventris,  
 Rana berlandieri and Rana dipiens.";  
 RL Bur. J. Biochem. 267:894-900(2000).  
 CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium  
 S. aureus. Weak activity against Gram-negative bacterium E.coli and  
 C. albicans.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- MASS SPECTROMETRY: MW=1603.1; METHOD=Electrospray; RANGE=1-14;  
 CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC Brevitin subfamily.  
 KW Amidation: Amphibian defense peptide; Antibiotic;  
 KW Direct protein sequencing; Fungicide.  
 FT MOD\_RES 14 Leucine amide.  
 FT SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;

Query Match 34.7%; Score 21.5; DB 1; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 1e+04; 0; Indels 1; Gaps 1;  
 Matches 4; Conservative 4; Mismatches 0;

QY 4 LPPV-VNVL 11  
 |||::|  
 DB 1 FLPIILNLI 9

RESULT 29  
 Q9P8B5 PRELIMINARY; PRT; 9 AA.  
 AC Q9P8B5;  
 DT 01-OCT-2000 (TRENBLREL. 15, Created)  
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)  
 DE His4 protein (Fragment).  
 GN Name=His4;  
 OS Kluyveromyces lacticis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NRRL-Y1140.  
 RC MEDLINE=99448382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;  
 RA Lamas-Maceliras M., Bisperanza Cerdan E., Freire-Picos M.A.;  
 RT "Kluyveromyces lacticis His4 transcriptional regulation: similarities  
 and differences to Saccharomyces cerevisiae His4 gene.";  
 RL FEBS Lett. 458:72-76(1999).  
 DR EMBL; AJ238494; CAB87125.1; -.  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1015 MW; 5770D2D772DD2D767 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 LPPVNV 10  
 |||||  
 DB 2 LPPVNV 7

RESULT 30  
 Q9TQSO PRELIMINARY; PRT; 11 AA.  
 AC Q9TQSO;  
 DT 01-MAY-2000 (TRENBLREL. 13, Created)  
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
 DE C-kit (Fragment).  
 GN Name=kit;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=20154958; PubMed=10690368;  
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;  
 RT "A polymorphism in the bovine c-kit gene.";  
 RL Anim. Genet. 31:71-71(2000).  
 DR EMBL; AJ243424; CAB60775.1; -.  
 DR EMBL; AJ243506; CAB60774.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 9.8e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPPVNV 10  
 |||||  
 DB 4 VPVSV 9

RESULT 31  
 CRBL\_VESAN STANDARD; PRT; 13 AA.  
 ID CRBL\_VESAN  
 AC P17233;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vespid chemotactic peptide A (VESCP-A).  
 OS Vespa analis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7449;  
 [1]  
 RN SEQUENCE.  
 RP TISSUE=Venom;  
 RC RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,  
 RA Fujino M.;  
 RL (In) Munekata E. (eds.);  
 RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation, Osaka  
 (1984).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 of neutrophils.  
 CC Amidation; Chemotaxis; Direct protein sequencing;  
 KW Mast cell degranulation.  
 FT MOD\_RES 13  
 FT SEQUENCE 13 AA; 1386 MW; C8554365DF9233D CRC64;

Query Match 33.9%; Score 21; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPPV 8  
 |||||  
 DB 1 FLPPV 5

RESULT 32  
 ID CRBL\_VESCR STANDARD; PRT; 13 AA.  
 AC P01518;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Crabrolin.  
 OS Vespa crabro (European hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 NCBI\_TaxID=7445;  
 OK NCBI\_TaxID=7445;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=84289390; PubMed=6206053;  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 crabrolin, from the venom of the European hornet, *Vespa crabro*.";  
 RL J. Biol. Chem. 259:10106-10111(1984).  
 RN [2]  
 RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
 RX MEDLINE=97419326; PubMed=9273892;  
 RA Krishnakumari V., Nagaraj R.;  
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
 peptide from the venom of the European hornet, *Vespa crabro*, and its  
 analogs.";  
 RL J. Pept. Res. 50:88-93(1997).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 of neutrophils. Has antimicrobial and hemolytic activity.  
 DR PIR: A01781; ZVHP1.  
 KW Amidation; Antibiotic; Chemotaxis; Direct protein sequencing;  
 KM Mast cell degranulation.  
 FT MOD\_RES 13 AA; 1497 MW; 51SEF8FCEA8D2407 CRC64;  
 SQ SEQUENCE 13 AA; 1497 MW; 51SEF8FCEA8D2407 CRC64;  
 QY Query Match 33.9%; Score 21; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 DB 4 FLPPV 8  
 1 FLPLI 5

RESULT 33  
 ID CRBL\_VESTR STANDARD; PRT; 13 AA.  
 AC P17231;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vespid Chemotactic Peptide T (VesCP-T).  
 OS Vespa tropica (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 NCBI\_TaxID=7450;  
 OK NCBI\_TaxID=7450;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Nakajima T., Erspamer V.;  
 RL (In) Sakakibara S. (eds.);  
 RL Peptide Chemistry 1982, pp.213-218, Protein Research Foundation, Osaka  
 RL (1983).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 of neutrophils.  
 KW Amidation; Chemotaxis; Direct protein sequencing;  
 KM Mast cell degranulation.  
 FT MOD\_RES 13 AA; 1354 MW; 220140365DFE5338 CRC64;  
 SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 33.9%; Score 21; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FLPPV 8  
 1 FLPLI 5

RESULT 34  
 ID HPB9\_RANES STANDARD; PRT; 13 AA.  
 AC P32416;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Hemolytic protein B9 (Fragment).  
 OS Rana esculenta (Edible frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8401;  
 OK NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90198965; PubMed=2317508; DOI=10.1016/0304-4165(90)90140-R;  
 RA Stimaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,  
 RA Barra D., Bossa F.;  
 RT "Purification and characterization of bioactive peptides from skin  
 extracts of *Rana esculenta*.";  
 RL Biochim. Biophys. Acta 1033:318-323(1990).  
 CC -1- FUNCTION: Shows hemolytic activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 DR PIR: S09019; S09019.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
 KM Hemolysis.  
 FT MOD\_RES 13 AA; 1402 MW; C6B41A765DF9287D CRC64;  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;  
 QY Query Match 33.9%; Score 21; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 DB 4 FLPPV 8  
 1 FLPLI 5

RESULT 35  
 ID TEMA\_RANTE STANDARD; PRT; 13 AA.  
 AC P56917;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Temporin A.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8407;  
 OK NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Stimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog *Rana  
 temporaria*.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive  
 bacteria.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

```

CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
KW Amidation: Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
DB 1 FLPLI 5

RESULT 36
TEMP_RANTE STANDARD; PRT; 13 AA.
ID TEMP_RANTE
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tempoxin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OK NCBI_TaxID=8407;
RN (1)
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Tempoxins", antimicrobial peptides from the European red frog Rana
RT temporaria."
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
CC Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
KW Amidation: Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
DB 1 FLPLI 5

RESULT 37
CRBL_VESOR STANDARD; PRT; 14 AA.
ID CRBL_VESOR
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Histamine releasing peptide II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespinoidea;
OC Vespidae; Vespinae; Vespa.
OK NCBI_TaxID=7447;
RN (1)
RP SEQUENCE.

```

```

RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Roznov B.V., Gubchik I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
DR PIR: JN0390; JN0390.
KW Amidation; Chemotaxis; Direct protein sequencing;
KW Mast cell degranulation.
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1524 MW; 22015B46CEDFD38 CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 1; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVV 8
DB 1 FLPLI 5

RESULT 38
Q9QVD7 PRELIMINARY; PRT; 15 AA.
ID Q9QVD7
AC Q9QVD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inositol 1,4,5-trisphosphate binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10118;
RN (1)
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanamatsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol."
RL J. Biol. Chem. 267:6518-6525(1992).
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1726 MW; 1F161D1E2ADF88BD CRC64;

Query Match
Best Local Similarity 33.9%; Score 21; DB 2; Length 15;
Matches 1; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFPLPVNV 10
DB 1 IYFFMAIIDI 10

RESULT 39
Q9URC6 PRELIMINARY; PRT; 17 AA.
ID Q9URC6
AC Q9URC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipid-binding protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OK NCBI_TaxID=4932;
RN (1)
RP SEQUENCE.
RX MEDLINE=91353077; PubMed=1882548;
RX Creutz C.E., Snyder S.L., Kamdouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding

```

RT proteins of Saccharomyces cerevisiae.";

RL Yeast 7:229-244(1991).

DR GO; GO:0005853; C:eukaryotic translation elongation factor 1. . . ; IEA.

DR GO; GO:0003746; F:translation elongation factor activity; IEA.

DR GO; GO:0006414; P:translational elongation; IEA.

DR InterPro; IPR001662; EFl\_G.

DR ProDom; PD006217; EFl\_G; 1.

FT NON\_TER 1

FT NON\_TER 17

SQ SEQUENCE 17 AA; 1959 MW; C2EB654328774AD2 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 33.3%; Pred. No. 1.5e+04;

Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 FLPVNVLP 12

Db 4 YVPFVDVAP 12

RESULT 40

O95795 PRELIMINARY; PRT; 17 AA.

AC O95795; 01-MAY-1999 (TRENBLER). 10, Created)

DT 01-MAY-1999 (TRENBLER). 10, Last sequence update)

DT 01-JUN-2003 (TRENBLER). 24, Last annotation update)

DE Advanced glycosylation end product-specific receptor (Fragment).

CN Name=RAGE;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI Taxid=9606;

RN [1] \_SEQUENCE FROM N.A.

RA Blazkova M., Kankova K.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF065211; AADI5888.1; .

DR GO; GO:004872; F:receptor activity; IEA.

KW Receptor.

FT NON\_TER 1

FT NON\_TER 17

SQ SEQUENCE 17 AA; 1727 MW; 38C7EB8959B00D72 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 1.5e+04;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FLPVV 8

Db 12 FLPAV 16

Search completed: June 7, 2005, 23:18:57  
Job time : 55.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-5  
Perfect score: 81  
Sequence: 1 DLEMPVLPEPPFV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneeqp19808:\*  
2: geneeqp19908:\*  
3: geneeqp20008:\*  
4: geneeqp20015:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20038:\*  
8: geneeqp20048:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	81	100.0	15	4 AAB72504	Aab72504 Colostrien
2	81	100.0	15	4 AAB59332	Aab59332 Ewe colos
3	81	100.0	15	4 AAB72250	Aab72250 Colostrien
4	81	100.0	15	4 AAB72536	Aab72536 Colostrien
5	81	100.0	15	5 AAO14581	Aao14581 Neural ce
6	81	100.0	15	5 AAM51040	Aam51040 Colostrien
7	81	100.0	15	5 AAE20232	Aae20232 Colostrien
8	81	100.0	15	5 ADN60299	Adn60299 Constitue
9	81	100.0	15	8 ADS74398	AdS74398 Ovine col
10	81	100.0	15	4 AAB59332	Aab59332 Ewe colos
11	57	70.4	10	4 AAE07187	Aae07187 Colostrien
12	51	63.0	10	4 AAE07187	Aae07187 Modified
13	39.5	48.8	15	5 AAD71712	Aad71712 Transcrip
14	39	48.1	17	7 ADF14579	Adf14579 Glutien-de
15	36	44.4	18	4 AAB72530	Aab72530 Colostrien
16	36	44.4	18	4 AAB59330	Aab59330 Ewe colos
17	36	44.4	18	4 AAB72267	Aab72267 Colostrien
18	36	44.4	18	4 AAB72552	Aab72552 Colostrien
19	36	44.4	18	5 AAO14584	Aao14584 Neural ce
20	36	44.4	18	5 AAM51056	Aam51056 Colostrien
21	36	44.4	18	5 AAE20239	Aae20239 Colostrien
22	36	44.4	18	8 ADN60316	Adn60316 Constitue
23	36	44.4	18	8 ADS74406	AdS74406 Ovine col
24	35	43.2	12	8 ADH14551	Adh14551 Barley ho
25	35	43.2	12	8 ADH14849	Adh14849 Gliadin r

26	34	42.0	14	2 AAR93469	Aar93469 GST-SRC p
27	34	42.0	15	4 AAB72507	Aab72507 Colostrien
28	34	42.0	15	4 AAB59313	Aab59313 Ewe colos
29	34	42.0	15	4 AAB72253	Aab72253 Colostrien
30	34	42.0	15	4 AAB72539	Aab72539 Colostrien
31	34	42.0	15	5 AAO14584	Aao14584 Neural ce
32	34	42.0	15	5 AAM51043	Aam51043 Colostrien
33	34	42.0	15	5 AAE20235	Aae20235 Colostrien
34	34	42.0	15	5 AAB09569	Aab09569 Human LI
35	34	42.0	15	5 ADN60302	Adn60302 Constitue
36	34	42.0	15	8 ADR31999	AdR31999 Heat ehoc
37	34	42.0	15	8 ADS74389	AdS74389 Ovine col
38	34	42.0	16	4 AAB59344	Aab59344 Ewe colos
39	34	42.0	17	8 ADH14830	Adh14830 Gliadin r
40	34	42.0	18	6 AAE34144	Aae34144 T-cell st
41	33	40.7	12	8 ADM96406	Adm96406 Immature
42	33	40.7	14	2 AAR58339	Aar58339 Hypotensi
43	33	40.7	14	7 ADF14537	Adf14537 Eptlope o
44	33	40.7	14	7 ADF14521	Adf14521 Eptlope o
45	33	40.7	14	7 ADF14850	Adf14850 T cell st
46	33	40.7	14	7 ADF14513	Adf14513 Glutien-de
47	33	40.7	14	7 ADF14529	Adf14529 Eptlope o
48	33	40.7	14	8 ADG37024	Adg37024 Bovine ca
49	33	40.7	15	8 ADC38553	AdC38553 HSV-2 U12
50	33	40.7	16	8 ADH14805	Adh14805 Gliadin r
51	33	40.7	17	8 ADH14823	Adh14823 Gliadin r
52	33	40.7	17	8 ADH14828	Adh14828 Gliadin r
53	33	40.7	17	8 ADH14826	Adh14826 Gliadin r
54	32	39.5	13	8 ADO15567	Ado15567 Targeting
55	32	39.5	15	2 AAW85209	Aaw85209 Helper T-
56	32	39.5	15	2 AAW85195	Aaw85195 Helper T-
57	32	39.5	15	2 AAW85329	Aaw85329 Helper T-
58	32	39.5	15	4 ABR24651	AbR24651 HIV DR su
59	32	39.5	15	4 ABR24658	AbR24658 HIV DR su
60	32	39.5	15	8 ADH14851	Adh14851 Gliadin r
61	32	39.5	16	2 AAR29099	Aar29099 Chymotryp
62	32	39.5	16	8 ADH14810	Adh14810 Gliadin r
63	32	39.5	16	8 ADR31998	AdR31998 Heat shoc
64	31.5	38.9	18	6 ADB12816	AdB12816 Antihyper
65	31	38.3	10	2 AAR93548	Aar93548 Random 10
66	31	38.3	10	4 AAB75678	Aab75678 HLA class
67	31	38.3	10	6 ABR47334	AbR47334 Staphyloc
68	31	38.3	12	6 ABR47208	AbR47208 Staphyloc
69	31	38.3	12	6 ABR75157	AbR75157 Elemental
70	31	38.3	12	7 ADB67069	AdB67069 GaAs bind
71	31	38.3	12	7 AAO24131	Aao24131 Chaperoni
72	31	38.3	12	7 AOC91636	Aoc91636 Phage bin
73	31	38.3	12	8 ADL99339	AdL99339 Nanostruc
74	31	38.3	12	8 ADO07136	Ado07136 GaAs seml
75	31	38.3	13	3 AAD07345	Aad07345 M13 colip
76	31	38.3	17	8 AAY57715	Aay57715 Human clu
77	31	38.3	17	8 ADH14703	Adh14703 Gliadin r
78	31	38.3	18	3 AAY57716	Aay57716 Human clu
79	30	37.0	9	6 ABR25398	AbR25398 Human can
80	30	37.0	9	6 ABR24394	AbR24394 Human can
81	30	37.0	9	6 ABR24628	AbR24628 Human can
82	30	37.0	9	6 ABR25632	AbR25632 Human can
83	30	37.0	9	6 ABR24838	AbR24838 Human can
84	30	37.0	9	6 ABR25012	AbR25012 Human can
85	30	37.0	10	6 ADH14530	Adh14530 Gliadin r
86	30	37.0	10	6 ABR24490	AbR24490 Human can
87	30	37.0	11	7 ADE19622	AdE19622 Antigenic
88	30	37.0	11	7 ADE15738	AdE15738 E. coli t
89	30	37.0	10	6 ABR25070	AbR25070 Human can
90	30	37.0	10	6 ABR24761	AbR24761 Human can
91	30	37.0	11	7 ADE15739	AdE15739 E. coli t
92	30	37.0	11	7 ADE19622	AdE19622 Antigenic
93	30	37.0	12	7 ADE15738	AdE15738 E. coli t
94	30	37.0	13	4 AAY71992	Aay71992 Autotaxin
95	30	37.0	13	7 ADE15737	AdE15737 E. coli t
96	30	37.0	13	7 ADM74834	Adm74834 Potential
97	30	37.0	13	8 ADH14550	Adh14550 Barley ho
98	30	37.0	13	8 ADH14819	Adh14819 Gliadin r

99 30 37.0 14 7 ADE15736  
100 30 37.0 14 7 ADP14522

Adel5736 E. coli t  
Adf14522 Epitope o

## ALIGNMENTS

```
RESULT 1
AAB72504
ID AAB72504 strand; peptide; 15 AA.
XX
XX AAB72504;
AC
XX
XX 09-MAY-2001 (first entry)
XX
XX DE Colostrinin peptide #5.
XX
XX KM Dermatological; oxidative stress regulator; colostrinin.
XX
XX OS Unidentified.
XX
XX PN WO200112650-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US022665.
XX
XX PR 17-AUG-1999; 99US-0149310P.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX
XX DR WPI; 2001-218342/22.
XX
XX PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.
XX
XX PS Claim 6; Page 25; 48pp; English.
XX
XX CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidizing species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient
XX
XX SQ Sequence 15 AA;

Query Match          100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPPFPV 15
   |||||
Db 1 DLEMPVLPEPPFPV 15

RESULT 2
AAB59322
ID AAB59322 strand; peptide; 15 AA.
XX
XX AAB59322;
AC
XX
XX 21-MAR-2001 (first entry)
XX
XX DE Ewe colostrinin peptide fragment B-7.
XX
XX KM Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; Beta-amyloid plaque.
XX
```

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OS Ovis sp.
XX
XX PN WO200075173-A2.
XX
XX PD 14-DEC-2000.
XX
XX PF 02-JUN-2000; 2000WO-GB002128.
XX
XX PR 02-JUN-1999; 99GB-00012852.
XX
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX
XX PI Georgiades JA;
XX
XX DR WPI; 2001-071058/08.
XX
XX PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
XX PS Claim 7; Page 27; 63pp; English.
XX
XX CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
XX SQ Sequence 15 AA;

Query Match          100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPPFPV 15
   |||||
Db 1 DLEMPVLPEPPFPV 15

RESULT 3
AAB72250
ID AAB72250 strand; peptide; 15 AA.
XX
XX AC AAB72250;
XX
XX DT 14-MAY-2001 (first entry)
XX
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 5.
XX
XX KM Colostrinin; immune response; cytokine; blood cell proliferation;
XX central nervous system disorder; neurological disorder; mental disorder;
XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX neurosis; infection.
XX
XX OS Synthetic.
XX
XX PN WO200111937-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US022818.
XX
XX PR 17-AUG-1999; 99US-0149311P.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
```

DR WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 81; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLPEPPPPV 15  
 DB 1 DLEMPVLPEPPPPV 15  
 RESULT 4  
 AAB72536  
 ID AAB72536 standard; peptide; 15 AA.  
 XX  
 XX AAB72536;  
 AC  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 XX Colostrinin peptide #5.  
 DB  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US022774.  
 PF  
 XX 17-AUG-1999; 99US-0149633P.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLPEPPPPV 15  
 DB 1 DLEMPVLPEPPPPV 15  
 RESULT 5  
 AA014581  
 ID AA014581 standard; peptide; 15 AA.  
 XX  
 XX AA014581;  
 AC  
 XX 27-MAY-2002 (first entry)  
 DT  
 XX  
 DE Neural cell regulatory colostrinin peptide 5.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FT Key Location/Qualifiers  
 FT Modified-site 15 /note="Optional C-terminal amide"  
 XX  
 XX WO200213851-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US022777.  
 PF  
 XX 17-AUG-2000; 2000WO-US022777.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I, Stanton JG, Hughes TK;  
 PI  
 XX WPI; 2002-269152/31.  
 DR  
 XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 81; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLPEPPPPV 15  
 DB 1 DLEMPVLPEPPPPV 15  
 RESULT 6  
 AAM51040

ID AAMS1040 standard; peptide; 15 AA.

XX AAMS1040;

XX 30-MAY-2002 (first entry)

XX Colostriin constituent peptide.

XX Colostriin; colostrum; immunomodulator; cardiovascular;  
XX blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 15 /note="optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US022775.

XX 17-AUG-2000; 2000WO-US022775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of blood  
XX cell regulator selected from colostriin, its constituent peptide and/or  
XX analog.

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostriin constituent peptide that is  
XX preferred for use as an immunological regulator and as a blood cell  
XX regulator in claimed methods of the invention. It is classified as having  
XX a beta-casein homologue precursor. Methods are claimed for: inducing a  
XX cytokine in a cell by contact with an immunological regulator, where the  
XX cell is present in a cell culture, a tissue, an organ or an organism, and  
XX the cell is mammalian, including human; modulating an immune response in  
XX a cell by contact with the immunological regulator under conditions  
XX effective to induce a cytokine; modulating an immune response in a  
XX patient by administering an immunological regulator under conditions  
XX effective to induce a cytokine, where the immunological regulator is  
XX administered topically or as part of a dietary supplement, and where the  
XX immune response is specific or non specific, an interferon response or an  
XX antibody response; modulating blood cell proliferation by contacting  
XX blood cells with a blood cell regulator, where the blood cells are  
XX present in a cell culture or an organism, are mammalian or human, and  
XX where the blood cells are increased in number or differentiated; and a  
XX method for modulating blood cell proliferation in a patient. A claimed  
XX cytokine-inducing composition comprises a pharmaceutical carrier and an  
XX active agent such as the present peptide. Cytokines induced by this  
XX peptide in human leucocyte cultures include interferon-gamma, tumour  
XX necrosis factor-alpha, interleukin-6 and interleukin-10

XX Sequence 15 AA;

XX Query Match 100.0%; Score 81; DB 5; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-05;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 DLEMPVLVPEPPFPV 15

XX 1 DLEMPVLVPEPPFPV 15

RESULT 7

AAE20232  
ID AAE20232 standard; peptide; 15 AA.

XX AAE20232;

XX 18-JUN-2002 (first entry)

XX Colostriin constituent peptide #5.

XX Blood cell regulator; colostriin; constituent peptide; oxidative stress;  
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX transplantation; implantation; dermatological; vulnary.

XX Unidentified.

XX Key Location/Qualifiers

XX Modified-site 15 /note="Optionally C-terminal amide"

XX WO200213850-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US022776.

XX 17-AUG-2000; 2000WO-US022776.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2002-269151/31.

XX Composition useful for the modulation of blood cell proliferation in a  
XX patient comprises a blood cell regulator selected from colostriin, its  
XX constituent peptide and/or analog.

XX Claim 6; Page 25; 51pp; English.

XX The invention relates to a composition which comprises a blood cell  
XX regulator selected from colostriin, its constituent peptide and/or  
XX analogue. The invention is used for modulating the oxidative stress level  
XX in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
XX organ, or organism; or for treating oxidative damage to the skin of a  
XX patient e.g. animal or human; to modulate oxidative stress during/ after  
XX a premature birth or normal birth, preventing/delaying aging in a  
XX patient; enhancing wound healing, and the reduction of side effects of  
XX cosmetic procedures. The method changes the level of an oxidising species  
XX in the cell, such as decreases or prevents increase in the level of  
XX damage to a biomolecule of the patient selected from DNA, protein and/or  
XX lipid, compared to the same conditions when the oxidative stress  
XX regulator is not present. The modulation of oxidative stress results in  
XX enhanced repair, regeneration, and replacement of cells, tissues and  
XX organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
XX external organs), as well as enhanced preservation of such organs for  
XX transplantation, implantation, or scientific research. The present  
XX sequence is a colostriin constituent peptide

XX Sequence 15 AA;

XX Query Match 100.0%; Score 81; DB 5; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-05;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 DLEMPVLVPEPPFPV 15

XX 1 DLEMPVLVPEPPFPV 15

RESULT 8

ADN60299  
ID ADN60299 standard; peptide; 15 AA.



XX AC ADN60299;  
 XX XX  
 DT 29-JUL-2004 (first entry)  
 XX DE Constituent peptide of colostrinin SEQ ID NO:5.  
 XX XX  
 XX modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
 KW 4HNE damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.  
 XX OS Synthetic.  
 XX XX  
 XX WO2004037851-A2.  
 XX PD 06-MAY-2004.  
 XX PF 22-OCT-2003; 2003WO-US033423.  
 XX PR 22-OCT-2002; 2002US-0420369P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (BOLD/) BOLDOGH I.  
 XX PA (STAN/) STANTON J G.  
 XX PA (GEOR/) GEORGIADIS J A.  
 XX PA (HUGH/) HUGHES T K.  
 XX PA (KRUZ/) KRUZEL M.  
 XX PI Bolodogh I, Stanton JG, Georgiades JA, Hughes TK, Kruznel M;  
 XX DR WPI; 2004-365494/34.  
 XX PT Use of colostrinin for e.g. modulating an intracellular signaling  
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 PT a cell.  
 XX PS Claim 6; SEQ ID NO 5; 46pp; English.  
 CC The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLPIVPEPPFV 15  
 |||||  
 DB 1 DLEMPVLPIVPEPPFV 15  
 RESULT 9  
 ADS74398  
 ID ADS74398 standard; peptide; 15 AA.

XX AC ADS74398;  
 XX XX  
 DT 16-DEC-2004 (first entry)  
 XX DE Ovine colostrinin peptide.  
 XX DE Colostrum; colostrinin; sheep; peptide purification.  
 XX KW  
 XX OS Ovis aries.  
 XX PN WO2004081038-A1.  
 XX PD 23-SEP-2004.  
 XX PF 10-MAR-2004; 2004WO-GB001014.  
 XX PR 11-MAR-2003; 2003GB-00005552.  
 XX PR 08-MAR-2004; 2004GB-00005190.  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX PI Georgiades JA, Polanowski A, Wilusz T, Kruznel M;  
 XX DR WPI; 2004-677519/66.  
 XX PT Recovering peptides such as colostrinin from mammalian colostrum, by  
 PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 PT and precipitate, separating alcohol phase from precipitate, and  
 PT recovering alcohol phase.  
 XX PS Example; SEQ ID NO 15; 41pp; English.  
 CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrum using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids. In an example from the invention, the antigenic profile of  
 CC peptides recovered from sheep colostrum using the alcohol precipitation  
 CC methods was determined by ELISA using antibodies prepared against 9  
 CC synthetic peptides, including a peptide having the present sequence  
 CC (denoted antigen class B-8).  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLPIVPEPPFV 15  
 |||||  
 DB 1 DLEMPVLPIVPEPPFV 15  
 RESULT 10  
 AAB59352  
 ID AAB59352 standard; peptide; 16 AA.  
 XX AC AAB59352;  
 XX XX  
 DT 21-MAR-2001 (first entry)

```

XX DE Ewe colostrinin peptide fragment derived sequence #12.
XX PR
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KM central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX PI
XX OS Ovis sp.
XX PN WO20075173-A2.
XX PD 14-DEC-2000.
XX PF 02-JUN-2000; 200WO-GB002128.
XX PR 02-JUN-1999; 99GB-00012852.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX DR WPI; 2001-071058/08.
XX PT Peptides having an N-terminal amino acid sequence isolated from
XX PT colostrinin for treating e.g. disorders of the central nervous system and
XX PT immune system, viral and bacterial infections, and diseases characterized
XX PT by amyloid plaques.
XX PS Claim 8; Page 27; 63pp; English.
XX CC The present invention provides the sequences of a number of peptides
XX CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX CC fragment of colostrum. These peptides can be used in the treatment of
XX CC central nervous system disorders such as senile dementia, Parkinson's
XX CC disease, Alzheimer's disease, psychosis and neurosis, immune system
XX CC disorders such as bacterial and viral infections, to improve the
XX CC development of a child's immune system, as a dietary supplement, and to
XX CC promote the dissolution of beta-amyloid plaques
XX SQ Sequence 16 AA;

Query Match          100.0%; Score 81; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPEPPFPV 15
   |||||
Db 2 DLEMPVLPEPPFPV 16

RESULT 11
AAE07187
ID AAE07187 standard; peptide; 10 AA.
XX AC
XX AC AAE07187;
XX DT 06-NOV-2001 (first entry)
XX DE Colostrinin peptide 3.
XX KM Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KM Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KM central nervous system disorder; neurodegenerative disorder; weight loss;
XX KM beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KM acquired immunological deficiency; neurological disorder; dementia;
XX KM antiviral.
XX OS Unidentified.
XX PN WO200155199-A1.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-GB000329.

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XX XX 26-JAN-2000; 2000GB-00001825.
XX PR
XX KW (REGG-) REGEN THERAPEUTICS PLC.
XX KM Georgiades JA;
XX PI
XX OS WPI; 2001-488775/53.
XX PN
XX DR Peptide useful as an interalia in the treatment of e.g. disorders of the
XX PT immune system and the central nervous system comprises ten amino-terminal
XX PT amino acid sequence derived from peptides present in colostrinin.
XX PS Claim 1; Page 15; 40pp; English.
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child. The
XX CC present sequence is colostrinin peptide 3 related to the invention
XX SQ Sequence 10 AA;

Query Match          70.4%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLPEPPFPF 14
   |||||
Db 1 PVLPEPPFPF 10

RESULT 12
AAE07197
ID AAE07197 standard; peptide; 10 AA.
XX AC
XX AC AAE07197;
XX DT 06-NOV-2001 (first entry)
XX DE Modified colostrinin cyclic peptide #3.
XX KM Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KM Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KM central nervous system disorder; neurodegenerative disorder; weight loss;
XX KM beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KM acquired immunological deficiency; neurological disorder; dementia;
XX KM antiviral; cyclic.
XX OS Synthetic.
XX FH Key
XX FT Modified-site 1 location/Qualifiers
XX FT /note= "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Pro found at the C-terminal end"
XX PN WO200155199-A1.
XX PD 02-AUG-2001.

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PF    26-JAN-2001; 2001WO-GB0000329.
XX
PR    26-JAN-2000; 2000GB-00001825.
XX
PA    (REGEN-) REGEN THERAPEUTICS PLC.
PI    Georgiadis JA;
XX
DR    WPI; 2001-488775/53.
XX
PT    Peptide useful as an interalia in the treatment of e.g. disorders of the
PT    immune system and the central nervous system comprises ten amino-terminal
PT    amino acid sequence derived from peptides present in colostrinin.
XX
PS    Example 2; Page 8; 40pp; English.
XX
CC    The invention relates to colostrinin peptide fragments which are useful,
CC    inter alia, in the treatment of chronic disorders of the immune system
CC    and the central nervous system. Colostrinin peptides are used as a
CC    neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC    disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC    neuromuscular diseases characterized by the presence of beta-amyloid plaques and as a dietary supplement for babies, small children,
CC    adults and senile persons, who have been subjected to chemotherapy or
CC    have suffered from cachexia or weight loss due to the chronic disease.
CC    Colostrinin peptides are also used as food additives and as an auxiliary
CC    withdrawal treatment for drug addicts, after a period of detoxification
CC    and in persons dependent on stimulants. Colostrinin peptides are used to
CC    prepare antibodies and to treat emotional disturbances, e.g. emotional
CC    disturbances of psychiatric patients in a state of depression. These
CC    colostrinin peptides improves the development of immune system in a new
CC    born child and to correct the immunological deficiencies in a child. The
CC    present sequence is modified colostrinin cyclic peptide #3 related to the
CC    invention
XX
SQ    Sequence 10 AA;
XX
Query Match      63.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY    5 PVLPEVPEPP 13
     PVLPEVPEPP 13
DB    2 PVLPEVPEPP 10
RESULT 13
AAU77172
ID    AAU77172 standard; peptide; 15 AA.
XX
AC    AAU77172;
XX
DT    02-JUL-2002 (first entry)
XX
DE    Transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide.
XX
KW    Human; transcriptional control factor ZFM1 isomer 25.63; HIV;
KW    malignant tumour; haemopathy; human immunodeficiency virus; cancer;
KW    immunological diseases; inflammation; cytostatic; haemostatic; virucide;
KW    immunomodulatory; antiinflammatory; gene therapy.
XX
OS    Homo sapiens.
XX
PN    WO200220588-A1.
XX
PD    14-MAR-2002.
XX
PE    02-JUL-2001; 2001WO-CN001127.
XX
PR    07-JUL-2000; 2000CN-00117050.

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XX	(BIOM-) BIONINDOW GENE DEV INC SHANGHAI.
PA	
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2002-339796/37.
XX	
PT	Human transcriptional control factor ZFMI isomer 25.63 and encoding
PT	polynucleotide, used in diagnosis and treatment of malignant tumors,
PT	hemopathy, human immunodeficiency virus infection, immunological diseases
XX	and inflammation.
XX	
PS	Example 5; Page 14; 38pp; Chinese.
XX	
CC	The invention relates to the human transcriptional control factor ZFMI
CC	isomer 25.63 and the polynucleotide encoding it. The sequences of the
CC	invention are used in diagnosis and treatment of malignant tumours,
CC	hemopathy, human immunodeficiency virus (HIV) infection, immunological
CC	diseases and various inflammations. This sequence represents the human
CC	transcriptional control factor ZFMI isomer 25.63 N-terminal peptide, used
CC	in ELISA
XX	
SO	Sequence 15 AA;
	Query Match 48.8%; Score 39.5; DB 5; Length 15;
	Best Local Similarity 75.0%; Pred. No. 29;
	Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1
OY	4 MPVLPEPPPPFV 15
DB	1 MPIL-VEKPPFV 11
	RESULT 14
ID	ADP14579
XX	ADP14579 standard; peptide; 17 AA.
AC	
XX	ADP14579;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Gluten-derived peptide - SEQ ID 74.
XX	
KX	plant; deamidation; tissue transglutaminase; CTG; celiac disease; CD;
KW	gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
KW	systemic lupus erythematosus; Sjogren syndrome; diabetes;
KW	immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW	dermatological; antiinflammatory.
OS	
XX	Unidentified.
XX	
XX	EP1332760-A1.
XX	
PD	06-AUG-2003.
XX	
XX	04-FEB-2002; 2002EP-00075456.
XX	
XX	04-FEB-2002; 2002EP-00075456.
XX	
PR	(ZIEK-) ACAD ZIEKENHUIS LEIDEN.
PA	
XX	WPI; 2003-647889/62.
DR	
XX	
PT	New gluten peptides or epitopes prone to deamidation by tissue
PT	transglutaminase, useful for treating celiac disease or an autoimmune
PT	disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
PT	erythematosus, or diabetes.
XX	
PS	Disclosure; SEQ ID NO 74; 143pp; English.
XX	
CC	The invention relates to a novel peptide or epitope which is prone to
CC	deamidation by tissue transglutaminase (TtG) and is a causative factor of
CC	celiac disease (CD, gluten intolerance) or an autoimmune disease such as
CC	

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
 CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates  
 CC immunosuppressive, antirheumatic, antidiabetic, antidiabetic,  
 CC dermatological and antiinflammatory activities whilst pharmaceutical  
 CC compositions comprising the peptides or epitopes may be useful for the  
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren  
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
 CC preparation of therapeutic agents capable of eliminating a subset of  
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
 CC The current sequence is that of the gluten-derived peptide of the  
 CC invention.

CC Sequence 17 AA;

Query Match 48.1%; Score 39; DB 7; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 39;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVLPEVPEPP 13  
 ||| :|||  
 Db 1 PVLPEVPEPP 9

RESULT 15  
 AAB72520  
 ID AAB72520 standard; peptide; 18 AA.

AC AAB72520;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #21.

KW Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

PI WPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostriin, its  
 PT constituent peptide, analog or their combinations.

PS Claim 6; Page 26; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostriin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12

Db 3 EMPPEKYVEPP 14  
 ::| |||||

RESULT 16

ID AAB59330 standard; peptide; 18 AA.

AC AAB59330;

DT 21-MAR-2001 (first entry)

DE Ewe colostriin peptide fragment C-5.

KW Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGB-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR WPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostriin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostriin. Colostriin is the proline-rich polypeptide  
 CC fragment of colostriin. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12  
 ::| |||||  
 Db 3 EMPPEKYVEPP 14

RESULT 17

ID AAB72267 standard; peptide; 18 AA.

AC AAB72267;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 22.

KW Colostriin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis, infection.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200111937-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US022818.  
 PF  
 XX  
 XX 17-AUG-1999; 99US-0149311P.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 PI WPI; 2001-202804/20.  
 DR  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 PS  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 CC  
 SQ Sequence 18 AA;  
 XX  
 XX Query Match 44.4%; Score 36; DB 4; Length 18;  
 XX Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 DLEMPVLPVEPF 12  
 XX : : | | | | |  
 Db 3 EMPFPKYPVEPF 14

RESULT 18  
 AAB72552  
 ID AAB72552 standard; peptide; 18 AA.  
 XX  
 XX AAB72552;  
 AC  
 XX  
 XX 09-MAY-2001 (first entry)  
 DT  
 XX  
 XX Colostrinin peptide #21.  
 DE  
 XX  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 KW  
 OS Unidentified.  
 XX  
 XX WO200112651-A2.  
 PN  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US022774.  
 PF  
 XX  
 XX 17-AUG-1999; 99US-0149633P.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA

XX  
 PI Boldogh I;  
 XX  
 XX WPI; 2001-226545/23.  
 DR  
 XX  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 PT  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 18 AA;  
 XX  
 XX Query Match 44.4%; Score 36; DB 4; Length 18;  
 XX Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 DLEMPVLPVEPF 12  
 XX : : | | | | |  
 Db 3 EMPFPKYPVEPF 14

RESULT 19  
 AA014598  
 ID AA014598 standard; peptide; 18 AA.  
 XX  
 XX AA014598;  
 AC  
 XX  
 XX 27-MAY-2002 (first entry)  
 DT  
 XX  
 XX Neural cell regulatory colostrinin peptide 21.  
 DE  
 XX  
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 KW  
 OS Unidentified.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note="Optional C-terminal amide"  
 XX  
 XX WO200213851-A1.  
 PN  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US022777.  
 PF  
 XX  
 XX 17-AUG-2000; 2000WO-US022777.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Boldogh I, Stanton GJ, Hughes TK;  
 PI  
 XX  
 XX WPI; 2002-269152/31.  
 DR  
 XX  
 XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 PT  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostroin peptide used in  
CC the method of the invention  
XX  
XX Sequence 18 AA;  
SQ

CC method for modulating blood cell proliferation in a patent. A claimed  
CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
CC active agent such as the present peptide. Cytokines induced by this  
CC peptide in human leucocyte cultures include interferon-gamma, tumour  
CC necrosis factor-alpha and interleukin-10

Query Match	44.4%	Score	36	DB	5	Length	18
Best Local Similarity	50.0%	Pred. NO.	1.2e+02				
Matches	6	Conservative	2	Mismatches	4	Indels	0
						Gaps	0

Query Match	44.4%	Score 36;	DB 5;	length 18;
SQ Sequence 18 AA;				

QY	1	DLEMPVLPEVEPF	12
	:	:	
Db	3	EMPFPPKYPVEVEPF	14

Db 3 EMPFPKYPVEPF 14

Db 3 EMPFPKYPEVEPF 14

RESULT 20
AAM51056
ID AAM51056 standard; peptide; 18 AA

XX	AAE20249
AC	ID AAE20249 standard; peptide; 18 AA
AA	...

XX	30-MAY-2002 (first entry)	XX
DT		AC
...		AAE20249;

XX	Colostrinin constituent peptide (casein amino acids 121-138).	XX	18-JUN-2002 (first entry)
DE		DT	

XX	Colostrinin; colostrum; immunomodulator; cardiovascular;
KM	Colostrinin; colostrum; immunomodulator; cardiovascular;
KM	blood cell regulator; cytokine inducer; beta-casein; human.
XX	Colostrinin constituent peptide #21.
XX	Colostrinin constituent peptide #21.

XX	KM	Blood cell re
OS	KM	therapy; oxid
Homo sapiens.		

XX	Location/Qualifiers	KW
FH Key		tissue; organ; cosmetic procedure; transplantation; implantation; derm

FT	Modified-site	18	XX
FT	/note= "optional C-terminal amidation"	05	Unidentified.

XX	XX
PN	WO200213849-A1.
XX	XX
FH	Key

XX	FT	Modified-site	18
PD	FT	/note="Optid	
21-FEB-2002.			

XX	17-AUG-2000; 2000WO-US022775.	XX	WO200213850
PF		PN	

XX	17-AUG-2000; 2000WO-US022775.	XX	21-FEB-2002.
PR		PD	
...		...	

XX	XX
PA (TEXA ) UNIV TEXAS SYSTEM,	PF 17-AUG-2000; 2000MO-US022776

PA (KEGE-) REGEN THERAPEUTICS PLC.	XX
XX	PR 17-AUG-2000; 2000MO-US022776

PI	stanton Gu, Hughes JK, Boldogh L, Georgiades J;	.XX
XX		PA (TEXA ) UNIV TEXAS SYSTEM.

DR	WPI; 2002-269150/31.	XX
XX		PI Stanton GJ, Hughes TK, Boldogh I;

PT	Modulation of bloodcell proliferation in a patient involves use of blood	XX
PT	cell regulator selected from colostrinin, its constituent peptide and/or	WPI; 2002-269151/31.
DR		

XX	Composition useful for the modulation
PT	
XX	
PT	analog.

XX  
PT constituent peptide selected from colostriin, lactoalbumin, or albumin.  
PT patient comprises a B100a cell regulator and/or analog.

PS Claim 1; Page 34; 54pp; English.

CC The present sequence is that of a colostrinin constituent peptide that is  
CC preferred for use as an immunological regulator and as a blood cell  
PS Claim 6; Page 26; 51pp; English

CC The invention relates to a composition which comprises a blood cell  
CC regulator in claimed methods of the invention. It is classified as having  
CC a beta-casein homologue precursor, and corresponds to casein amino acids  
XX

CC contact with an immunological regulator, where the cell is present  
CC 121-138. Methods are claimed for: inducing a cytokine in a cell by  
CC selected from co-stimatin, its constitutent peptide analogs and/or  
CC analogues. The invention is used for modulating the oxidative stress

cell culture, an organ or an organism, and the cell is in a cell culture, or for treating oxidative damage to the skin of a mammalian, including human, modulating an immune response in a cell by

[illegible]

CC administering an immunological regulator under conditions effective to  
CC inducing a cytokine, where the immunological regulator is administered  
CC to a patient, and the reduction or side effects  
CC associated with the method changes the level of an oxidizing  
CC cosmetic procedures. The method

CC damage to a biomolecule of the patient selected from DNA, protein  
CC in the cell, such as decreases or prevents increase in the level of  
CC topically or as part of a dietary supplement, and wherein the immune  
CC response is specific or non specific, an interferon response or an

CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results

CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal  
CC organs) are increased in number or differentiated; and a  
CC where the blood cells are increased in number or differentiated; and a  
CC present in a cell culture or an organism, are mammalian or human, and  
CC present in a cell culture or an organism, are mammalian or human, and  
CC CC

CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide

XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12  
 :: |||||  
 Db 3 EMPFPKYPVEPP 14

RESULT 22

ID ADN60316 standard; peptide; 18 AA.

XX ADN60316;

XX 29-JUL-2004 (first entry)

XX Constituent peptide of colostrinin SEQ ID NO:22.

XX modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
 KW DNA damage; beta-amyloid; retinoic acid; cytoskeletal; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.

XX Synthetic.

XX WO2004037851-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033423.

XX 22-OCT-2002; 2002US-0420369P.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (BOLD/) STANTON J G.

PA (GEOR/) GEORGIADIS J A.

PA (HUGH/) HUGHES T K.

PA (KRUIZ/) KRUIZEL M.

XX Bolodogh I, Stanton JG, Georgiades JA, Hughes TK, Krusel M,

PI WPI; 2004-365494/34.

XX Use of colostrinin for e.g. modulating an intracellular signaling

PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a

PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in

PT a cell.

XX Claim 6; SEQ ID NO 22; 46pp; English.

XX The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,

CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.

XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 8; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12  
 :: |||||  
 Db 3 EMPFPKYPVEPP 14

RESULT 23

ID AD574406 standard; peptide; 18 AA.

XX AD574406;

XX 16-DEC-2004 (first entry)

XX Ovine colostrinin peptide.

XX Colostrum; colostrinin; sheep; peptide purification.

XX Ovis aries.

XX WO2004081038-A1.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-GB001014.

XX 11-MAR-2003; 2003GB-00005552.

XX 08-MAR-2004; 2004GB-00005190.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA, Polanowski A, Wilusz T, Krusel ML,

XX WPI; 2004-67519/66.

XX Recovering peptides such as colostrinin from mammalian colostrum, by

PT mixing colostrum with alcohol to form alcohol phase containing peptides

PT and precipitate, separating alcohol phase from precipitate, and

PT recovering alcohol phase.

XX Disclosure; SEQ ID NO 23; 41pp; English.

XX The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrinin using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.

XX Sequence 18 AA;

Query Match 44.4%; Score 36; DB 8; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPEVPP 12  
 :: |||||  
 Db 3 EMPFKYVPEPP 14

RESULT 24  
 ADH14551  
 ID ADH14551 standard; peptide; 12 AA.  
 AC ADH14551;  
 DT 11-MAR-2004 (first entry)  
 DE Barley hordein related gliadin peptide SEQ ID NO:41.  
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 KM vaccine.  
 OS Synthetic.  
 XX  
 PN WO2003104273-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 05-JUN-2003; 2003WO-GB002450.  
 XX  
 PR 05-JUN-2002; 2002GB-00012885.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 PI Anderson RP, Hill AVS, Jewell DP;  
 XX  
 DR MPI; 2004-043640/04.  
 XX  
 PT Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T  
 PT cell receptor.  
 XX  
 PS Claim 1; SEQ ID NO 41; 177pp; English.  
 XX  
 CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.  
 CC  
 SQ Sequence 12 AA;

Query Match 43.2%; Score 35; DB 8; Length 12;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEVPP 13  
 | : | : |||  
 Db 1 PLOPOQPP 9

RESULT 25  
 ADH14849  
 ID ADH14849 standard; peptide; 12 AA.  
 AC ADH14849;  
 XX

DT 11-MAR-2004 (first entry)  
 XX  
 DE Gliadin related epitope peptide.  
 XX  
 KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 KM vaccine.  
 OS Synthetic.  
 XX  
 PN WO2003104273-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 05-JUN-2003; 2003WO-GB002450.  
 XX  
 PR 05-JUN-2002; 2002GB-00012885.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 PI Anderson RP, Hill AVS, Jewell DP;  
 XX  
 DR MPI; 2004-043640/04.  
 XX  
 PT Preventing or treating coeliac disease comprises administering agent  
 PT which are wheat gliadin T cell epitope capable of being recognized by T  
 PT cell receptor.  
 XX  
 PS Example 13; Page 96; 177pp; English.  
 XX  
 CC The present invention describes a method (M1) for preventing or treating  
 CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 CC be used in the preparation of a medicament for treating or preventing  
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 CC disease, in an individual, which involves determining whether T cells of  
 CC the individual recognise the agent, recognition by the T cells indicating  
 CC that the individual has, or is susceptible to, coeliac disease. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.  
 CC  
 SQ Sequence 12 AA;

Query Match 43.2%; Score 35; DB 8; Length 12;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEVPP 13  
 | : | : |||  
 Db 1 PLOPOQPP 9

RESULT 26  
 AAR93469  
 ID AAR93469 standard; peptide; 14 AA.  
 AC AAR93469;  
 DT 09-MAY-1996 (first entry)  
 DE GST-SRC protein tyrosine kinase derived peptide #3.  
 XX  
 KM SH3 ligand; SH3 binding agent; biased phage library;  
 KM recognition sequence; src SH3 domain; Paget's disease; restenosis;  
 KM rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;  
 KM p67; complex; chronic myelogenous leukaemia; cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9524419-A1.  
 XX



PD 14-SEP-1995.  
 XX  
 PF 13-MAR-1995; 95WO-US003208.  
 XX  
 PR 11-MAR-1994; 94US-00209835.  
 PR 06-JAN-1995; 95US-00369832.  
 XX  
 PA (ARIA-) ARIAD PHARM INC.  
 XX  
 PI Rickles RJ, Brugge JS, Bortfield MC, Zoller MJ;  
 DR WPI; 1995-328231/42.  
 XX  
 PT Identification of peptide(s) binding specifically to SH3 domains - for  
 PT use in inhibiting interactions mediated by SH3 domains in treatment of  
 PT e.g. osteoporosis and cancer.  
 XX  
 PS Disclosure; Fig 5; 74pp; English.  
 XX  
 CC The sequences given in AAR93457-71 represent peptides which are SH3  
 CC ligands/SH3 binding agents. They represent a biased phage library which  
 CC comprises five random amino acids flanking the decapeptide -RSRRPVPVP or  
 CC derivatives of this, which was identified as a recognition sequence for  
 CC the Src SH3 domain. These sequences were identified using the method of  
 CC the invention. The method comprises contacting the SH3 domain with a  
 CC mixture of peptides under conditions permitting a ligand to bind to an  
 CC SH3 domain to form a complex. Any unbound peptides are removed and the  
 CC complexed peptide ligands are dissociated from the complexes. The  
 CC selected peptides are enriched by re-contacting them with the SH3 domain  
 CC and then candidates which bind to the SH3 domain are detected. The  
 CC isolated SH3 binding peptides may be used in the diagnosis, prevention  
 CC and treatment of conditions or diseases resulting from cellular processes  
 CC mediated by an SH3-based interaction. Such diseases include Paget's  
 CC disease. Other conditions treatable with these peptides include  
 CC osteoporosis, rheumatoid arthritis, gout and other problems in which an SH3  
 CC of neutrophil oxidase p47 and p67 complex is implicated, etc  
 XX  
 SQ Sequence 14 AA;  
 Query Match 42.0%; Score 34; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 LEMPVPVPVP 13  
 Db 3 LPPPLPAPRP 14  
 XX  
 RESULT 27  
 AAB72507  
 ID AAB72507 standard; peptide; 15 AA.  
 XX  
 AC AAB72507;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostriin peptide #8.  
 XX  
 KW Dermatological; oxidative stress regulator; colostriin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 200WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;

XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostriin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostriin, or its constituent peptide (e.g. the present prepat),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 15 AA;  
 Query Match 42.0%; Score 34; DB 4; Length 15;  
 Best Local Similarity 70.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 PVLVPVPVP 14  
 Db 5 PVLKVPVPVP 14  
 XX  
 RESULT 28  
 AAB59313  
 ID AAB59313 standard; peptide; 15 AA.  
 XX  
 AC AAB59313;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostriin peptide fragment A-4.  
 XX  
 KW Sheep; colostriin; proline rich polypeptide; colostriin; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 200WO-GB002128.  
 XX  
 PR 02-JUN-1999; 99GB-00012852.  
 XX  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostriin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostriin. Colostriin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;  
 Best Local Similarity 70.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPPF 14  
 | | | | |  
 DB 5 PRLKVEVFPF 14

RESULT 29

AAB72253  
 ID AAB72253 standard; peptide; 15 AA.

AC AAB72253;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 8.

Colostriin: immune response; cytokine; blood cell proliferation;  
 central nervous system disorder; neurological disorder; mental disorder;  
 dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

(TEXA ) UNIV TEXAS SYSTEM.  
 (REGS-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

Inducing a cytokine and modulating an immune response, useful for  
 treating central nervous system diseases and bacterial and viral  
 infections, comprises administering colostriin as an immunological  
 regulator.

PS Claim 1; Page 34; 50pp; English.

Sequences AAB72246 - AAB72275 represent peptides derived from colostriin,  
 a proline rich polypeptide aggregate contained in colostrum. The peptides  
 have immune response modulatory activity, and are capable of inducing  
 cytokines. Colostriin and its derived peptides are useful for inducing  
 cytokine production, for modulating an immunological response and for  
 inducing blood cell proliferation. The peptides are useful in the  
 treatment of disorders of the central nervous system, neurological  
 disorders, mental disorders, dementia, neurodegenerative diseases,  
 Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 disorders of the immune system, bacterial and viral infections and  
 acquired immunological deficiencies

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;  
 Best Local Similarity 70.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPPF 14  
 | | | | |  
 DB 5 PRLKVEVFPF 14

RESULT 30

AAB72539  
 ID AAB72539 standard; peptide; 15 AA.

AC AAB72539;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #8.

Neuroprotective; neural cell differentiation regulator; colostriin;  
 colostrum.

OS Unidentified.

PN WO200112651-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022774.

PR 17-AUG-1999; 99US-0149633P.

(TEXA ) UNIV TEXAS SYSTEM.  
 PI Boldogh I;

XX WPI; 2001-226545/23.

Use of colostriin, its constituent peptide or analog as a neural cell  
 regulator, for promoting neural cell differentiation and treating damaged  
 neural cells in a patient.

PS Claim 6; Page 21; 35pp; English.

The present invention relates to a method for promoting neural cell  
 differentiation and treating damaged neural cells, using colostriin and  
 colostriin constituent peptides (e.g. the present peptide) as a neural  
 cell regulator. Colostriin is a polypeptide complex found in colostrum

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;  
 Best Local Similarity 70.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPPF 14  
 | | | | |  
 DB 5 PRLKVEVFPF 14

RESULT 31

AA014584  
 ID AA014584 standard; peptide; 15 AA.

AC AA014584;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostriin peptide 8:

Neural cell differentiation; neural cell regulator; colostriin peptide;  
 neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 neural cell treatment.

OS Unidentified.

FH Key Location/Qualifiers

Modified-site 15  
 /note="Optional C-terminal amide"

XX WO200213851-A1.  
 XX

PD 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022777.  
XX  
XX 17-AUG-2000; 2000WO-US022777.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX PA Boldogh I, Stanton JG, Hughes TK;  
XX PI  
XX DR WPI; 2002-269152/31.  
XX  
XX Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog.  
XX  
XX Claim 7, Page 21, 37pp; English.  
XX  
XX The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neutral cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention  
SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPPF 14  
| | | | |  
Db 5 PRLKVEVFPF 14

## RESULT 32

AAM51043  
ID AAM51043 standard; peptide; 15 AA.  
XX  
XX

AC AAM51043;  
XX

DT 30-MAY-2002 (first entry)  
XX

DE Colostrinin constituent peptide.  
XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
XX blood cell regulator; cytokine inducer; human.  
XX

OS Homo sapiens.  
XX

FT Key Location/Qualifiers  
XX Modified-site 15  
XX /note="optional C-terminal amidation"

PN WO200213849-A1.  
XX

PD 21-FEB-2002.  
XX

PF 17-AUG-2000; 2000WO-US022775.  
XX

PR 17-AUG-2000; 2000WO-US022775.  
XX

PA (TEXA ) UNIV TEXAS SYSTEM.  
XX (REGG-) REGEN THERAPEUTICS PLC.  
XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
XX WPI; 2002-269150/31.  
XX

PT Modulation of blood cell proliferation in a patient involves use of blood  
PT cell regulator selected from colostrinin, its constituent peptide and/or  
PT analog.  
XX  
XX Claim 1, Page 34, 54pp; English.  
XX

XX The present sequence is that of a colostrinin constituent peptide that is  
CC preferred for use as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. Methods are claimed for:  
CC inducing a cytokine in a cell by contact with an immunological regulator,  
CC where the cell is present in a cell culture, a tissue, an organ or an  
CC organism, and the cell is mammalian, including human; modulating an  
CC immune response in a cell by contact with the immunological regulator  
CC under conditions effective to induce a cytokine; modulating an immune  
CC response in a patient by administering an immunological regulator under  
CC conditions effective to induce a cytokine, where the immunological  
CC regulator is administered topically or as part of a dietary supplement,  
CC and where the immune response is specific or non specific, an interferon  
CC response or an antibody response; modulating blood cell proliferation by  
CC contacting blood cells with a blood cell regulator, where the blood cells  
CC are present in a cell culture or an organism, are mammalian or human, and  
CC where the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patient. A claimed  
CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
CC active agent such as the present peptide. Cytokines induced by this  
CC peptide in human leucocyte cultures include interferon-gamma, tumour  
CC necrosis factor-alpha, interleukin-6 and interleukin-10  
XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPPF 14  
| | | | |  
Db 5 PRLKVEVFPF 14

## RESULT 33

AAE20235  
ID AAE20235 standard; peptide; 15 AA.  
XX  
XX

AC AAE20235;  
XX

DT 18-JUN-2002 (first entry)  
XX

DE Colostrinin constituent peptide #8.  
XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX transplantation; implantation; dermatological; vulnery.  
XX

OS Unidentified.  
XX

FT Key Location/Qualifiers  
XX Modified-site 15  
XX /note="Optionally C-terminal amide"

PN WO200213850-A1.  
XX

PD 21-FEB-2002.  
XX

PF 17-AUG-2000; 2000WO-US022776.  
XX

PR 17-AUG-2000; 2000WO-US022776.  
XX

PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX

PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
XX WPI; 2002-269151/31.  
XX

XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog.  
PS Claim 6; Page 25; 51pp; English.  
XX  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress level  
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
CC organ, or organism; or for treating oxidative damage to the skin of a  
CC patient e.g. animal or human; to modulate oxidative stress during/ after  
CC a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide  
SQ Sequence 15 AA;  
Query Match 42.0%; Score 34; DB 5; Length 15;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 5 PVLVPEPPF 14  
| | | | |  
Db 5 PVLVPEPPF 14  
RESULT 34  
ABB09569  
ID ABB09569 strand; peptide; 15 AA.  
XX  
XX ABB09569;  
AC  
XX  
XX 06-SEP-2002 (first entry)  
DT  
XX  
XX Human L1 factor ORF2 associated protein 10.45 N-terminal peptide.  
DE  
XX  
XX Human; L1 factor ORF2 associated protein 10.45; open reading frame;  
KW L1 element ORF2-like protein homologue; recombinant production; tumour;  
KW cancer; protein metabolism disorder; cytostatic; gene therapy;  
KW N-terminal peptide; enzyme linked immunosorbent assay; ELISA.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1338469-A.  
PN  
XX  
XX 06-MAR-2002.  
PD  
XX  
XX 21-AUG-2000; 2000CN-00119641.  
PF  
XX  
XX 21-AUG-2000; 2000CN-00119641.  
PR  
XX  
XX 21-AUG-2000; 2000CN-00119641.  
PA  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX WPI; 2002-384269/42.  
DR  
XX  
XX New polypeptide-human L1 factor ORF2 associated protein 10.45 for  
PT treating diseases such as a tumor, or a protein metabolism disorder.  
PT  
XX  
XX Example 6; Page 21 (Disclosure); 33pp; Chinese.  
XX

CC The invention relates to human L1 factor ORF2 associated protein 10.45  
CC (ABB09568) and nucleic acids encoding it (AB155410). The protein has a  
CC molecular weight of 10.45 kD and has 65% identity and 77% homology over a  
CC 95 amino acid stretch with a human L1 element ORF2-like protein given in  
CC Genbank accession number AF003535. The invention also relates to a method  
CC for the recombinant production of the protein, an antagonist of the  
CC protein, and the use of the protein, gene and antagonist in therapeutic  
CC applications. L1 factor ORF2 associated protein 10.45 can be used in the  
CC treatment of a variety of diseases such as tumours and disorders of  
CC protein metabolism. The present sequence represents the 15 N-terminal  
CC amino acids of human L1 factor ORF2 associated protein 10.45 used in  
CC ELISA (enzyme linked immunosorbent assay) in an exemplification of the  
CC invention  
SQ Sequence 15 AA;  
Query Match 42.0%; Score 34; DB 5; Length 15;  
Best Local Similarity 45.5%; Pred. No. 2e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
OY 2 LEMPVLPVPPF 12  
| | | | |  
Db 5 LEMPVLPVPPF 12  
RESULT 35  
ADN60302  
ID ADN60302 strand; peptide; 15 AA.  
XX  
XX ADN60302;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Constituent peptide of colostrinin SEQ ID NO:8.  
DE  
XX  
XX modulator; colostrinin; intracellular signaling molecule modulator;  
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
KW DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor;  
KW 4HNE-protein adduct formation reduction;  
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
KW c-Jun NH2-terminal kinase inhibition.  
XX  
XX Synthetic.  
OS  
XX  
XX WO2004037851-A2.  
PN  
XX  
XX 06-MAY-2004.  
PD  
XX  
XX 22-OCT-2003; 2003WO-US033423.  
PF  
XX  
XX 22-OCT-2002; 2002US-0420369P.  
PR  
XX  
XX (TEXA ) UNTV TEXAS SYSTEM.  
PA (BOLD/) BOLDGCH I.  
PA (STAN/) STANTON J G.  
PA (GEOR/) GEORGIADES J A.  
PA (HUGH/) HUGHES T K.  
PA (KRUZ/) KRUZEL M.  
XX  
XX Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruznel M;  
PI  
XX  
XX WPI; 2004-365494/34.  
DR  
XX  
XX Use of colostrinin for e.g. modulating an intracellular signaling  
PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
PT a cell.  
PT  
XX  
XX Claim 6; SEQ ID NO 8; 46pp; English.  
PS  
XX  
XX The present invention describes the use of a modulator selected from  
CC colostrinin, its constituent peptide, its active analogue, and a  
CC combination of these, for modulating an intracellular signaling molecule  
CC

CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytoprotective activity and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostriin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostriin, which can be used as a modulator in the present invention.  
 CC  
 XX  
 XX  
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 8; Length 15;  
 Best Local Similarity 70.0%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPE 14  
 | | | | |  
 Db 5 PVLKVEVPFP 14

## RESULT 36

ADRI31999  
 ID ADRI31999 standard; peptide; 15 AA.

AC ADRI31999;

DT 02-DEC-2004 (first entry)

DE Heat shock protein 20-derived peptide SEQ ID NO:313;

XX heat shock protein 20; HSP20; scar; wound healing; vulnery;

KM gene therapy.

XX Synthetic.

FN WO2004075914-A1.

PD 10-SBP-2004.

PF 20-FEB-2004; 2004WO-US004999.

PR 21-FEB-2003; 2003US-0448954P.

PR 17-OCT-2003; 2003US-0512211P.

PR 16-DEC-2003; 2003US-0530306P.

XX (UNVAR-) UNIV ARIZONA STATE.

PI Brophy C, Panitch A, Parmiter C, Furnish E, Komalavilas P,

DR WPI; 2004-653328/63.

XX Reducing scar formation and/or promoting wound healing comprises

PT administering to an individual an amount of heat shock protein 20-derived

PT polypeptides.

XX Disclosure; SEQ ID NO 313; 113pp; English.

CC The invention relates to a novel method for reducing scar formation or  
 CC promoting wound healing, comprising administering to an individual an  
 CC amount to reduce scar formation or promote wound healing of a polypeptide  
 CC comprising a sequence of formula X1-A(X2)APLP-X3. Within the formula X1 =  
 CC 0-14 amino acids of the sequence of heat shock protein 20 (HSP20) between  
 CC residues 1 and 14 of a sequence having 160 amino acids fully defined in  
 CC the specification (ADRI31985); X2 = Ser, Thr, Tyr, Asp, Glu,  
 CC hydroxylysine, hydroxyproline, phosphoserine analogues and  
 CC phosphotyrosine analogues; and X3 = 0-140 amino acids of hsp20 between  
 CC residues 21 and 160 of ADRI31985; or 0, 1, 2 or 3 amino acids of a  
 CC sequence of genus Z1-Z2-Z3, where Z1 is Gly or Asp, Z2 is Leu or Lys, and

CC '23 is Ser, Thr or Lys. A polypeptide of the invention has vulnery  
 CC activity, and may have a use in gene therapy. The method is useful for  
 CC reducing initial scar formation and/or for promoting wound healing. The  
 CC present sequence represents a HSP20-derived peptide of the invention.  
 CC  
 XX  
 XX  
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 8; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEMPVLPVP 11  
 : | : | : | : |  
 Db 1 MEIPVPVMP 10

## RESULT 37

ADST74389  
 ID ADST74389 standard; peptide; 15 AA.

AC ADST74389;

DT 16-DEC-2004 (first entry)

DE Ovine colostriin peptide.

XX Colostrium; colostriin; sheep; peptide purification.

OS Ovis aries.

PN WO2004081038-A1.

PD 23-SEP-2004.

PF 10-MAR-2004; 2004WO-GB001014.

PR 11-MAR-2003; 2003GB-00005552.

PR 08-MAR-2004; 2004GB-00005190.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Georgiades JA, Polanowski A, Wilusz T, Kruszal ML;

DR WPI; 2004-677519/66.

XX Recovering peptides such as colostriin from mammalian colostrium, by

PT mixing colostrium with alcohol to form alcohol phase containing peptides

PT and precipitate, separating alcohol phase from precipitate, and

PT recovering alcohol phase.

XX Disclosure; SEQ ID NO 4; 41pp; English.

CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostriin using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostriin)  
 CC from colostrium in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrium with an alcohol to  
 CC form an alcohol phase containing the colostriin and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostriin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostriin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostriin-rich phase  
 CC to induce precipitation of the colostriin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.  
 XX  
 XX  
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 8; Length 15;



PR 12-APR-2001; 2001EP-00201377.  
 PR 16-NOV-2001; 2001EP-00204383.

XX  
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX PI Drijfhout JW, Koning P, Mcadam SN, Sollid LM;  
 XX DR WPI; 2003-093000/08.

XX  
 PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-  
 PT cell receptor for treating food-related immune enteropathy, such as celiac  
 PT sprue, tropical sprue, giardiasis and food allergies of childhood.

PS Disclosure; Fig 2; 64pp; English.

XX  
 CC The present invention relates to novel isolated or recombinant human  
 CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional  
 CC equivalent and/or fragment, capable of recognising a prolamine-derived  
 CC peptide. The invention relates to recombinant or synthetic prolamine  
 CC derived peptides involved in food-related immune enteropathy. The  
 CC pharmaceutical composition is useful to treat food-related immune  
 CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food  
 CC allergies of childhood. It is useful to induce tolerance, treat gluten-  
 CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the  
 CC invention are useful to decrease the amount of toxic prolamine-derived  
 CC peptides in food or food components and to select and/or breed a cereal.  
 CC The cereal is useful for inclusion in a diet for a gluten sensitive  
 CC individual. Blocking substances are useful to decrease the binding of HLA  
 CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in  
 CC food-related immune enteropathy for depletion of T-cells bearing the HLA-  
 CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory  
 CC gluten peptide. This sequence is used in the invention

XX  
 SQ Sequence 18 AA:

Query Match 42.0%; Score 34; DB 6; Length 18;  
 Best Local Similarity 45.5%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPVPEFP 13  
 : | : : | | |  
 DB 4 QQPYLQLQPPF 14

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OM protein - protein search, using sw model

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Title: US-10-691-157-5  
Perfect score: 81  
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Searched: 513545 seqs, 74649064 residues

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Maximum DB seq length: 18

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Maximum Match 100%  
Listing first 100 summaries

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- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	4	US-09-641-803-5
2	36	44.4	18	4	US-09-641-803-22
3	34	42.0	15	4	US-09-641-803-8
4	32	39.5	15	4	US-09-009-953-97
5	32	39.5	15	4	US-09-009-953-111
6	32	39.5	16	1	US-07-702-771-5
7	32	39.5	16	1	US-08-438-883-5
8	32	39.5	16	1	US-08-741-599-5
9	31	38.3	8	1	US-08-360-239B-2
10	31	38.3	12	4	US-09-914-259-179
11	30	37.0	15	2	US-08-687-956A-8
12	30	37.0	15	3	US-08-743-168B-15
13	30	37.0	15	3	US-09-807-278-5
14	30	37.0	15	5	PCT-US96-10435-15
15	30	37.0	16	5	US-08-602-999A-451
16	30	37.0	16	4	US-09-500-124-451
17	29	35.8	13	1	US-08-205-938A-21
18	29	35.8	13	5	PCT-US95-02626-21
19	29	35.8	14	3	US-08-630-916A-56
20	29	35.8	15	2	US-08-687-956A-7
21	29	35.8	16	3	US-08-602-999A-202
22	29	35.8	16	3	US-08-602-999A-406
23	29	35.8	16	4	US-09-500-124-202
24	29	35.8	16	4	US-09-500-124-406
25	29	35.8	17	3	US-08-987-743-11
26	29	35.8	18	1	US-08-205-938A-22
27	29	35.8	18	5	PCT-US95-02626-22

28	34.6	10	4	US-09-239-043D-2314	Sequence 2314, Ap
29	34.6	15	3	US-08-684-187-1	Sequence 1, Appl
30	34.6	15	4	US-09-009-953-120	Sequence 120, App
31	34.6	16	2	US-08-844-312-9	Sequence 9, Appl
32	34.6	17	3	US-08-602-999A-360	Sequence 360, App
33	34.6	17	4	US-09-500-124-360	Sequence 360, App
34	34.6	18	3	US-08-630-916A-103	Sequence 103, App
35	34.6	18	3	US-08-602-999A-317	Sequence 317, App
36	34.6	18	3	US-08-630-916A-159	Sequence 159, App
37	34.6	18	4	US-09-500-124-317	Sequence 317, App
38	34.6	18	4	US-09-879-957-159	Sequence 159, App
39	33.3	6	2	US-08-672-805-6	Sequence 6, Appl
40	33.3	8	3	US-08-828-712-12	Sequence 12, Appl
41	33.3	8	3	US-08-993-165-25	Sequence 25, Appl
42	33.3	8	3	US-08-993-165-30	Sequence 30, Appl
43	33.3	8	3	US-08-993-165-30	Sequence 30, Appl
44	33.3	8	3	US-09-063-276-12	Sequence 12, Appl
45	33.3	8	4	US-09-540-448-25	Sequence 25, Appl
46	33.3	8	4	US-09-540-448-28	Sequence 28, Appl
47	33.3	8	4	US-09-496-761-1	Sequence 1, Appl
48	33.3	8	4	US-09-496-761-6	Sequence 6, Appl
49	33.3	8	4	US-09-324-782-12	Sequence 12, Appl
50	33.3	8	4	US-09-668-143-12	Sequence 12, Appl
51	33.3	8	4	US-09-668-143-12	Sequence 12, Appl
52	33.3	8	4	US-08-913-612A-46	Sequence 46, Appl
53	33.3	8	4	US-08-929-847-26	Sequence 26, Appl
54	33.3	8	4	US-08-929-847-29	Sequence 29, Appl
55	33.3	8	4	US-09-813-484-26	Sequence 26, Appl
56	33.3	8	4	US-09-813-484-29	Sequence 29, Appl
57	33.3	8	4	US-10-046-801-25	Sequence 25, Appl
58	33.3	8	4	US-10-046-801-28	Sequence 28, Appl
59	33.3	8	4	US-10-266-463A-46	Sequence 46, Appl
60	33.3	9	3	US-08-828-712-13	Sequence 13, Appl
61	33.3	9	3	US-08-828-712-14	Sequence 14, Appl
62	33.3	9	3	US-09-063-276-13	Sequence 13, Appl
63	33.3	9	3	US-09-063-276-13	Sequence 13, Appl
64	33.3	9	4	US-09-324-782-13	Sequence 13, Appl
65	33.3	9	4	US-09-324-782-14	Sequence 14, Appl
66	33.3	9	4	US-09-668-143-13	Sequence 13, Appl
67	33.3	9	4	US-09-668-143-14	Sequence 14, Appl
68	33.3	9	4	US-08-913-612A-47	Sequence 47, Appl
69	33.3	9	4	US-10-266-463A-47	Sequence 47, Appl
70	33.3	10	1	US-08-214-650-40	Sequence 40, Appl
71	33.3	10	4	US-09-051-380-16	Sequence 16, Appl
72	33.3	10	4	US-09-239-043D-2313	Sequence 2313, Ap
73	33.3	14	3	US-09-208-966-11	Sequence 11, Appl
74	33.3	14	4	US-09-775-052A-11	Sequence 11, Appl
75	33.3	14	6	5164482-18	Patent No. 5164482
76	33.3	15	1	US-08-230-047-27	Sequence 27, Appl
77	33.3	15	3	US-08-602-999A-467	Sequence 467, App
78	33.3	15	4	US-09-500-124-467	Sequence 467, App
79	33.3	15	4	US-09-500-124-467	Sequence 467, App
80	33.3	15	4	US-09-647-372B-74	Sequence 74, Appl
81	33.3	16	2	US-08-844-312-10	Sequence 10, Appl
82	33.3	16	3	US-08-602-999A-200	Sequence 200, App
83	33.3	16	3	US-08-602-999A-220	Sequence 220, App
84	33.3	16	4	US-09-500-124-200	Sequence 200, App
85	33.3	16	4	US-09-500-124-220	Sequence 220, App
86	33.3	17	4	US-08-469-260A-251	Sequence 251, App
87	33.3	17	4	US-08-488-446-251	Sequence 251, App
88	33.3	17	4	US-08-467-344A-251	Sequence 251, App
89	33.3	17	4	US-08-428-088B-272	Sequence 272, App
90	33.3	17	4	US-08-424-550B-251	Sequence 251, App
91	33.3	18	2	US-08-374-655C-30	Sequence 30, Appl
92	33.3	18	2	US-08-179-984-3	Sequence 3, Appl
93	33.3	15	4	US-09-205-256-379	Sequence 379, App
94	32.1	6	2	US-08-540-118-5	Sequence 5, Appl
95	32.1	6	2	US-08-747-117-167	Sequence 167, App
96	32.1	6	4	US-09-185-818-5	Sequence 5, Appl
97	32.1	7	3	US-09-365-581A-2	Sequence 2, Appl
98	32.1	7	4	US-09-626-821A-2	Sequence 2, Appl
99	32.1	8	1	US-08-360-239B-1	Sequence 1, Appl
100	32.1	8	3	US-08-993-165-34	Sequence 34, Appl

## ALIGNMENTS

## RESULT 1

US-09-641-803-5  
; Sequence 5, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-5

## Query Match

Best Local Similarity 100.0%; Score 81; DB 4; Length 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPYLPVEPPFV 15  
| | | | | | | | | | | | | | | | |

DB 1 DLEMPYLPVEPPFV 15

## RESULT 2

US-09-641-803-22  
; Sequence 22, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-22

## Query Match

Best Local Similarity 44.4%; Score 36; DB 4; Length 18;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPYLPVEPPF 12  
: : | | | | |

DB 3 EMPFPCYVPEPPF 14

## RESULT 3

US-09-641-803-8  
; Sequence 8, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-8

## Query Match

Best Local Similarity 42.0%; Score 34; DB 4; Length 15;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLXVPEPPF 14  
| | | | |

DB 5 PVLXVPEPPF 14

## RESULT 4

US-09-009-953-97  
; Sequence 97, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; REACTIVE DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-JAN-1997  
; APPLICATION NUMBER: US 60/037,432  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 97:  
US-09-009-953-97

Query Match 39.5%; Score 32; DB 4; Length 15;  
Best Local Similarity 41.7%; Pred. No. 95;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVLPEVPP 13  
DB 2 LNFPIPIETVP 13

RESULT 5  
US-09-009-953-111  
Sequence 111, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
REACTIVE DR RESTRICTED EPITOPES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
TELEFAX: 415-576-0300  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-09-009-953-111

Query Match 39.5%; Score 32; DB 4; Length 15;  
Best Local Similarity 41.7%; Pred. No. 95;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVLPEVPP 13  
DB 4 LNFPIPIETVP 15

RESULT 6  
US-07-702-771-5  
Sequence 5, Application US/07702771  
Patent No. 5610276  
GENERAL INFORMATION:  
APPLICANT: Wong, Gail L.  
APPLICANT: McCormick, Frank  
TITLE OF INVENTION: Cloning and Purification of p62  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cetus Corporation  
STREET: 1400 Fifty-Third Street  
CITY: Emeryville  
STATE: California  
ZIP: 94608-2997  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/702,771  
FILING DATE: 17-MAY-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Giotta, Gregory J.  
REGISTRATION NUMBER: 32,028  
REFERENCE/DOCKET NUMBER: 2594  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-420-3300  
TELEFAX: 415-658-5239  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-07-702-771-5

Query Match 39.5%; Score 32; DB 1; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 EMPVLPEVPP 13  
DB 4 EMVLIPVQYP 14

RESULT 7  
US-08-438-883-5  
Sequence 5, Application US/08438883  
Patent No. 5731427  
GENERAL INFORMATION:  
APPLICANT: Wong, G.  
APPLICANT: McCormick, F.  
TITLE OF INVENTION: Purification and Cloning of p62  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America

ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,883  
FILING DATE: 10-MAY-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/702,771  
FILING DATE: 17-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pochopien, Donald J.  
REGISTRATION NUMBER: 32,167  
REFERENCE/DOCKET NUMBER: 27527/33275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: Mus musculus  
US-08-438-883-5

Query Match 39.5%; Score 32; DB 1; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPEPFP 13  
Db 4 EMVLIPVKQYP 14

RESULT 8  
US-08-741-599-5  
Sequence 5, Application US/08741599  
Patent No. 5773237  
GENERAL INFORMATION:  
APPLICANT: Wong, G.  
TITLE OF INVENTION: Purification and Cloning of p62  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,599  
FILING DATE: 01-NOV-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/702,771  
FILING DATE: 17-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pochopien, Donald J.  
REGISTRATION NUMBER: 32,167  
REFERENCE/DOCKET NUMBER: 0892.003/33583  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: Mus musculus  
US-08-741-599-5

Query Match 39.5%; Score 32; DB 1; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1e+02;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPEPFP 13  
Db 4 EMVLIPVKQYP 14

RESULT 9  
US-08-360-239B-2  
Sequence 2, Application US/08360239B  
Patent No. 5801222  
GENERAL INFORMATION:  
APPLICANT: Pettit, George R.  
TITLE OF INVENTION: Isolation and Structure of  
TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Richard R. Mybeck  
STREET: 8010 East Morgan Trail, #10  
CITY: Scottsdale  
STATE: Arizona  
COUNTRY: USA  
ZIP: 85258-1234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: DOS 5  
SOFTWARE: Microsoft Word for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,239B  
FILING DATE: 12/20/94  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard R. Mybeck  
REGISTRATION NUMBER: 17,886  
REFERENCE/DOCKET NUMBER: 4997  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (602)-483-1285  
TELEFAX: (602)-483-7452  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acid residues  
TYPE: amino acid  
TOPOLOGY: cyclic  
MOLECULE TYPE:  
DESCRIPTION: Cyclooctapeptide  
DESCRIPTION: phakellistatin 11  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE: circular  
ORIGINAL SOURCE:  
ORGANISM: Phakellia sp.  
DEVELOPMENTAL STAGE: whole organism  
FEATURE:

NAME/KEY: phakellistatin 11  
NAME/KEY: amino acid analysis, high resolution  
NAME/KEY: nuclear magnetic resonance and mass  
NAME/KEY: spectral MS/MS techniques  
OTHER INFORMATION: Phakellistatin is a  
OTHER INFORMATION: cell growth inhibitory peptide with  
OTHER INFORMATION: activity in murine lymphocytic leukemia  
OTHER INFORMATION: cell line of 0.20 mg/ml.  
US-08-360-239B-2

Query Match 38.3%; Score 31; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 BPPPV 15  
DB 2 QPPPV 7

RESULT 10  
US-09-914-259-179  
Sequence 179, Application US/09914259  
Patent No. 6495336  
GENERAL INFORMATION:  
APPLICANT: Makowski, Lee  
APPLICANT: Hyman, Paul  
APPLICANT: Williams, Mark  
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
FILE REFERENCE: 8471-010-999  
CURRENT APPLICATION NUMBER: US/09/914,259  
CURRENT FILING DATE: 2000-11-21  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 179  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Identified from M13 bacteriophage peptide display library.  
US-09-914-259-179

Query Match 38.3%; Score 31; DB 4; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPP 13  
DB 5 LPVTPP 11

RESULT 11  
US-08-687-956A-8  
Sequence 8, Application US/08687956A  
Patent No. 5861157  
GENERAL INFORMATION:  
APPLICANT: BURNIE, JAMES P  
APPLICANT: MATHERS, RUTH C  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PILLSBURY, MADISON & SUTRO, LLP  
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH  
FLOOR  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,956A  
FILING DATE: 29-JUL-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9401689.6  
FILING DATE: 28-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 50885/222892  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/861-3000  
TELEFAX: 202/822-0944  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus sobrinus  
STRAIN: Streptococcus sobrinus MUCOB 263  
US-08-687-956A-8

Query Match 37.0%; Score 30; DB 2; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVPP 11  
DB 4 DONIDKPPV 14

RESULT 12  
US-08-743-168B-15  
Sequence 15, Application US/08743168B  
Patent No. 6271015  
GENERAL INFORMATION:  
APPLICANT: Glitula, No. 6271015ton B  
APPLICANT: Cravatt, Benjamin F  
APPLICANT: Ierner, Richard A  
TITLE OF INVENTION: PATTY-ACID AMIDE HYDROLASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: The Scripps Research Institute  
STREET: 10550 No. 6271015th Torrey Pines Road  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/743,168B  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/489,535  
FILING DATE: 12-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 485.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-743-168B-15

Query Match 37.0%; Score 30; DB 3; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLVPEPPF 14  
|:|:|:|:  
DB 5 PTVP--PPPF 12

RESULT 13  
US-09-807-278-5  
Sequence 5, Application US/09807278  
Patent No. 6753310  
GENERAL INFORMATION:  
APPLICANT: Otsuka Pharmaceutical Co., Ltd.  
TITLE OF INVENTION: NEOVASCULAR-SPECIFIC PEPTIDES  
FILE REFERENCE: Q64027  
CURRENT APPLICATION NUMBER: US/09/807,278  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: JP 1998-295198  
PRIOR FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patent version 3.0  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: phage library  
US-09-807-278-5

Query Match 37.0%; Score 30; DB 4; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEPPF 13  
|:|:|:|:  
DB 5 PALPVLPF 13

RESULT 14  
PCT-US96-10435-15  
Sequence 15, Application PC/TUS9610435  
GENERAL INFORMATION:  
APPLICANT: The Scripps Research Institute  
TITLE OF INVENTION: CIS-9, 10-OTRIDECEMOMITASE  
NUMBER OF SEQUENCES: 32  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10435  
FILING DATE: 12-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/489,535  
FILING DATE: 12-JUN-1995  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal

PCT-US96-10435-15

Query Match 37.0%; Score 30; DB 5; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLVPEPPF 14  
|:|:|:|:  
DB 5 PTVP--PPPF 12

RESULT 15  
US-08-602-999A-451  
Sequence 451, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOLKES, Dana M.  
APPLICANT: RIDER, James B.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 451:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-451

Query Match 37.0%; Score 30; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVPEPP 11  
|:|:|:|:  
DB 6 PLPPIKP 12

RESULT 16  
US-09-500-124-451  
Sequence 451, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.

```

/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: OUILIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/500,124
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mastrock, S. Leslie
/ REGISTRATION NUMBER: 18, 872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 451:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/
/ US-09-500-124-451
/
Query Match 37.0%; Score 30; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVPEPP 11
DB 6 PLLPKIP 12

RESULT 17
US-08-205-938A-21
/ Sequence 21, Application US/08205938A
/ Patent No. 5466671
/ GENERAL INFORMATION:
/ APPLICANT: TEMPEST, PAUL
/ APPLICANT: CASTELS, PETER
/ TITLE OF INVENTION: APIADACIN-TYPE PEPTIDE ANTIBIOTICS WITH
/ TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
/ TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: COOPER & DUNHAM LLP
/ STREET: 1185 AVENUE OF THE AMERICAS
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/
```

```

/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/205,938A
/ FILING DATE: 02-MAR-1994
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WHITE, JOHN P
/ REGISTRATION NUMBER: 28, 678
/ REFERENCE/DOCKET NUMBER: 45061
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
/ US-08-205-938A-21
/
Query Match 35.8%; Score 29; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 2.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLVPEPP 13
DB 1 QVPIRPSQPP 11

RESULT 18
PCT-US95-02626-21
/ Sequence 21, Application PC/TUS9502626
/ GENERAL INFORMATION:
/ APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
/ APPLICANT: TEMPEST, PAUL
/ APPLICANT: CASTELS, PETER
/ TITLE OF INVENTION: APIADACIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED
/ TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIBACTERIAL SPECTRUM
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: COOPER & DUNHAM LLP
/ STREET: 1185 AVENUE OF THE AMERICAS
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/02626
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/205,938
/ FILING DATE: 02-MAR-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WHITE, JOHN P
/ REGISTRATION NUMBER: 28, 678
/ REFERENCE/DOCKET NUMBER: 45061-A-PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/
```

MOLECULE TYPE: peptide  
PCT-US95-02626-21

Query Match 35.8%; Score 29; DB 5; Length 13;  
Best Local Similarity 36.4%; Pred. No. 2.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPEVPEP 13  
DB 1 QVPIRPSQRP 11

## RESULT 19

US-08-630-916A-56  
Sequence 56, Application US/08630916A  
Patent No. 6011137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
TITLE OF INVENTION: POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ. ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-56

Query Match 35.8%; Score 29; DB 3; Length 14;  
Best Local Similarity 45.5%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 EMPVLPEVPEP 13  
DB 1 EYPPYPPPPYP 11

## RESULT 20

US-08-687-956A-7  
Sequence 7, Application US/08687956A  
Patent No. 5861157  
GENERAL INFORMATION:  
APPLICANT: BURKE, JAMES P  
APPLICANT: MATTHEWS, RUTH C  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI

NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PILLSBURY, MADISON & SUTRO, LLP  
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH  
STREET: FLOOR  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,956A  
FILING DATE: 29-JUL-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9401689.6  
FILING DATE: 28-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 50885/222892  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/861-3000  
TELEFAX: 202/822-0944  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORGANISM: Streptococcus sobrinus  
STRAIN: Streptococcus sobrinus MUCCB 263  
US-08-687-956A-7

Query Match 35.8%; Score 29; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EMPVLPEVPEP 11  
DB 6 ELVDLPVEP 14

## RESULT 21

US-08-602-999A-202  
Sequence 202, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711



COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 202:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-202

Query Match 35.8%; Score 29; DB 3; Length 16;  
Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLEMPVLP 8  
| | | | |  
Db 3 DERPVLVP 10

RESULT 22  
US-08-602-999A-406  
Sequence 406, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: OUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-406

Query Match 35.8%; Score 29; DB 3; Length 16;  
Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMPVLP 8  
| | | | |  
Db 4 LKLPVLP 10

RESULT 23  
US-09-500-124-202  
Sequence 202, Application US/09500124  
Patent No. 643920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: OUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 202:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-202

Query Match 35.8%; Score 29; DB 4; Length 16;  
Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLEMPVLP 8  
| | | | |

Db 3 DERPVLP 10

RESULT 24

US-09-500-124-406  
Sequence 406, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILTER, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION/DOCKET NUMBER: 18,872  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-406

Query Match 35.8%; Score 29; DB 4; Length 16;  
Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMPVLP 8  
Db 4 LKLPVLP 10

RESULT 25

US-08-987-743-11  
Sequence 11, Application US/08987743  
Patent No. 6123938

GENERAL INFORMATION:  
APPLICANT: Stern, Robert  
APPLICANT: Csoka, Anthony  
APPLICANT: Frost, Gregory I.  
APPLICANT: Wong, Tim M.  
TITLE OF INVENTION: Purification and Microsequencing of  
TITLE OF INVENTION: Hyaluronidase Isozymes

FILE REFERENCE: 9076/088CIP2  
CURRENT APPLICATION NUMBER: US/08/987,743  
CURRENT FILING DATE: 1997-12-09  
EARLIER APPLICATION NUMBER: 08/733,360  
EARLIER FILING DATE: 1996-10-17  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 17  
TYPE: PRT  
ORGANISM: H. sapiens  
US-08-987-743-11

Query Match 35.8%; Score 29; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVLPEPPPPV 15  
Db 4 PLLPNXPPTTV 14

RESULT 26

US-08-205-938A-22  
Sequence 22, Application US/08205938A  
Patent No. 5466671

GENERAL INFORMATION:  
APPLICANT: TEMPEST, PAUL  
APPLICANT: CASTELLS, PETER  
TITLE OF INVENTION: APIDACIN-TYPE PEPTIDE ANTIBIOTICS WITH  
TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT  
TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM LLP  
STREET: 1185 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,938A  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WHITE, JOHN P  
REGISTRATION/DOCKET NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-205-938A-22

Query Match 35.8%; Score 29; DB 1; Length 18;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPEPPPP 13  
Db 6 QVPIRSPDRP 16

RESULT 27  
PCT-US95-02626-22  
Sequence 22, Application PC/TUS9502626  
GENERAL INFORMATION:  
APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH  
APPLICANT: TEMPEST, PAUL  
APPLICANT: CASTEELS, PETER  
TITLE OF INVENTION: APIRACIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED  
TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIMICROBIAL SPECTRUM  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM LLP  
STREET: 1185 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02626  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/205,938  
FILING DATE: 02-MAR-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WHITE, JOHN P  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45061-A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid.  
TOPOLOGY: linear  
MOLBUCLE TYPE: peptide  
PCT-US95-02626-22

Query Match 35.8%; Score 29; DB 5; Length 18;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMPVLPEPPF 13  
Db 6 QVPIRPSQPRP 16

RESULT 28  
US-09-239-043D-2314  
Sequence 2314, Application US/09239043D  
Patent No. 6689363  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Vitello, Maria A.  
APPLICANT: Livingston, Brian D.  
APPLICANT: Kubo, Esteban  
APPLICANT: Cells, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Cheanu, Robert  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus  
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0060007  
CURRENT APPLICATION NUMBER: US/09/239,043D

CURRENT FILING DATE: 1999-01-27  
PRIOR APPLICATION NUMBER: US 09/189,702  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/978,291  
PRIOR FILING DATE: 1997-11-25  
PRIOR APPLICATION NUMBER: US 08/820,360  
PRIOR FILING DATE: 1997-03-12  
PRIOR APPLICATION NUMBER: US 60/013,363  
PRIOR FILING DATE: 1996-03-13  
PRIOR APPLICATION NUMBER: US 08/461,603  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
PRIOR APPLICATION NUMBER: US 08/344,824  
PRIOR FILING DATE: 1994-11-23  
PRIOR APPLICATION NUMBER: US 08/278,634  
PRIOR FILING DATE: 1994-07-21  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/197,484  
PRIOR FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2314  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HBV analog peptide  
US-09-239-043D-2314

Query Match 34.6%; Score 28; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVPEPPFV 15  
Db 2 LPVDPPFSV 10

RESULT 29  
US-08-684-187-1  
Sequence 1, Application US/08684187A  
Patent No. 6020171  
GENERAL INFORMATION:  
APPLICANT: SAITO, ATSUSHI  
APPLICANT: SHINAGAWA, HIDEO  
APPLICANT: NAKATA, ATSUGO  
TITLE OF INVENTION: METHOD OF PREPARING PLASMID HAVING BOTH EXPRESSING  
TITLE OF INVENTION: ABILITY OF RETROVIRAL GENE AND PROCESSING ABILITY AFTER  
TITLE OF INVENTION: TRANSLATION, AND RESULTANT PLASMID AND EXPRESSION  
FILE REFERENCE: 96-0747/1c(lmc)/553  
CURRENT APPLICATION NUMBER: US/08/684,187A  
CURRENT FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: N-TERMINAL  
US-08-684-187-1

Query Match 34.6%; Score 28; DB 3; Length 15;  
Best Local Similarity 44.4%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEPPF 13  
Db 1 PVLPEPPF 13

Db 1 PISPIETVP 9

RESULT 30  
US-09-009-953-120  
Sequence 120, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-Jan-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 120:  
US-09-009-953-120

Query Match 34.6%; Score 28; DB 4; Length 15;  
Best Local Similarity 44.4%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLVPEVPP 13  
Db 3 PISPIETVP 11

RESULT 31  
US-08-844-312-9  
Sequence 9, Application US/08844312  
Patent No. 5948639  
GENERAL INFORMATION:  
APPLICANT: Carlos J. Gimeno and Dean A. Falb  
TITLE OF INVENTION: No. 5948639el TGF-{SYMBOL 98 \f "symbol"} Pathway Genes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,312  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silveri, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MN1-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-844-312-9

Query Match 34.6%; Score 28; DB 2; Length 16;  
Best Local Similarity 38.5%; Pred. No. 4.1e+02;  
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DEMPVPEVPP 13  
Db 4 ELESPPAPYSRY 16

RESULT 32  
US-08-602-999A-360  
Sequence 360, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 360:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-360

Query Match 34.6%; Score 28; DB 3; Length 17;  
Best Local Similarity 45.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVPPPPF 14  
DB 4 LPPPPPPPLPF 14

RESULT 33  
US-09-500-124-360  
Sequence 360, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWIKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
TITLE OF INVENTION: ISOLATING AND USING SAME  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 360:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-360

Query Match 34.6%; Score 28; DB 4; Length 17;

Best Local Similarity 45.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVPPPPF 14  
DB 4 LPPPPPPPLPF 14

RESULT 34  
US-08-630-916A-103  
Sequence 103, Application US/08630916A  
Patent No. 6011137

GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWIKES, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-103

Query Match 34.6%; Score 28; DB 3; Length 18;  
Best Local Similarity 30.8%; Pred. No. 4.6e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLPVPPPPV 15  
DB 6 QLPVPPKPPPL 18

RESULT 35  
US-08-602-999A-317  
Sequence 317, Application US/08602999A  
Patent No. 6184205

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWIKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 317:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-317

Query Match 34.6%; Score 28; DB 3; Length 18;  
Best Local Similarity 30.8%; Pred. No. 4.6e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPVEPPPV 15  
Db 6 QLPVPVPRPRL 18

RESULT 36  
US-08-630-915A-159  
Sequence 159, Application US/08630915A  
Patent No. 6309820  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6309820h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,915A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 159:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-915A-159

Query Match 34.6%; Score 28; DB 3; Length 18;  
Best Local Similarity 30.8%; Pred. No. 4.6e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPVEPPPV 15  
Db 6 QLPVPVPRPRL 18

RESULT 37  
US-09-500-124-317  
Sequence 317, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: OUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 317:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-09-500-124-317

Query Match 34.6%; Score 28; DB 4; Length 18;  
Best Local Similarity 30.8%; Pred. No. 4.6e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLPVEPPFV 15  
DB 6 QLPVPVPPKRPRL 18

## RESULT 38

US-09-879-957-159  
Sequence 159, Application US/09879957  
Patent No. 6709821

## GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
HOFFMAN, No. 6709821h  
KAY, Brian K.  
FOWLES, Dana M.  
McCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME

NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edwards LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-Apr-1996

## ATTORNEY/AGENT INFORMATION:

NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Query Match 34.6%; Score 28; DB 4; Length 18;  
Best Local Similarity 30.8%; Pred. No. 4.6e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLPVEPPFV 15  
DB 6 QLPVPVPPKRPRL 18

## RESULT 39

US-08-672-805-6  
Sequence 6, Application US/08672805  
Patent No. 5831003

## GENERAL INFORMATION:

APPLICANT: Baumbach, George A.,  
Baumbach, Joseph A.,  
APPLICANT: Baumbach, Joseph A.,  
APPLICANT: Dadd, Christopher A.,  
APPLICANT: Hammond, David J.  
TITLE OF INVENTION: Peptides which bind to Prothrombin  
and Thrombin  
NUMBER OF SEQUENCES: 21

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Bayer Corporation  
STREET: 800 Dwight Way  
STREET: P. O. Box 1966  
CITY: Berkeley  
STATE: California  
COUNTRY: USA

ZIP: 94701-1986

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb Storage

COMPUTER: IBM

OPERATING SYSTEM: DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,805

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gbilia, James A.

REGISTRATION NUMBER: 25772

REFERENCE/DOCKET NUMBER: MSB-7236

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 705-7910

TELEFAX: (510) 705-7904

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 6

TYPE: amino acid

STRANDEDNESS: single strand

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: peptide

US-08-672-805-6

Query Match 33.3%; Score 27; DB 2; Length 6;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPFV 15  
DB 1 PPFV 5

## RESULT 40

US-08-828-712-12  
Sequence 12, Application US/08828712  
Patent No. 6015884

## GENERAL INFORMATION:

APPLICANT: Schneck, Jonathan P.

APPLICANT: O'Herrin, Sean

TITLE OF INVENTION: Soluble Divalent and Multivalent  
Heterodimeric Analogs of Proteins

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

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ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,712
FILING DATE: 28-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.73713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)508-9100
TELEFAX: (202)508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide p2Ca
US-08-828-712-12

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFPP 14
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Db 1 LSPFPP 6
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Search completed: June 7, 2005, 23:23:15  
Job time : 21.4545 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds

(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-5

Perfect score: 81  
Sequence: 1 DLEMPVLPVPPFPV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_Aa.\*

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22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	14	US-10-281-652-5
2	81	100.0	15	16	US-10-691-157-5
3	81	100.0	15	16	US-10-691-330-5
4	57	70.4	10	17	US-10-182-110-3
5	36	44.4	18	14	US-10-281-652-22
6	36	44.4	18	16	US-10-691-157-22
7	36	44.4	18	17	US-10-691-330-22
8	34	42.0	15	14	US-10-281-652-8
9	34	42.0	15	16	US-10-691-157-8
10	34	42.0	15	17	US-10-691-330-8
11	34	42.0	18	16	US-10-474-955-67

12	32	39.5	13	16	US-10-706-391-63	Sequence 63, Appl
13	32	39.5	15	13	US-10-103-395-97	Sequence 97, Appl
14	32	39.5	15	13	US-10-103-395-111	Sequence 111, Appl
15	31	38.3	12	14	US-10-158-596A-10	Sequence 10, Appl
16	31	38.3	12	14	US-10-157-775B-10	Sequence 10, Appl
17	31	38.3	12	14	US-10-254-446A-10	Sequence 10, Appl
18	31	38.3	12	14	US-10-155-883B-10	Sequence 10, Appl
19	31	38.3	12	14	US-10-080-608A-179	Sequence 179, Appl
20	31	38.3	12	15	US-10-370-665-88	Sequence 88, Appl
21	30	37.0	15	16	US-10-788-992-15	Sequence 15, Appl
22	30	37.0	16	14	US-10-161-791-451	Sequence 451, Appl
23	30	37.0	17	14	US-10-211-088-97	Sequence 97, Appl
24	30	37.0	18	14	US-10-225-567A-1382	Sequence 1382, Ap
25	29	35.8	6	17	US-10-433-709-6	Sequence 6, Appl
26	29	35.8	9	14	US-10-353-929-171	Sequence 171, Appl
27	29	35.8	14	14	US-10-185-050-56	Sequence 56, Appl
28	29	35.8	16	14	US-10-161-791-202	Sequence 202, Appl
29	29	35.8	16	14	US-10-161-791-406	Sequence 406, Appl
30	28	34.6	9	15	US-10-398-104-34	Sequence 34, Appl
31	28	34.6	10	10	US-09-572-404B-218	Sequence 218, Appl
32	28	34.6	10	10	US-09-572-404B-220	Sequence 220, Appl
33	28	34.6	10	10	US-09-572-404B-222	Sequence 222, Appl
34	28	34.6	10	14	US-10-200-708-513	Sequence 513, Appl
35	28	34.6	10	14	US-10-200-708-538	Sequence 538, Appl
36	28	34.6	10	17	US-10-654-601-2314	Sequence 2314, Ap
37	28	34.6	11	15	US-10-398-104-174	Sequence 174, Appl
38	28	34.6	12	14	US-10-226-007-1252	Sequence 1252, Ap
39	28	34.6	13	14	US-10-226-007-1253	Sequence 1253, Ap
40	28	34.6	13	14	US-10-226-007-1261	Sequence 1261, Ap
41	28	34.6	13	15	US-10-467-209-21	Sequence 21, Appl
42	28	34.6	13	15	US-10-468-370-75	Sequence 75, Appl
43	28	34.6	13	16	US-10-468-496-66	Sequence 66, Appl
44	28	34.6	13	16	US-10-468-496-1465	Sequence 1465, Ap
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46	28	34.6	14	14	US-10-226-007-1254	Sequence 1254, Ap
47	28	34.6	14	14	US-10-226-007-1262	Sequence 1262, Ap
48	28	34.6	14	14	US-10-226-007-1269	Sequence 1269, Ap
49	28	34.6	14	16	US-10-474-955-1	Sequence 1, Appl
50	28	34.6	14	17	US-10-794-514A-250	Sequence 250, Appl
51	28	34.6	14	17	US-10-794-514A-261	Sequence 261, Appl
52	28	34.6	14	17	US-10-794-514A-282	Sequence 282, Appl
53	28	34.6	14	17	US-10-794-514A-530	Sequence 530, Appl
54	28	34.6	15	13	US-10-103-395-120	Sequence 120, Appl
55	28	34.6	15	14	US-10-226-007-1255	Sequence 1255, Ap
56	28	34.6	15	14	US-10-226-007-1263	Sequence 1263, Ap
57	28	34.6	15	14	US-10-226-007-1270	Sequence 1270, Ap
58	28	34.6	15	14	US-10-226-007-1276	Sequence 1276, Ap
59	28	34.6	15	16	US-10-475-853-11	Sequence 11, Appl
60	28	34.6	16	14	US-10-226-007-1256	Sequence 1256, Ap
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62	28	34.6	16	14	US-10-226-007-1271	Sequence 1271, Ap
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71	28	34.6	17	14	US-10-161-791-360	Sequence 360, Appl
72	28	34.6	17	16	US-10-788-400-26	Sequence 26, Appl
73	28	34.6	18	9	US-09-879-957-159	Sequence 159, Appl
74	28	34.6	18	14	US-10-185-050-103	Sequence 103, Appl
75	28	34.6	18	14	US-10-226-007-1258	Sequence 1258, Ap
76	28	34.6	18	14	US-10-226-007-1266	Sequence 1266, Ap
77	28	34.6	18	14	US-10-226-007-1273	Sequence 1273, Ap
78	28	34.6	18	14	US-10-226-007-1279	Sequence 1279, Ap
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80	28	34.6	18	14	US-10-226-007-1288	Sequence 1288, Ap
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85 27.5 34.0 10 10 US-09-895-298-138 Sequence 138, App  
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87 27 33.3 8 9 US-09-813-484-26 Sequence 26, Appl  
88 27 33.3 8 9 US-09-813-484-29 Sequence 29, Appl  
89 27 33.3 8 9 US-09-954-166-12 Sequence 12, Appl  
90 27 33.3 8 9 US-09-761-534A-3 Sequence 3, Appl  
91 27 33.3 8 9 US-09-434-965-2 Sequence 2, Appl  
92 27 33.3 8 14 US-10-145-396-2 Sequence 25, Appl  
93 27 33.3 8 14 US-10-046-801-25 Sequence 28, Appl  
94 27 33.3 8 14 US-10-046-801-28 Sequence 46, Appl  
95 27 33.3 8 15 US-10-266-463A-46 Sequence 338, App  
96 27 33.3 8 16 US-10-785-472-2 Sequence 2, Appl  
97 27 33.3 8 17 US-10-885-523-3 Sequence 3, Appl  
98 27 33.3 9 17 US-08-344-824-97 Sequence 97, Appl  
99 27 33.3 9 9 US-09-954-166-13 Sequence 13, Appl  
100 27 33.3 9 9

## ALIGNMENTS

RESULT 1  
US-10-281-652-5  
; Sequence 5, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265 00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-5  
Query Match 100.0%; Score 81; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLEMPVLVPEPPFV 15  
Db 1 DLEMPVLVPEPPFV 15  
RESULT 2  
US-10-691-157-5  
; Sequence 5, Application US/10691157  
; Publication No. US2004026681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUZEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265 00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-5

Query Match 100.0%; Score 81; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVPEPPFV 15  
Db 1 DLEMPVLVPEPPFV 15  
RESULT 3  
US-10-691-330-5  
; Sequence 5, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, G. John  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Kruzel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265 00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-5  
Query Match 100.0%; Score 81; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLEMPVLVPEPPFV 15  
Db 1 DLEMPVLVPEPPFV 15  
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US-10-182-110-3  
; Sequence 3, Application US/10182110  
; Publication No. US20040171553A1  
; GENERAL INFORMATION:  
; APPLICANT: Regen Therapeutics Plc  
; APPLICANT: Georgiades, Jerzy A  
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use  
; FILE REFERENCE: AAT-14173  
; CURRENT APPLICATION NUMBER: US/10/182,110

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/ CURRENT FILING DATE: 2003-04-21
/ PRIOR APPLICATION NUMBER: GB0001825.9
/ PRIOR FILING DATE: 2000-01-26
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 10
/ TYPE: PRF
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-3

Query Match
Best Local Similarity 70.4%; Score 57; DB 16; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLPEVPEPP 14
DB 1 PVLPEVPEPP 10

RESULT 5
US-10-281-652-22
/ Sequence 22, Application US/10281652
/ Publication No. US20030091606A1
/ GENERAL INFORMATION:
/ APPLICANT: STANTON, G. John
/ APPLICANT: HUGHES, Thomas K.
/ APPLICANT: BOLDGHI, Istvan
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
/ FILE REFERENCE: 265, 00220101
/ CURRENT APPLICATION NUMBER: US/10/281,652
/ CURRENT FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US/09/641,803
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/149,310
/ PRIOR FILING DATE: 1999-08-17
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-22

Query Match
Best Local Similarity 44.4%; Score 36; DB 14; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12
DB 3 EMPFPKYPVEPP 14

RESULT 6
US-10-691-157-22
/ Sequence 22, Application US/10691157
/ Publication No. US2004026661A1
/ GENERAL INFORMATION:
/ APPLICANT: BOLDGHI, Istvan
/ APPLICANT: STANTON, G. John
/ APPLICANT: GEORGIADIS, Jerzy
/ APPLICANT: HUGHES, Thomas
/ APPLICANT: KRUEL, Marian
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
/ FILE REFERENCE: 265, 00440101
/ CURRENT APPLICATION NUMBER: US/10/691,157
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/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 10/281,652
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: 09/641,803
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/149,310
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 60/420,369
/ PRIOR FILING DATE: 2002-10-22
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptides
US-10-691-157-22

Query Match
Best Local Similarity 44.4%; Score 36; DB 16; Length 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPP 12
DB 3 EMPFPKYPVEPP 14

RESULT 8
US-10-281-652-8
/ Sequence 8, Application US/10281652
/ Publication No. US20030091606A1
/ GENERAL INFORMATION:
/ APPLICANT: STANTON, G. John
/ APPLICANT: HUGHES, Thomas K.
/ APPLICANT: BOLDGHI, Istvan
/ TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
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; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
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US-10-281-652-8
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Query Match          42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 5 PKLKEVFPF 14
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RESULT 9
US-10-691-157-8
; Sequence 8, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDGOCH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265.0040101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
;
US-10-691-157-8
```

```

Query Match          42.0%; Score 34; DB 16; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 PVLPEPPF 14
   |||||
Db 5 PKLKEVFPF 14
```

```

RESULT 10
US-10-691-330-8
; Sequence 8, Application US/10691330
```

```

; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Boldgoch, Istvan
; APPLICANT: Stanton, G. John
; APPLICANT: Georgiades, Jerzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265.00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
;
US-10-691-330-8
```

```

Query Match          42.0%; Score 34; DB 17; Length 15;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 PVLPEPPF 14
   |||||
Db 5 PKLKEVFPF 14
```

```

RESULT 11
US-10-474-955-67
; Sequence 67, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Driffoht, Jan W.
; APPLICANT: Koning, Eric
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; TITLE OF INVENTION: DQ BINDING PROLAMINE-DERIVED PEPTIDES
; FILE REFERENCE: 279/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide sequence in pool 57
; NAME/KEY: MISC FEATURE
; LOCATION: (7)-(8)
; OTHER INFORMATION: "Y" on position 7 is P/S
;
US-10-474-955-67
```

```

Query Match          42.0%; Score 34; DB 16; Length 18;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 EMPVLPEPPF 13
   |||||
Db 4 QOPLYQLQPPF 14
```

```

RESULT 12
US-10-706-391-63
; Sequence 63, Application US/10706391
```

```
Publication No. US20040137482A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: WASHINGTON DENTAL SERVICE
APPLICANT: Eckert, Randal
APPLICANT: Qi, Fengxia
APPLICANT: Shi, Wenyuan
APPLICANT: Anderson, Maxwell H.
FILE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 2101363-991600
CURRENT APPLICATION NUMBER: US/10/706,391
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 10/077,624
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Design peptide
US-10-706-391-63
```

```
Query Match      39.5%; Score 32; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 MPVLPVEPP 11
        |||||
Db      4 LPVLPVLP 11
```

```
RESULT 13
US-10-103-395-97
Sequence 97, Application US/10103395
Publication No. US20020160019A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
FILE REFERENCE: 39963-20016.01
CURRENT APPLICATION NUMBER: US/10/103,395
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 09/009,953
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: PCT/US98/01373
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: US 60/036,713
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 60/037,432
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 274
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-395-97
```

```
Query Match      39.5%; Score 32; DB 13; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 LEMPVLVEBPP 13
        ||:|:|
Db      5 LPVTPVPP 13
```

```
Db      2 LNPISPIETVP 13

RESULT 14
US-10-103-395-111
Sequence 111, Application US/10103395
Publication No. US20020160019A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
FILE REFERENCE: 39963-20016.01
CURRENT APPLICATION NUMBER: US/10/103,395
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 09/009,953
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: PCT/US98/01373
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: US 60/036,713
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 60/037,432
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 274
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-395-111
```

```
Query Match      39.5%; Score 32; DB 13; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 LEMPVLVEBPP 13
        ||:|:|
Db      4 LNPISPIETVP 15
```

```
RESULT 15
US-10-158-596A-10
Sequence 10, Application US/10158596A
Publication No. US20030068900A1
GENERAL INFORMATION:
APPLICANT: Belcher, Angela
APPLICANT: Flynn, Christine
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL
FILE REFERENCE: 119927-1052
CURRENT APPLICATION NUMBER: US/10/158,596A
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/296,013
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 12
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-10
```

```
Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 LPVTPPP 13
        ||:|:|
Db      5 LPVTPPP 11
```

```
RESULT 16
US-10-157-775B-10
; Sequence 10, Application US/10157775B
; Publication No. US20030073104A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Lee, Seung-Muk
; TITLE OF INVENTION: NANOSCALING ORDERING OF HYBRID MATERIALS USING GENETICALLY ENGINE
; TITLE OF INVENTION: MESOSCALE VIRUS
; FILE REFERENCE: 11927-1051
; CURRENT APPLICATION NUMBER: US/10/157,775B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/326,583
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide recognition sequence retrieved from phage biopanning
US-10-157-775B-10

Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 LPVPPFP 13
Db      5 LPMTFPF 11

RESULT 17
US-10-254-446A-10
; Sequence 10, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Escher
; APPLICANT: Lee, Seung-Muk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 11927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopat
US-10-254-446A-10

Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 LPVPPFP 13
Db      5 LPMTFPF 11

RESULT 18
US-10-155-883B-10
; Sequence 10, Application US/10155883B
; Publication No. US20030148380A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; TITLE OF INVENTION: MOLECULAR RECOGNITION OF MATERIALS
; FILE REFERENCE: 11927-1049
; CURRENT APPLICATION NUMBER: US/10/155,883B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide binding sequence retrieved from phage biopanning
US-10-155-883B-10

Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 LPVPPFP 13
Db      5 LPMTFPF 11

RESULT 19
US-10-080-608A-179
; Sequence 179, Application US/10080608A
; Publication No. US2003018956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Identified from M13 bacteriophage peptide display library.
US-10-080-608A-179

Query Match      38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 LPVPPFP 13
Db      5 LPMTFPF 11

RESULT 20
US-10-370-685-88
; Sequence 88, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF-P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
```

LENGTH: 12  
TYPE: PRT  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: binds to GAs

US-10-370-685-88

Query Match 38.3%; Score 31; DB 15; Length 12;  
Best Local Similarity 71.4%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVPPPP 13  
|:|:|  
DB 5 LPVPPPP 11

## RESULT 21

US-10-788-992-15  
Sequence 15, Application US/10788992  
Publication No. US20040265958A1  
GENERAL INFORMATION:  
APPLICANT: Gilula, Norton B  
Cravatt, Benjamin F  
Lerner, Richard A

TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: The Scripps Research Institute  
STREET: 10550 North Torrey Pines Road  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/788,992  
FILING DATE: 26-Feb-2004  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/743,168  
FILING DATE: 01-May-1998  
APPLICATION NUMBER: US 08/489,535  
FILING DATE: 12-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 485.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-788-992-15

Query Match 37.0%; Score 30; DB 16; Length 15;  
Best Local Similarity 60.0%; Pred. No. 8.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PVLVPPPP 14  
|:|:|  
DB 5 PTVV-PPPP 12

## RESULT 22

US-10-161-791-451  
Sequence 451, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: OULLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 451:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-10-161-791-451

Query Match 37.0%; Score 30; DB 14; Length 16;  
Best Local Similarity 57.1%; Pred. No. 9.4e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVPP 11  
|:|:|  
DB 6 PVLVPP 12

## RESULT 23

US-10-211-088-97  
Sequence 97, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai

TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins and Assays for Molecular B  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/309,395  
PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/341,589  
PRIOR FILING DATE: 2001-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 97  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Binding domain  
US-10-211-088-97

Query Match 37.0%; Score 30; DB 14; Length 17;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8  
DB 7 DLEMPVLP 14

RESULT 24  
US-10-225-567A-1382  
Sequence 1382, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burmer, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1382  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-1382

Query Match 37.0%; Score 30; DB 14; Length 18;  
Best Local Similarity 41.7%; Pred. No. 1.1e+03;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVPEPF 12  
DB 6 NLAKPTLPPIKTF 17

RESULT 25  
US-10-433-709-6  
Sequence 6, Application US/10433709  
Publication No. US20050085422A1  
GENERAL INFORMATION:  
APPLICANT: Regen Therapeutics plc  
APPLICANT: Georgiadis, Jerry A.  
TITLE OF INVENTION: Peptides Derived from Colostretinun  
FILE REFERENCE: NAT-14866  
CURRENT APPLICATION NUMBER: US/10/433,709  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: GB0029777.0  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Ovis aries  
US-10-433-709-6

Query Match 35.8%; Score 29; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12  
DB 1 PVEPP 5

RESULT 26  
US-10-353-929-171  
Sequence 171, Application US/10353929  
Publication No. US20030175288A1  
GENERAL INFORMATION:  
APPLICANT: ITOH, Kyogo  
TITLE OF INVENTION: Tumor antigen  
FILE REFERENCE: GP01-1024  
CURRENT APPLICATION NUMBER: US/10/353,929  
CURRENT FILING DATE: 2003-01-30  
PRIOR APPLICATION NUMBER: JP P2000-231814  
PRIOR FILING DATE: 2000-07-31  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 171  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Designed peptide based on the amino acid sequence of SEQ ID NO:5  
US-10-353-929-171

Query Match 35.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 42.9%; Pred. No. 1.5e+06;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVEPP 13  
DB 2 LPVEPP 8

RESULT 27  
US-10-185-050-56  
Sequence 56, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozqi, Gregorio  
Kay, Brian K.  
Fowles, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE



REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: peptide  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-10-185-050-56

Query Match 35.8%; Score 29; DB 14; Length 14;  
Best Local Similarity 45.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 EMPVLPVEPP 13  
| | | | |  
| | | | |  
Db 1 EYPPYPPPPYP 11

RESULT 28  
US-10-161-791-202  
; Sequence 202, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 202:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

US-10-161-791-202

Query Match 35.8%; Score 29; DB 14; Length 16;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLEMPVLP 8  
| | | | |  
| | | | |  
Db 3 DPERPVLP 10

RESULT 29  
US-10-161-791-406  
; Sequence 406, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 406:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

US-10-161-791-406

Query Match 35.8%; Score 29; DB 14; Length 16;  
Best Local Similarity 71.4%; Pred. No. 1.3e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMPVLP 8  
| | | | |  
| | | | |  
Db 4 LKLPVLP 10

RESULT 30  
US-10-398-104-34  
; Sequence 34, Application US/10398104

```
Publication No. US20040047880A1
GENERAL INFORMATION:
APPLICANT: De Bolle, Xavier Thomas
APPLICANT: Lelesson, Jean-Jacques
APPLICANT: Lobet, Yves
APPLICANT: Mertens, Pascal Yvon
APPLICANT: Poolman, Jan
APPLICANT: Voet, Pierre
TITLE OF INVENTION: COMPONENT FOR VACCINE
FILE REFERENCE: B45242
CURRENT APPLICATION NUMBER: US/10/398,104
CURRENT FILING DATE: 2003-01-04
PRIOR APPLICATION NUMBER: PCT/EP01/11409
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: GB 0024200.8
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-34

Query Match
Best Local Similarity 34.6%; Score 28; DB 15; Length 9;
                          66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PVEPPF 13
DB 3 PYDPPF 8

RESULT 31
US-09-572-404B-218
Sequence 218, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 218
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 11-20 and may interact with Sequen
US-09-572-404B-218

Query Match
Best Local Similarity 34.6%; Score 28; DB 10; Length 10;
                          62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPVEP 11
DB 2 LPVTPGEP 9

RESULT 32
US-09-572-404B-220
Sequence 220, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
```

```
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 220
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 10-19 and may interact with Sequen
US-09-572-404B-220

Query Match
Best Local Similarity 34.6%; Score 28; DB 10; Length 10;
                          62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPVEP 11
DB 2 LPVTPGEP 9

RESULT 33
US-09-572-404B-222
Sequence 222, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 222
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in Unknown at 14-23 and may interact with Sequen
US-09-572-404B-222

Query Match
Best Local Similarity 34.6%; Score 28; DB 10; Length 10;
                          62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPVEP 11
DB 2 LPVTPGEP 9

RESULT 34
US-10-200-708-513
Sequence 513, Application US/10200708
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 17999-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 513
```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-513

Query Match
Best Local Similarity 34.6%; Score 28; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPFP 13
DB 2 PISPIETVP 10

RESULT 35
US-10-200-708-538
; Sequence 538, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-538

Query Match
Best Local Similarity 34.6%; Score 28; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEPPFP 13
DB 2 PISPIETVP 10

RESULT 36
US-10-654-601-2314
; Sequence 2314, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.006007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
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; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2314
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide
US-10-654-601-2314

Query Match
Best Local Similarity 34.6%; Score 28; DB 17; Length 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LPVDEPPFV 15
DB 2 LPVDPPFV 10

RESULT 37
US-10-398-104-174
; Sequence 174, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-174

Query Match
Best Local Similarity 34.6%; Score 28; DB 15; Length 11;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PVEPPFP 13
DB 4 PYDPPF 9
```

```
RESULT 38
US-10-226-007-1252
; Sequence 1252, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1252
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1252

Query Match          34.6%; Score 28; DB 14; Length 12;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVPEPF 12
      ||:| | | |
Db      1 DLDTPPTDPPPY 12

RESULT 39
US-10-226-007-1253
; Sequence 1253, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1253
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1253

Query Match          34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVPEPF 12
      ||:| | | |
Db      1 DLDTPPTDPPPY 12

RESULT 40
US-10-226-007-1261
; Sequence 1261, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
```

```
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1261
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1261

Query Match          34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 DLEMPVLPVPEPF 12
      ||:| | | |
Db      2 DLDTPPTDPPPY 13
```

Search completed: June 7, 2005, 23:31:37  
Job time : 68.5 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 13.9091 Seconds  
(without alignments)  
103.763 Million cell updates/sec

Title: US-10-691-157-5  
Perfect score: 81  
Sequence: 1 DLEMPVLVPEPFV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	33.3	17	2	S59481	hydroxyproline-ric
2	25	30.9	11	2	I33098	173K exoantigen -
3	25	30.9	15	2	B39109	hypothetical 1.5K
4	24	29.6	15	2	PA0088	protein QP200051 -
5	24	29.6	15	2	PS0455	superoxide dismuta
6	24	29.6	17	2	G85956	telomeric and tetr
7	23	28.4	16	2	PC4371	ribosomal protein
8	23	27.8	17	2	S17274	tetracenomycin A2
9	22	27.2	11	2	A55149	H+-transporting tw
10	22	27.2	14	2	G33160	Pax-QNR, long form
11	22	27.2	14	2	B56884	protein QP200037 -
12	22	27.2	15	2	PA0060	superoxide dismuta
13	22	27.2	16	2	E58503	melanin-omochrome
14	22	27.2	16	2	A23892	hydroxymethylgluta
15	22	27.2	18	2	S56715	guinaldine oxidore
16	22	27.2	18	2	S29166	tetrameric protein
17	21	25.9	9	2	S66419	32K protein 3306 -
18	21	25.9	15	2	PS0452	protein kinase (EC
19	21	25.9	15	2	S20410	hypodermin B - ear
20	21	25.9	16	2	A20190	insulin-like growt
21	21	25.9	17	2	E23734	45/47K antigen - M
22	21	25.9	18	2	A49237	elastase inhibitor
23	21	25.9	18	2	A28060	chromoprotein rec
24	21	25.9	18	2	I78841	halo-toxin - Pseud
25	20	24.7	6	2	A61049	alpha-2-macroglobu
26	20	24.7	9	2	S66635	peptide-N4-(N-acet
27	20	24.7	10	2	B59272	protein QA300042 -
28	20	24.7	11	2	PA0028	statmin - mouse (
29	20	24.7	11	2	PN0042	

30	20	24.7	13	2	B47415	mannose-1-phosphat
31	20	24.7	13	2	S21152	tryptophyllin-rela
32	20	24.7	14	2	H64008	hypothetical prote
33	20	24.7	15	2	PA0024	protein QA300050 -
34	20	24.7	16	1	A49761	locustacyprokinin -
35	20	24.7	16	2	A60551	leucocyte elastase
36	20	24.7	18	2	A42576	steroid receptor c
37	20	24.7	18	2	I52614	u-plasminogen acti
38	20	24.7	18	2	A28027	protein P2 - curle
39	20	24.7	18	2	A40760	basic fibroblast g
40	19	23.5	10	2	B61218	alpha-gliadin 6Ha
41	19	23.5	11	2	PQ0231	beta-glucosidase (
42	19	23.5	13	2	A59387	VCAM-1 5'UTR bindi
43	19	23.5	13	2	A05174	tryptophyllin-13 -
44	19	23.5	15	2	S29207	avenin gamma-4 - o
45	19	23.5	15	2	PA0026	protein QA300027 -
46	19	23.5	15	2	C61511	milk band B protei
47	19	23.5	15	2	A41436	alpha-macroglobuli
48	19	23.5	15	2	I40665	ILVFN leader pepti
49	19	23.5	16	2	T37075	hypothetical prote
50	19	23.5	16	2	A45454	ankyrin-binding gl
51	19	23.5	17	2	UQ2030	hypothetical 1.9K
52	19	23.5	17	2	I55612	thyroid hormone re
53	19	23.5	17	4	I51887	hypothetical BMSR1
54	19	23.5	18	2	S04229	N4-(beta-N-acetylgl
55	19	23.5	18	2	PN0149	beta-Gliadin 13 -
56	19	23.5	18	2	A60915	enkephalin-degrad
57	19	23.5	18	2	A54651	insulin-like growt
58	19	23.5	18	2	I51427	hemoglobin alpha c
59	18	22.2	9	2	A60356	bHtH transcription
60	18	22.2	9	2	S26508	118K stomach cance
61	18	22.2	10	2	S18396	collagen alpha 2(V
62	18	22.2	10	2	B33710	probable glucose-6
63	18	22.2	10	2	B33710	ornithine decarbox
64	18	22.2	11	2	A54348	N-acetylglucosamin
65	18	22.2	11	2	S21727	gamma-Interferon-1
66	18	22.2	12	2	S67528	napin - rape (frag
67	18	22.2	12	2	S70344	amine oxidase (cop
68	18	22.2	14	2	S21247	H+-transporting tw
69	18	22.2	14	2	PL0152	metal-binding prot
70	18	22.2	14	2	A60158	disaggregatase - M
71	18	22.2	15	2	PA0071	superoxide dismuta
72	18	22.2	15	2	A56963	acid phosphatase (
73	18	22.2	16	2	C45133	casein kinase II (
74	18	22.2	16	2	PA0048	protein QA100047 -
75	18	22.2	16	2	B23692	transcription fact
76	18	22.2	17	2	I49593	cystic fibrosis tr
77	18	22.2	17	2	I84733	gene CPTP protein
78	18	22.2	18	2	S29264	ovomemerythrin - d
79	18	22.2	18	2	S09722	2S albumin small c
80	18	22.2	18	2	S07223	T-cell receptor de
81	18	22.2	18	2	I46653	serine proteinase
82	18	22.2	18	2	S71592	caldesmon, car
83	18	22.2	18	2	A39040	ubiquitin-carrier
84	17	21.6	15	2	A54397	catch-relaxing pep
85	17	21.0	8	2	ECMWCR	hypothetical prote
86	17	21.0	8	2	S16324	enamelin f - bovin
87	17	21.0	8	2	S10783	spasmodic toxin
88	17	21.0	8	2	A46306	coat protein beta
89	17	21.0	9	2	S13636	locustacyprotopin I
90	17	21.0	9	2	A61620	translation elonga
91	17	21.0	9	2	PC7074	angiotensin I - Ja
92	17	21.0	10	2	A60624	angiotensin precu
93	17	21.0	10	2	A90917	angiotensin precu
94	17	21.0	10	2	A90345	angiotensin precu
95	17	21.0	11	1	XAVIBH	bradykinin-potent
96	17	21.0	11	2	PC2254	cytochrome P450 3A
97	17	21.0	11	2	S07207	Critia-angiotensin
98	17	21.0	12	2	C36201	1-aminocyclopropan
99	17	21.0	12	2	S01749	collagen alpha 1(I
100	17	21.0	12	2	B45691	probable minor cap

## ALIGNMENTS

## RESULT 1

S59481  
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
C/Species: Phaseolus vulgaris (kidney bean)  
C/Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: S59481  
R/Mojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A/Title: Specificity in the immobilisation of cell wall proteins in response to different  
A/Reference number: S59481; MUID:96011753; PMID:7548825  
A/Accession: S59481

A/Molecule type: protein  
A/Residues: 1-17 <MOJ>

A/Cross-references: UNIPROT:Q7M113  
C/Keywords: glycoprotein; hydroxyproline  
F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

## Query Match

Best Local Similarity 33.3%; Score 27; DB 2; Length 17;  
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLEMPVLPEPPPEPV 15  
| : | | | | |  
DB 1 DMTLP--PVPPPPVV 13

## RESULT 2

I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C/Species: Plasmodium falciparum  
C/Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C/Accession: I33098  
R/Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A/Reference number: A33098  
A/Accession: I33098  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <NIC>

## Query Match

Best Local Similarity 30.9%; Score 25; DB 2; Length 11;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLPPV 9  
| : | : | : |  
DB 5 ELPLPPI 11

## RESULT 3

B39109  
hypothetical 1.5K protein - hepatitis C virus  
N/Alternate names: hypothetical protein 2  
C/Species: hepatitis C virus  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C/Accession: B39109; JQ1585  
R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
A/Reference number: A39109; MUID:91156678; PMID:11705704  
A/Accession: B39109

A/Status: not compared with conceptual translation  
A/Molecule type: mRNA

A/Residues: 1-15 <HAN>

A/Cross-references: GB:M58406

R/Kumar, U.; Cheng, D.; Thomas, H.; Nonjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A/Title: Cloning and sequencing of the structural region and expression of putative core  
A/Reference number: JQ1584; MUID:92300349; PMID:1318944

A/Accession: JQ1585

A/Molecule type: genomic RNA

A/Residues: 1-15 <KUM>

A/Experimental source: strain U.K.

## Query Match

Best Local Similarity 30.9%; Score 25; DB 2; Length 15;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEVP 11  
| : | | | |  
DB 9 PPLPGERP 15

## RESULT 4

PA0088  
protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)  
C/Species: Fusarium sporotrichioides  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C/Accession: PA0088  
R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
A/Reference number: PA0051  
A/Accession: PA0088  
A/Molecule type: protein  
A/Residues: 1-15 <CHO>

## Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 15;  
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMPVLPEPPPP 13  
| : | : | : |  
DB 1 QKPDIPXDYP 11

## RESULT 5

PS0455  
superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: PS0455  
R/Tsugita, A.  
submitted to JIPID, April 1993  
A/Reference number: PS0206  
A/Accession: PS0455  
A/Molecule type: protein  
A/Residues: 1-15 <TSU>  
A/Cross-references: UNIPROT:Q7M105  
A/Experimental source: germ  
C/Function:

A/Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C/Keywords: metalloprotein; oxidoreductase

## Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 15;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLPEV 10  
| : | : | : |  
DB 6 LPLPYD 12

## RESULT 6

G85956  
hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: G85956  
R/Berna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grobcock, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85956  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-17 <SR>  
 A:Cross-references: UNIPROT:Q6X444; GB:AE005174; MID:912517539; PIDN:AAG58115.1; GSPDB:Q  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: 24331

Query Match 29.6%; Score 24; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 8.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFP 13  
 |||||  
 Db 4 VSPFP 8

RESULT 7  
 PC4371  
 telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
 C:Accession: PC4371  
 R:Sarig, G.; Weisman-Shomer, P.; Fry, M.  
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CP  
 A:Reference number: PC4371; MUID:97445086; PMID:9299414  
 A:Accession: PC4371  
 A:Molecule type: protein  
 A:Residues: 1-16 <SR>  
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 28.4%; Score 23; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEP 11  
 |||||  
 Db 5 PVEP 8

RESULT 8  
 S17274  
 ribosomal protein YmlJ5, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 A:Variety: strain 07173  
 C:Date: 23-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
 C:Accession: S17274  
 R:Grothmann, L.; Graack, H.R.; Knift, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.  
 F8BS Lett. 284, 51-56, 1991  
 A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from  
 A:Reference number: S17255; MUID:91285106; PMID:2060626  
 A:Accession: S17274  
 A:Molecule type: protein  
 A:Residues: 1-17 <SR>  
 A:Cross-references: UNIPROT:P36530  
 C:Comment: A coding region for this protein could not be identified in the genome of Sac  
 C:Genetics:  
 A:Genome: nuclear  
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.8%; Score 22.5; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 LPVP-PPV 15  
 |||||  
 Db 8 LPVPVPPV 17

RESULT 9

A55149  
 tetracenomycin A2 oxygenase (EC 1.-.-.-) - Streptomyces glaucescens (fragment)  
 N:Alternate names: tcmA2 oxygenase; tcmA  
 C:Species: Streptomyces glaucescens  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: A55149  
 R:Shen, B.; Hutchinson, C.R.  
 J. Biol. Chem. 269, 30726-30733, 1994  
 A:Title: Triple hydroxylation of tetracenomycin A2 to tetracenomycin C in Streptomyces  
 A2 oxygenase.  
 A:Reference number: A55149; MUID:95074090; PMID:7982994  
 A:Accession: A55149  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <SR>  
 A:Cross-references: UNIPROT:Q7M0K6  
 C:Genetics:  
 A:Start codon: TTG  
 C:Keywords: antibiotic biosynthesis; PAD; monomer; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 11;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLV 9  
 |||||  
 Db 5 EMPVLV 11

RESULT 10  
 G33160  
 H+-transporting two-sector ATPase (EC 3.6.3.14) 9K chain - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 03-Jun-2002  
 C:Accession: G33160  
 R:Godinot, C.  
 submitted to the Protein Sequence Database, February 1991  
 A:Reference number: A33160  
 A:Accession: G33160  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <GOD>  
 C:Keywords: hydrolase

Query Match 27.2%; Score 22; DB 2; Length 14;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 VLPVPPPV 15  
 |||||  
 Db 1 VLPVQVSPV 10

RESULT 11  
 B56884  
 Pax-QNR, long form - quail (fragment)  
 C:Species: Coturnix coturnix (quail)  
 C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: B56884  
 R:Dozier, C.; Carriere, C.; Grevin, D.; Martin, P.; Quatanens, B.; Stehelin, D.; Saule,  
 Cell Growth Differ. 4, 281-289, 1993  
 A:Title: Structure and DNA-binding properties of Pax-QNR, a paired box- and homeobox-con  
 A:Reference number: A56884; MUID:93264300; PMID:8096617  
 A:Accession: B56884  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <DOZ>  
 A:Cross-references: UNIPROT:007378; GB:X68169; MID:9311558; PIDN:CAA48271.1; PID:9311559  
 A:Experimental source: neuroretina cells  
 C:Keywords: alternative splicing; retina

Query Match 27.2%; Score 22; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVLPEPP 12  
| | | |  
1 PTPVSSSF 8

Db

#### RESULT 12

PA0060  
protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C:Accession: PA0060

R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

Submitted to JFID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PA0051

A:Accession: PA0060

A:Molecule type: protein

A:Residues: 1-15 <CHO>

Query Match 27.2%; Score 22; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PVLPEPP 13  
| | | |  
1 PLRPLP 6

Db

#### RESULT 13

ES5503  
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)

N:Alternate names: 21.3K bladder and kidney stone protein

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004

C:Accession: ES5503

R:Binette, J.P.; Binette, M.B.

Submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: AS5501

A:Accession: ES5503

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BIN>

A:Cross-references: UNIPROT:Q7M137

A:Experimental source: human bladder and kidney stones

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Keywords: metalloprotein; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPE 10  
| | | |  
5 LPPLPYR 11

Db

#### RESULT 14

A23992  
melanin-omochrome-stimulating hormone III - silkworm (fragment)

N:Alternate names: melanization and reddish coloration hormone III; MRCH III

C:Species: Bombyx mori (silkworm)

C:Date: 30-Jan-1988 #sequence\_revision 30-Jan-1988 #text\_change 09-Jul-2004

C:Accession: A23992

R:Matsumoto, S.; Isogai, A.; Suzuki, A.

FEBS Lett. 189, 115-118, 1985

A:Title: N-terminal amino acid sequence of an insect neurohormone, melanization and red

A:Reference number: A23992; PMID:85285612; PMID:3896851

A:Accession: A23992

A:Molecule type: protein

5

A:Residues: 1-16 <MAT>

A:Cross-references: UNIPROT:Q17211

C:Keywords: hormone

Query Match 27.2%; Score 22; DB 2; Length 16;

Best Local Similarity 37.5%; Pred. No. 1.7e+03;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMPVLPE 10  
| | | |  
5 DMFATPAD 12

Db

#### RESULT 15

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) - potato (frag

C:Species: Solanum tuberosum (potato)

C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S56715

R:Bhattacharyya, M.K.; Palva, N.L.; Dixon, R.A.; Korth, K.L.; Stermer, B.A.

Plant Mol. Biol. 28, 1-15, 1995

A:Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in potato.

A:Reference number: S56710; PMID:95306778; PMID:7787174

A:Accession: S56715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-18 <BNA>

A:Cross-references: UNIPROT:Q41458; EMBL:L34830; NID:9529524; PIDN:AAC37437.1; PID:95531

C:Superfamily: hydroxymethylglutaryl-CoA reductase (NADPH)

C:Keywords: coenzyme A; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;

Best Local Similarity 57.1%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLPEPP 11  
| | | |  
7 PVKPLYP 13

Db

#### RESULT 16

S29166  
quinoline oxidoreductase (EC 1.5.99.-) beta chain - Arthrobacter sp. (isolate Rue 61a)

C:Species: Arthrobacter sp.

A:Variety: isolate Rue 61a

C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

C:Accession: S29166

R:de Beyer, A.; Lingens, F.

Biol. Chem. Hoppe-Seyler 374, 101-110, 1993

A:Title: Microbial metabolism of quinoline and related compounds. XVI. Quinoline oxidoreductase.

A:Reference number: S29165; PMID:93228843; PMID:8471177

A:Accession: S29166

A:Molecule type: protein

A:Residues: 1-18 <BBY>

A:Experimental source: isolate Rue 61a

C:Complex: heterohexamer; two alpha, two beta and two gamma chains

A:Description: catalyzes the oxidation of quinoline to 1H-4-oxoquinoline

C:Pathway: quinoline degradation

C:Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;

Best Local Similarity 42.9%; Pred. No. 1.9e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 VEPPEPV 15  
| | | |  
2 MHPFOFI 8

Db

RESULT 17

S66419

S66419



tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)  
C:Species: Spinacia oleracea (spinach)  
C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S66419

R:Kuwabara, T.

FEBS Lett. 371, 195-198, 1995

A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spi  
A:Reference number: S66419; MWID:95402209; PMID:7672127

A:Accession: S66419

A:Molecule type: protein

A:Residues: 1-9 <KDW>

A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 9;  
Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLTP 8

DB 2 PVLTP 5

RESULT 18

PS0452

32K protein 3306 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995

C:Accession: PS0452

R:Tangita, A.; Miyatake, N.

submitted to JIPID, April 1993

A:Reference number: PS0208

A:Accession: PS0452

A:Molecule type: protein

A:Residues: 1-15 <TSU>

A:Experimental source: bran, strain Nihonbare

C:Comment: molecular weight 32K, pI 5.3.

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 15;  
Pred. No. 2.2e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PVPV 15

DB 6 PVPV 10

RESULT 19

S20410

protein kinase (BC 2.7.1.37) - spinach chloroplast (fragment)

N:Alternate names: LHCI protein kinase

C:Species: chloroplast Spinacia oleracea (spinach)

C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C:Accession: S20410

R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.

FEBS Lett. 298, 33-35, 1992

A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyto

A:Reference number: S20410; MWID:92183823; PMID:1544419

A:Accession: S20410

A:Molecule type: protein

A:Residues: 1-15 <GAL>

A:Cross-references: UNIPROT:Q9T2K8

A:Genome: chloroplast

C:Function:

A:Description: is responsible for the regulation of energy distribution between photosyn

A>Note: does not exhibit redox-controlled activation

C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 15;  
Pred. No. 2.2e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLTP 8

DB 2 PVLTP 5

RESULT 20

A20190

hypodermis B - early cattle grub (fragment)

C:Species: Hypoderma lineatum (early cattle grub)

C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004

C:Accession: A20190

R:Leclercq, A.; Tong, N.T.; Keil, B.

Eur. J. Biochem. 134, 261-267, 1983

A:Title: Hypodermis B, a trypsin-related enzyme from the insect Hypoderma lineatum.

A:Reference number: A20190; MWID:83261874; PMID:6307690

A:Accession: A20190

A:Molecule type: protein

A:Residues: 1-16 <LEC>

A:Cross-references: UNIPROT:P35588

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 16;  
Pred. No. 2.4e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VBPVP 14

DB 9 IEDFPW 14

RESULT 21

E23734

insulin-like growth factor-binding protein 3 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993

C:Accession: E23734

R:Shimazaki, S.; Gao, L.; Shimonaka, M.; Ling, N.

Mol. Endocrinol. 5, 938-948, 1991

A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6

A:Reference number: A23734; MWID:92049376; PMID:1719383

A:Accession: E23734

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <SHI>

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 17;  
Pred. No. 2.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVLTPVP 11

DB 9 PVLTPVP 11

RESULT 22

A49237

45/47K antigen - Mycobacterium bovis (fragment)

C:Species: Mycobacterium bovis

C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A49237

R:Romanin, F.; Laqueyrie, A.; Miltzer, P.; Pescher, P.; Chavaret, P.; Lagranderie, M.,

Infect. Immun. 61, 742-750, 1993

A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a

A:Reference number: A49237; MWID:93138802; PMID:8423100

A:Accession: A49237

A:Contents: BCG

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <ROM>

A:Cross-references: UNIPROT:P80069

Query Match

Best Local Similarity 25.9%; Score 21; DB 2; Length 17;  
Pred. No. 2.6e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PVLPEP 11  
DB 4 PAPVPP 10

## RESULT 23

A28060  
elastase inhibitor, leukocyte - horse (fragment)  
C/Species: Equus caballus (domestic horse)  
C/Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 09-Jul-2004  
C/Accession: A28060  
R/Potempa, J.; Dubin, A.; Marorek, W.; Travis, J.  
J. Biol. Chem. 263, 7364-7369, 1988  
A/Title: An elastase inhibitor from equine leukocyte cytosol belongs to the serpin super  
A/Reference number: A28060; MUID:88213423; PMID:3366785  
A/Accession: A28060  
A/Molecule type: protein  
A/Residues: 1-18 <POT>  
A/Cross-references: UNIPROT:P05619  
C/Superfamily: Serpin

Query Match 25.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 35.7%; Pred. No. 2.8e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 6 VLPEPP---PPV 15  
DB 4 LMPENFNADHPFI 17

## RESULT 24

I78841  
thrombopoietin receptor - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C/Accession: I78841  
R/Alexander, W.S.; Dunn, A.R.  
Oncogene 10, 795-803, 1995  
A/Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep  
A/Reference number: I58350; MUID:9516571; PMID:7662460  
A/Accession: I78841  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-18 <RMS>  
A/Cross-references: GB:S76842; NID:9912990; PIRN:AAB33462.1; PID:9912991  
C/Genetics:  
A/Genes: c-mpl

Query Match 25.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 PVEPPFPV 15  
DB 2 PHGPAPPL 9

## RESULT 25

A61049  
halo-toxin - Pseudomonas syringae pv. mori  
C/Species: Pseudomonas syringae pv. mori  
A/Note: host mulberry tree  
C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
C/Accession: A61049  
R/Kajimoto, T.; Yokonizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;  
Chem. Lett. 00, 679-680, 1989  
A/Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri  
A/Reference number: A61049  
A/Accession: A61049  
A/Molecule type: protein  
A/Residues: 1-6 <KAJ>  
A/Note: sequence confirmed by synthesis

C/Comment: This toxin is one of the etiological agents of halo bright disease in mulberry  
C/Keywords: toxin

Query Match 24.7%; Score 20; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13  
DB 1 PFP 3

## RESULT 26

S66635  
alpha-2-macroglobulin isoform 1 - bovine (fragment)  
C/Species: Bos primigenius indicus (zebu cattle)  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S66635  
R/Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottru  
FEBS Lett. 372, 93-95, 1995  
A/Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o  
A/Reference number: S66634; MUID:96032553; PMID:7556651  
A/Accession: S66635  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <DOL>  
A/Cross-references: UNIPROT:Q7M2N8

Query Match 24.7%; Score 20; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EPFP 14  
DB 2 DEFP 6

## RESULT 27

B59272  
peptide-N-(N-acetyl-beta-glucosaminyl) asparagine amidase (EC 3.5.1.52) A, small chain -  
N/Alternate names: peptide N-glycosidase  
C/Species: Prunus dulcis var. sativa (sweet almond)  
C/Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
C/Accession: B59272  
R/Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.  
Eur. J. Biochem. 252, 118-123, 1998  
A/Title: Characterisation of peptide-N-(N-acetyl-beta-glucosaminyl) asparagine amidase  
A/Reference number: B59272; MUID:98181894; PMID:9523720  
A/Accession: B59272  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <ALT>  
A/Cross-references: UNIPROT:P81898  
C/Keywords: hydrolase

Query Match 24.7%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PVEPP 13  
DB 4 PLHDFP 9

## RESULT 28

PA0028  
protein QA300042 - Arabidopsis thaliana (fragment)  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C/Accession: PA0028  
R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPED, July 1994  
A/Description: Separation and characterization of Arabidopsis proteins by two-dimension

A:Reference number: PA0001  
A:Accession: PA0028  
A:Molecule type: protein  
A:Residues: 1-11 <XAM>  
A:Experimental source: seed  
C:Keywords: seed

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 11;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13  
DB 6 PFP 8

RESULT 29  
PN0042  
stathmin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 09-Jul-2004  
C:Accession: PN0042  
R:Kato, H.  
Kawasaki Igakkaishi 22, 245-259, 1996  
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neur  
A:Reference number: PN0041  
A:Accession: PN0042  
A:Molecule type: protein  
A:Residues: 1-11 <KAT>  
A:Cross-references: UNIPROT:Q9DCP3; UNIPROT:Q91XT3  
A:Experimental source: neuroblastoma cell  
C:Comment: The molecular mass is 17,500 and the pI is 5.63. The amino-terminus is blocke  
C:Keywords: brain

Query Match  
Best Local Similarity 37.5%; Score 20; DB 2; Length 11;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MPVLPVFP 11  
DB 3 VPDPPLSP 10

RESULT 30  
B47415  
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)  
N:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 25-Feb-1994 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C:Accession: B47415  
R:Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.  
J. Biol. Chem. 268, 17943-17950, 1993  
A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and ucl  
A:Reference number: A47415; MUID:93352609; PMID:7688733  
A:Accession: B47415  
A:Molecule type: protein  
A:Residues: 1-13 <SZU>  
A:Experimental source: liver  
C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.  
C:Function:  
A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP  
A>Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac  
C:Keywords: blocked amino end, nucleotidyltransferase

Query Match  
Best Local Similarity 60.0%; Score 20; DB 2; Length 13;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PFPV 15  
DB 8 PFPPL 12

RESULT 31  
S21152  
tryptophyllin-related peptide - two-colored leaf frog  
C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004  
C:Accession: S21152  
R:Mignogna, G.; Severini, C.; Sismaco, M.; Negri, L.; Falconieri Brspamer, G.; Krell, G  
FEBS Lett. 302, 151-154, 1992  
A:Title: Identification and characterization of two dermorphins from skin extracts of ti  
A:Reference number: S21152; MUID:92339502; PMID:1633846  
A:Accession: S21152  
A:Molecule type: protein  
A:Residues: 1-13 <MIG>  
A:Cross-references: UNIPROT:Q7LZ51  
A:Experimental source: skin

Query Match  
Best Local Similarity 60.0%; Score 20; DB 2; Length 13;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVPV 9  
DB 9 PVPV 13

RESULT 32  
H64008  
hypothetical protein H10492 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
C:Accession: H64008  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, .  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, .  
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: H64008  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-14 <TIGR>  
A:Cross-references: GB:U32731; GB:I42023; NID:G1573465; PID:G1573478; TIGR:H10492

Query Match  
Best Local Similarity 42.9%; Score 20; DB 2; Length 14;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVPVFP 11  
DB 6 PKMPKPK 12

RESULT 33  
PA0024  
protein QA300050 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0024  
R:Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimension  
A:Reference number: PA0001  
A:Accession: PA0024  
A:Molecule type: protein  
A:Residues: 1-15 <XAM>  
A:Experimental source: seed

Query Match  
Best Local Similarity 100.0%; Score 20; DB 2; Length 15;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13

Db 6 PFP 8

## RESULT 34

A49761

A:Experimental source: migratory locust

C:Species: locusta migratoria (migratory locust)

C&gt;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C/Accession: A49761

R/Schoof, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.

Gen. Comp. Endocrinol. 81, 97-104, 1991

A&gt;Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide

A/Reference number: A49761; PMID:91224474; PMID:2026322

A/Accession: A49761

A/Molecule type: protein

A/Residues: 1-16 &lt;SCH&gt;

A/Cross-references: UNIPROT:P20404

C/Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut as

C/Superfamily: pyrokinin

C/Keywords: amidated carboxyl end, neuropeptide; pyroglutamic acid

F1/Modified site: pyroglutamic acid (Gln) #status experimental

F16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 24.7%; Score 20; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PVPF 12  
Db 8 PQPF 12

## RESULT 35

A60551

A:leukocyte elastase (EC 3.4.21.37) - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C&gt;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C/Accession: A60551

R/Axelsson, L.; Bergentfeldt, M.; Björk, P.; Olsson, R.; Ohlsson, K.

Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A&gt;Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin A

A/Reference number: A60551; PMID:90193608; PMID:1690443

A/Accession: A60551

A/Molecule type: protein

A/Residues: 1-16 &lt;AXB&gt;

A/Cross-references: UNIPROT:Q8MJD1

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 24.7%; Score 20; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 8 PVPF--PPVF 15  
Db 6 PQPFHMPF 15

## RESULT 36

A42576

A:steroid receptor complex Hsp56 60K component - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C&gt;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998

C/Accession: A42576

R/Yam, A.W.; Tomaselli, A.G.; Heinrichson, R.L.; Zürcher-Neely, H.; Ruff, V.A.; Johnson, J.

J. Biol. Chem. 267, 2868-2871, 1992

A&gt;Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 an

A/Reference number: A42576; PMID:92147620; PMID:1371107

A/Accession: A42576

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 &lt;YEM&gt;

A:Experimental source: thymus  
A>Note: sequence extracted from NCBI backbone (NCBIP:80696)  
C:Superfamily: human FK506-binding protein FKBP51; BKB-type peptidylprolyl isomerase ho  
C/Keywords: steroid hormone receptor

Query Match 24.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 4e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 VLPVPPFP 14  
Db 9 VPEVBLFER 17

## RESULT 37

I52614

A:plasma/ogen activator receptor precursor - human (fragment)

C/Species: Homo sapiens (man)

C&gt;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004

C/Accession: I52614

R/Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

Blood 86, 624-635, 1995

A&gt;Title: A conserved XRTA-less proximal promoter drives basal transcription from the ur

A/Reference number: I52614; PMID:95329719; PMID:7605992

A/Accession: I52614

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-18 &lt;RES&gt;

A/Cross-references: UNIPROT:Q03405; GB:878532; NID:g999207; PIDN:AAD14289.1; PID:g42619f

A/Genes: UPAR

C/Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 24.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 4e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVPV 9  
Db 5 PVLPL 9

## RESULT 38

A28027

A:protein P2 - curled-leaved tobacco (fragment)

C/Species: Nicotiana glauca (curled-leaved tobacco)

C&gt;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C/Accession: A28027

R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A&gt;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid

A/Reference number: A94167

A/Accession: A28027

A/Molecule type: protein

A/Residues: 1-18 &lt;BAU&gt;

A/Note: 14-Arg was also found

Query Match 24.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 4e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 VLPVFP 11  
Db 8 IVPLAP 13

## RESULT 39

A40760

A:basic fibroblast growth factor, long form - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C&gt;Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 09-Jul-2004

C/Accession: A40760

R/Nice, E.C.; Fabri, L.; Whitehead, R.H.; James, R.; Simpson, R.J.; Burgess, A.W.

J. Biol. Chem. 266, 14425-14430, 1991  
A:Title: The major colonic cell mitogen extractable from colonic mucosa is an N terminal  
A:Reference number: A40760; MUID:91317799; PMID:1860849  
A:Accession: A40760  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <NTC>  
A:Cross-references: UNIPROT:Q7M2P3

Query Match 24.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLP 8  
: |||  
Db 14 LPALP 18

## RESULT 40

B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Daespyrum villosum  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: B61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
A:Reference number: A61218; MUID:91315394; PMID:1859356  
A:Accession: B61218  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHB>  
A:Cross-references: UNIPROT:Q7M1F6  
C:Keywords: seed; storage protein

Query Match 23.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 30.0%; Pred. No. 3e+03;  
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMPVLPVPE 11  
: |||::|  
Db 1 VRVPVQLQP 10

Search completed: June 7, 2005, 23:20:40  
Job time : 14.9091 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-5

Perfect score: 81  
Sequence: 1 DLEMPYLVEPPFPV 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	33.3	17	2 Q7MI13	Q7MI13 phaseolus v
2	27	33.3	18	2 Q9NSFO	Q9NSFO homo sapien
3	26	32.1	8	2 Q9TRX8	Q9TRX8 bos taurus
4	26	32.1	18	2 Q56610	Q56610 vibrio chol
5	25	30.9	9	2 Q9PE85	Q9PE85 kluyveromyc
6	25	30.9	12	2 Q83139	Q83139 barley stri
7	25	30.9	15	1 UC17_MAIZE	P80623 zea mays (m
8	24	29.6	8	1 NGIF_RAT	P82598 rattus norv
9	24	29.6	15	2 Q7MI05	Q7MI05 oryza sativ
10	24	29.6	16	2 Q64K00	Q64K00 sporophila
11	24	29.6	17	2 Q9TRH5	Q9TRH5 bos taurus
12	24	29.6	17	2 Q8X4A4	Q8X4A4 escherichia
13	23	28.4	12	1 TM2A_METMA	P80652 methanosarc
14	23	28.4	13	1 SODM_ARTDA	P83289 arthropoxy
15	23	28.4	13	2 Q69GDT	Q69GDT pleospora t
16	23	28.4	15	1 SODM_ENTAB	P22799 enterobacte
17	23	28.4	15	2 Q69EFJ1	Q69EFJ1 stemphylium
18	23	28.4	15	2 Q69EFJ3	Q69EFJ3 stemphylium
19	23	28.4	15	2 Q69GAI1	Q69GAI1 stemphylium
20	23	28.4	15	2 Q69GB9	Q69GB9 pleospora g
21	23	28.4	15	2 Q69GDI1	Q69GDI1 stemphylium
22	23	28.4	15	2 Q9TMO1	Q9TMO1 mus sp. bet
23	23	28.4	15	2 Q64KG2	Q64KG2 sporophila
24	23	28.4	16	2 Q69G98	Q69G98 pleospora s
25	23	28.4	16	2 Q69GB3	Q69GB3 pleospora e
26	23	28.4	16	2 Q69GB0	Q69GB0 pleospora t
27	23	28.4	16	2 Q69GCS	Q69GCS pleospora s
28	23	28.4	16	2 Q69GCS	Q69GCS stemphylium
29	23	28.4	16	2 Q69GCS	Q69GCS stemphylium
30	23	28.4	16	2 Q69GCS	Q69GCS pleospora g
31	23	28.4	16	2 Q64KB4	Q64KB4 volatintia j

32	23	28.4	16	2 Q64KB8	Q64KB8 sporophila
33	23	28.4	16	2 Q64KC6	Q64KC6 sporophila
34	23	28.4	16	2 Q64KD0	Q64KD0 sporophila
35	23	28.4	16	2 Q64KD2	Q64KD2 sporophila
36	23	28.4	16	2 Q64KD8	Q64KD8 sporophila
37	23	28.4	16	2 Q64KE0	Q64KE0 sporophila
38	23	28.4	16	2 Q64KE2	Q64KE2 sporophila
39	23	28.4	16	2 Q64KE4	Q64KE4 sporophila
40	23	28.4	16	2 Q64KE8	Q64KE8 sporophila
41	23	28.4	16	2 Q64KE2	Q64KE2 sporophila
42	23	28.4	16	2 Q64KE6	Q64KE6 sporophila
43	23	28.4	16	2 Q64KE8	Q64KE8 sporophila
44	23	28.4	16	2 Q64KG0	Q64KG0 sporophila
45	23	28.4	16	2 Q64KG6	Q64KG6 sporophila
46	23	28.4	16	2 Q64KH0	Q64KH0 sporophila
47	23	28.4	16	2 Q64KH4	Q64KH4 sporophila
48	23	28.4	16	2 Q64KH6	Q64KH6 pleospora s
49	23	28.4	17	2 Q69GAI4	Q69GAI4 pleospora p
50	23	28.4	17	2 Q69GAI7	Q69GAI7 stemphylium
51	23	28.4	17	2 Q69GB6	Q69GB6 stemphylium
52	23	28.4	17	2 Q9UC43	Q9UC43 homo sapien
53	23	28.4	17	2 Q8OX06	Q8OX06 mus sp. abd
54	23	28.4	18	2 Q9BRH2	Q9BRH2 homo sapien
55	23	28.4	18	2 Q8CJD4	Q8CJD4 rattus norv
56	22.5	27.8	11	2 Q48933	Q48933 mycobacteri
57	22.5	27.8	11	2 Q79C20	Q79C20 mycobacteri
58	22.5	27.8	11	2 Q79C22	Q79C22 mycobacteri
59	22.5	27.8	17	1 YX35_YEAST	P36530 saccharomyc
60	22	27.2	9	2 P83157	P83157 anabaena sp
61	22	27.2	10	2 Q6A3T8	Q6A3T8 archanglopt
62	22	27.2	10	2 Q9QVJ5	Q9QVJ5 rattus sp.
63	22	27.2	10	2 Q9QVJ6	Q9QVJ6 rattus sp.
64	22	27.2	11	2 Q7M0K6	Q7M0K6 streptomyce
65	22	27.2	12	2 P82441	P82441 nicotiana t
66	22	27.2	13	2 Q6GVJ5	Q6GVJ5 burkholderi
67	22	27.2	14	2 P82326	P82326 pismum sativ
68	22	27.2	14	2 Q07378	Q07378 coturnix co
69	22	27.2	15	2 Q68CX4	Q68CX4 homo sapien
70	22	27.2	15	2 Q9HCX8	Q9HCX8 homo sapien
71	22	27.2	15	2 Q6UTP9	Q6UTP9 dimerostemm
72	22	27.2	15	2 Q71H02	Q71H02 andrena inc
73	22	27.2	15	2 P83076	P83076 bacillus ce
74	22	27.2	15	2 Q6LEB7	Q6LEB7 rattus norv
75	22	27.2	16	2 Q00497	Q00497 homo sapien
76	22	27.2	16	2 Q77489	Q77489 tupia glis
77	22	27.2	16	2 Q9T0Y6	Q9T0Y6 cycloclagus
78	22	27.2	16	2 Q8407	Q8407 bacteriophag
79	22	27.2	16	2 Q6QVE1	Q6QVE1 phaseolus v
80	22	27.2	16	2 Q7M137	Q7M137 unidentified
81	22	27.2	16	2 Q9MMG6	Q9MMG6 sigma virus
82	22	27.2	17	2 Q9TRU8	Q9TRU8 bos taurus
83	22	27.2	18	2 Q9UCF9	Q9UCF9 homo sapien
84	22	27.2	18	2 Q41458	Q41458 solanum tub
85	22	27.2	18	2 Q9R5B0	Q9R5B0 arthropacte
86	21	25.9	8	2 Q6R408	Q6R408 bubalus bub
87	21	25.9	9	2 Q9UMF3	Q9UMF3 homo sapien
88	21	25.9	9	2 Q9TRV0	Q9TRV0 antrophleura
89	21	25.9	10	1 PAK6_PANRE	P82360 panagrellus
90	21	25.9	11	1 PVK3_BIACR	P83633 blaberus cr
91	21	25.9	11	1 PVK3_BIADU	P83334 blaptica du
92	21	25.9	11	1 PVK3_GROPO	P83335 giromphadori
93	21	25.9	11	1 PVK3_LETMA	P83331 leucophaea
94	21	25.9	11	1 PVK3_NAUCI	P83332 nauphoeta c
95	21	25.9	13	1 YP82_LACLC	P42021 lactococcus
96	21	25.9	14	2 Q71GK8	Q71GK8 andrena iml
97	21	25.9	14	2 Q85527	Q85527 chlamydia t
98	21	25.9	14	2 Q71IZ6	Q71IZ6 lactobacilli
99	21	25.9	14	2 Q9ZB42	Q9ZB42 streptococc
100	21	25.9	15	1 UC25_MAIZE	P80631 zea mays (m

## ALIGNMENTS

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RESULT 1
Q7MI13 PRELIMINARY; PRT; 17 AA.
AC 07MI13;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OC NCBI_TaxID=3885;
RN [1]
RP SEQUENCE.
RX MEDLINE=96011753; PubMed=7548825;
RA Wojtaszek P., Trethowan J., Bolwell G.P.;
RT "Specificity in the immobilisation of cell wall proteins in response
RT to different elicitor molecules in suspension-cultured cells of French
RT bean (Phaseolus vulgaris L.).";
RL Plant Mol. Biol. 28:1075-1087(1995).
DR PIR; S59481; S59481.
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE55 CRC64;

Query Match 33.3%; Score 27; DB 2; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLEMPVLPVPPV 15
DB 1 DMYLP--PVPPPPV 13

RESULT 2
Q9NSF0 PRELIMINARY; PRT; 18 AA.
AC Q9NSF0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MESPI (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Aultay C., Ansoorge W., Ballbio A., Ectivill X., Gibson K.,
RA Lehrach H., Pouscka A., Lundberg J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Carim L., Ectivill X., Escarceller M., Sunoy L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALJ57535; CAB93427.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 2196 MW; 0ACBE7DA3E2849F0 CRC64;

Query Match 33.3%; Score 27; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MPVLPVPPV 13
DB 5 MPVLPVPPV 14

RESULT 3
Q9TRX8 PRELIMINARY; PRT; 8 AA.
ID Q9TRX8

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AC Q9TRX8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovine; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Krumdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF7632D767 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LPVPPV 14
DB 1 LPVKPKXF 8

RESULT 4
Q56610 PRELIMINARY; PRT; 18 AA.
AC Q56610;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE Acca (Fragment).
GN Name=acca;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6706;
RX MEDLINE=97074686; PubMed=8917113; DOI=10.1016/0378-1119(96)00155-2;
RA Franco A., Peir-Eu Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from Vibrio cholerae strain
RT C6706.";
RL Gene 175:281-283 (1996).
DR EMBL; U30472; AAC44579.1; -.
FT NON_TER 18 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2154 MW; 18BECAD212842EF CRC64;

Query Match 32.1%; Score 26; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLEMPVLPV 10
DB 7 DFEKPIVELE 16

RESULT 5
Q9P8E5 PRELIMINARY; PRT; 9 AA.
ID Q9P8E5
AC Q9P8E5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

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DE HIS4 protein (Fragment).  
 GN Name=HIS4;  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=NRRL-Y1140;  
 RX MEDLINE=99448382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;  
 RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;  
 RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities  
 and differences to Saccharomyces cerevisiae HIS4 gene."  
 RL FEBS Lett. 458:72-76(1999).  
 DR EMBL; AJ238494; CAB87125.1; -  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;  
 Query Match 30.9%; Score 25; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVLPV 9  
 Db 2 LPVVPV 7  
 RESULT 6  
 OS8139 PRELIMINARY; PRT; 12 AA.  
 ID Q83139  
 AC Q83139;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (strain CV17) genomic RNA-gamma, 5' leader.  
 OS Barley stripe mosaic virus (BSMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.  
 OX NCBI\_TaxID=12327;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV17;  
 RX MEDLINE=91062385; PubMed=2247462;  
 RA Perty I.T., Edwards M.C., Jackson A.O.;  
 RT "Systemic movement of an RNA plant virus determined by a point  
 substitution in a 5' leader sequence."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897(1990).  
 DR EMBL; M38633; AAA75527.1; -  
 SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;  
 Query Match 30.9%; Score 25; DB 2; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 MPVLPV 12  
 Db 4 MPVLPV 12  
 RESULT 7  
 UC17\_MAIZE STANDARD; PRT; 15 AA.  
 ID UC17\_MAIZE  
 AC P80623;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 32)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACMAD clade; Panicoideae; Andropogonae; Zea.  
 OX NCBI\_TaxID=45777;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program."  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.5, its MW is: 42.7 kDa.  
 DR MaizeDB; 123949; -  
 DR MaizeDB; P80623; COLEOPTILE.  
 KW Direct protein sequencing.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1554 MW; COAFPI5FECEB8 CRC64;  
 Query Match 30.9%; Score 25; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEMPVLPV 11  
 Db 2 LSVFPAVAP 11  
 RESULT 8  
 NGIF\_RAT  
 ID NGIF\_RAT STANDARD; PRT; 8 AA.  
 AC P82598;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Non-arginase growth inhibitory factor (NGIF) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE, AND FUNCTION.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=20198203; PubMed=10731662;  
 RA Kim K.-Y., Choi I., Kim S.-S.;  
 RT "Purification and characterization of a novel inhibitor of the  
 RT proliferation and hepatic stellate cells."  
 RL J. Biochem. 127:23-27(2000).  
 CC -1- FUNCTION: Inhibitor of the proliferation of hepatic stellate cells  
 CC (HSC). Also inhibits the growth of bovine endothelial cells and  
 CC 3T6 fibroblasts.  
 CC Direct protein sequencing.  
 KW Direct protein sequencing.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76BID CRC64;  
 Query Match 29.6%; Score 24; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPVP 12  
 Db 3 PVEPVP 7  
 RESULT 9  
 Q7MIUS PRELIMINARY; PRT; 15 AA.  
 ID Q7MIUS  
 AC Q7MIUS;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE "Superoxide dismutase (EC 1.15.1.1) (Mn) (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.

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OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Tsugita A.; Submitted (APR-1993) to the PIR data bank.
RL PIR; PS0455; PS0455.
DR GO; GO:0004784; F:superoxide dismutase activity; IRA.
FT NON TER 1 1
FT SEQUENCE 15 AA; 1561 MW; 0596471D6F3DBEAE CRC64;
SQ
Query Match 29.6%; Score 24; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 MPVLVPE 10
DB 6 LPLLPYD 12

RESULT 10
Q64KC0 PRELIMINARY; PRT; 16 AA.
AC Q64KC0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Atpase subunit 8 (Fragment).
GN Name=Atp8;
OS Sporophylla telasco (chestnut-throated seedeater).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidae;
OC Fringillidae; Emberizinae; Sporophilla.
OX NCBI_TaxID=256699;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Lougheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophylla
RT (Aves: Passeriformes).";
RT Mol. Phylogenet. Evol. 0:0-0(2004).
RW EMBL; AY387478; AAR26793.1; -.
KM Mitochondrion.
FT NON TER 16
FT SEQUENCE 16 AA; 1902 MW; 0ADD11A3861D77C CRC64;
SQ
Query Match 29.6%; Score 24; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 5.3e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLVPEPPFV 15
DB 1 MPQINPFWLFI 12

RESULT 11
Q9TRH5 PRELIMINARY; PRT; 17 AA.
AC Q9TRH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-S1-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=3231344; PubMed=1299613; DOI=10.1016/0014-5793(92)80664-3;
RA Neuteboom B., Gufferida M.G., Conti A.;

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RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes.";
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;
Query Match 29.6%; Score 24; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 5.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 VEPFPPV 15
DB 2 VAPFPEV 8

RESULT 12
Q8X4A4 PRELIMINARY; PRT; 17 AA.
AC Q8X4A4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Z4331 protein.
GN OrderedLocusNames=Z4331;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca U., Antantharaman I.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RW EMBL; AE005528; AAG58115.1; -.
DR PIR; G85956; G85956.
KM Complete proteome.
FT SEQUENCE 17 AA; 1823 MW; 5A1C41BC7BF69D69 CRC64;
SQ
Query Match 29.6%; Score 24; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEPFP 13
DB 4 VSPFP 8

RESULT 13
TW2A METWA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (NS-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobialia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goe1 / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Ilendard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RA "Sodium ion translocation by NS-methyltetrahydromethanopterin";

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RT coenzyme M methyltransferase from Methanosarcina mazei G01  
 RT reconstituted in ether lipid liposomes."  
 RL Bur. J. Biochem. 239:857-864(1996).  
 CC -1- FUNCTION: This enzyme complex catalyzes an intermediate step in  
 CC methanogenesis, the formation of methyl-coenzyme M and  
 CC tetrahydromethanopterin from coenzyme M and N5-methyl-  
 CC tetrahydromethanopterin.  
 CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
 CC (methylthio)ethanesulfonate.  
 CC -1- SUBUNIT: Composed of six different subunits.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 KM Direct protein sequencing; Methanogenesis; Methyltransferase;  
 KM transferase; Transmembrane.  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A576623D76B CRC64;

Query Match 28.4%; Score 23; DB 1; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 5.7e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVP 9  
 |||:  
 Db 6 PVLPL 10

RESULT 14  
 SODM\_ARTDA STANDARD; PRT; 13 AA.  
 AC P83289;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1) (Fragment).  
 OS Archaeobacter dactyloides (Nematode-trapping fungus).  
 OC Bacteria; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;  
 OC Orbiliales; Orbiliaceae; mitosporic Orbiliaceae; Archaeobacterys.  
 OX NCBI\_TaxId=74499;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=072;  
 RA Zhao M., Zhang K.;  
 RL Submitted (FEB-2002) to Swiss-Prot.  
 CC -1- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems.  
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -1- COFACTOR: Binds 1 manganese or iron ion per subunit (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
 CC family.  
 DR InterPro: IPR001189; SODismutase.  
 DR PROSITE: PS00088; SOD\_MN; PARTIAL.  
 KM Direct protein sequencing; Iron; Manganese; Metal-binding;  
 KM Oxidoreductase.  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1515 MW; 699492028642672B CRC64;

Query Match 28.4%; Score 23; DB 1; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLP 8  
 |:|:  
 Db 3 ELPELP 8

RESULT 15  
 ID 069GD7 PRELIMINARY; PRT; 13 AA.  
 AC 069GD7;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE Hypothetical protein (Fragment).  
 OS Pleospora trichoclinalcola.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; Pleospora.  
 OX NCBI\_TaxId=183473;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EGS 36-118.  
 RA Underhitzin P., Berbee M.L.;

RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stemphylium."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY335167; AAR00945.1; -  
 KM Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 13 AA; 1345 MW; 6AD166DF073972CB CRC64;

Query Match 28.4%; Score 23; DB 2; Length 13;  
 Best Local Similarity 42.9%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7  
 |:|:  
 Db 4 DIEVPTI 10

RESULT 16  
 SODM\_ENTAB STANDARD; PRT; 15 AA.  
 AC P22799;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).  
 GN Name=SODA;  
 OS Enterobacter aerogenes (Enterobacter aerogenes).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 OX NCBI\_TaxId=548;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=91248479; PubMed=136858;  
 RA Kim S.W., Lee S.O., Lee T.H.;  
 RL "Purification and characterization of superoxide dismutase from  
 RT Aerobacter aerogenes."  
 RT Agric. Biol. Chem. 55:101-108(1991).  
 CC -1- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems.  
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
 CC family.  
 DR PIR: PNO615; PNO615.  
 DR InterPro: IPR001189; SODismutase.  
 DR Pfam: PR00081; Sod Fe N: 1.  
 DR PROSITE: PS00088; SOD\_MN; PARTIAL.  
 KM Direct protein sequencing; Iron; Metal-binding; Oxidoreductase.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1756 MW; 352F3D9492028642 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 7.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLP 8  
 |:|:  
 Db 3 ELPELP 8

RESULT 17  
 ID 069FJ1 PRELIMINARY; PRT; 15 AA.  
 AC 069FJ1;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

AC Q69FU1: 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stemphylium solani.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.  
 OX NCBI\_TaxID=110364;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EGS41-135;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stemphylium.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY339855; AAR04451.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1547 MW; 84F7BB8AD166DF45 CRC64;  
 Query Match 28.4%; Score 23; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DLEMPVL 7  
 ID 1:1:1:  
 DB 3 DIEVPTI 9

RESULT 18  
 ID Q69FU3: PRELIMINARY; PRT; 15 AA.  
 AC Q69FU3: 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stemphylium sarciniforme.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.  
 OX NCBI\_TaxID=119934;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EGS38-121;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stemphylium.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY339854; AAR04449.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;  
 Query Match 28.4%; Score 23; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DLEMPVL 7  
 ID 1:1:1:  
 DB 3 DIEVPTI 9

RESULT 19  
 ID Q69GA1: PRELIMINARY; PRT; 15 AA.  
 AC Q69GA1: 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stemphylium sp. EGS49-030.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.

OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.  
 OX NCBI\_TaxID=235041;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EGS 49-030;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stemphylium.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY335179; AAR00981.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1542 MW; 84EF0ABAD166DF45 CRC64;  
 Query Match 28.4%; Score 23; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DLEMPVL 7  
 ID 1:1:1:  
 DB 3 DIEVPTI 9

RESULT 20  
 ID Q69GB9: PRELIMINARY; PRT; 15 AA.  
 AC Q69GB9: 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Pleospora gracillariae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; Pleospora.  
 OX NCBI\_TaxID=91368;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EGS 37-073;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stemphylium.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY335173; AAR00963.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1512 MW; 84EF0ABAD166CF44 CRC64;  
 Query Match 28.4%; Score 23; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 7.2e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DLEMPVL 7  
 ID 1:1:1:  
 DB 3 DIEVPTI 9

RESULT 21  
 ID Q69GD1: PRELIMINARY; PRT; 15 AA.  
 AC Q69GD1: 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stemphylium sp. EGS08-174.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stemphylium.  
 OX NCBI\_TaxID=234989;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EGS 08-174;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of

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RT Stenophylum";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335169; AAR00951.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 15 AA; 1533 MW; 84EF1D8AD16DDF45 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
DB 3 DIEVPPT 9

RESULT 22
Q9TNO1 PRELIMINARY; PRT; 15 AA.
ID Q9TNO1;
AC Q9TNO1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta 2M-class I-binding PEPTIDE-MAJOR histocompatibility complex H-2Kb-specific molecule POORLY associated with beta 2-microglobulin (Fragment).
DS Mus sp.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=94240094; Pubmed=8183884;
RA Joyce S., Kuzushima K., Kepes G., Angeletti R.H., Nathenson S.G.;
RT "Characterization of an incompletely assembled major histocompatibility class I molecule (H-2Kb) associated with unusually long peptides: implications for antigen processing and presentation.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149 (1994).
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DLEMPVL 9
DB 5 LQLPVVKV 12

RESULT 23
Q64KG2 PRELIMINARY; PRT; 15 AA.
ID Q64KG2;
AC Q64KG2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
DS Name=ATP8;
OS Sporophila cinnamomea (chestnut seedeater).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256690;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0 (2004).
DR EMBL; AY387457; AAR26751.1; -.

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KW Mitochondrion.
FT NON TER 15
SQ SEQUENCE 15 AA; 1849 MW; 2D131A3861D99C5E CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 15;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPEVPFPFV 15
DB 1 MPQLNPWPFPF 12

RESULT 24
Q69G98 PRELIMINARY; PRT; 16 AA.
ID Q69G98;
AC Q69G98;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora sp. P327.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=234982;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=P327.
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stenophylum.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335180; AAR00984.1; -.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 16 AA; 1662 MW; 54D36D8AD16DDF07 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7
DB 4 DIEVPPT 10

RESULT 25
Q69GB0 PRELIMINARY; PRT; 16 AA.
ID Q69GB0;
AC Q69GB0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora etumuna.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=235069;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=EGS 29-099;
RA Inderbitzin P., Berbee M.L.;
RT "Mating type gene evolution in Pleospora, the sexual state of Stenophylum.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY335176; AAR00972.1; -.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 16
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD16DDF07 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DLEMPVL 7  
|:|:|:  
Db 4 DIEVPTI 10

## RESULT 26

QY 069GB3 PRELIMINARY; PRT; 16 AA.  
AC 069GB3;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)  
DE Hypothetical protein (Fragment).  
OS Pleospora tomatonis.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Pleospora.  
OX NCBI\_Taxid=235068;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EGS 29-089;  
RA Inderbitzin P., Berbee M.L.;  
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY335175; AAR00969.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD16DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7  
|:|:|:  
Db 4 DIEVPTI 10

## RESULT 27

QY 069GC2 PRELIMINARY; PRT; 16 AA.  
AC 069GC2;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)  
DE Hypothetical protein (Fragment).  
OS Pleospora sp. EGS37-067.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Pleospora.  
OX NCBI\_Taxid=234979;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EGS 37-067;  
RA Inderbitzin P., Berbee M.L.;  
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY335172; AAR00960.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD16DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7  
|:|:|:  
Db 4 DIEVPTI 10

## RESULT 28

QY 069GC5 PRELIMINARY; PRT; 16 AA.  
AC 069GC5;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)  
DE Hypothetical protein (Fragment).  
OS Stemphylium sp. EGS48-089.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Pleospora.  
OX NCBI\_Taxid=235021;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EGS 48-089;  
RA Inderbitzin P., Berbee M.L.;  
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY335171; AAR00957.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD16DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7  
|:|:|:  
Db 4 DIEVPTI 10

## RESULT 29

QY 069GC8 PRELIMINARY; PRT; 16 AA.  
AC 069GC8;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)  
DE Hypothetical protein (Fragment).  
OS Stemphylium sp. EGS48-074.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Pleospora.  
OX NCBI\_Taxid=235018;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EGS 48-074;  
RA Inderbitzin P., Berbee M.L.;  
RT "Mating type gene evolution in Pleospora, the sexual state of Stemphylium."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY335170; AAR00954.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD16DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLEMPVL 7  
|:|:|:  
Db 4 DIEVPTI 10

## RESULT 30

QY 069GD4 PRELIMINARY; PRT; 16 AA.  
AC 069GD4;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)  
DE Hypothetical protein (Fragment).

OS Pleospora gigaspora.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Pleospora.  
OX NCBI\_TaxID=235067;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=EGS 37-017;  
RT "Mating type gene evolution in Pleospora, the sexual state of  
Stemphylium."  
RL Submitted (Jul-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY331568; AAR00948.1; -.  
KW Hypothetical protein.  
FT NON TER  
SQ SEQUENCE 16 AA; 1641 MW; 54CF0ABAD166DF07 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLEMPVL 7  
| | | | |  
DB 4 DIEVPTI 10

## RESULT 31

OS 064KB4 PRELIMINARY; PRT; 16 AA.  
AC 064KB4;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE ATPase subunit 8 (Fragment).  
GN Name=ATP8;  
OS Volactinia jaccarina (blue-black grassquit).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;  
OC Fringillidae; Emberizinae; Volatilia.  
OX NCBI\_TaxID=135452;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lijlmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;  
RT "Molecular phylogenetics and diversification of the genus Sporophila  
(Aves: Passeriformes)."  
RL Mol. Phylogenet. Evol. 0:0-0 (2004).  
DR EMBL; AY387481; AAR26799.1; -.  
DR EMBL; AY387482; AAR26801.1; -.  
KW Mitochondrion.  
FT NON TER  
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 7.8e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15  
| | | | |  
DB 1 MPOLNPNPWFPI 12

## RESULT 32

OS 064KB8 PRELIMINARY; PRT; 16 AA.  
AC 064KB8;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE ATPase subunit 8 (Fragment).  
GN Name=ATP8;  
OS Sporophila zelichi (Narosky's seedeater).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;  
OC Fringillidae; Emberizinae; Sporophila.  
OX NCBI\_TaxID=256700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lijlmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;  
RT "Molecular phylogenetics and diversification of the genus Sporophila  
(Aves: Passeriformes)."  
RL Mol. Phylogenet. Evol. 0:0-0 (2004).  
DR EMBL; AY387479; AAR26799.1; -.  
DR EMBL; AY387480; AAR26797.1; -.  
KW Mitochondrion.  
FT NON TER  
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 7.8e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15  
| | | | |  
DB 1 MPOLNPNPWFPI 12

## RESULT 33

OS 064KC6 PRELIMINARY; PRT; 16 AA.  
AC 064KC6;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE ATPase subunit 8 (Fragment).  
GN Name=ATP8;  
OS Sporophila ruficollis (dark-throated seedeater).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;  
OC Fringillidae; Emberizinae; Sporophila.  
OX NCBI\_TaxID=200161;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lijlmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;  
RT "Molecular phylogenetics and diversification of the genus Sporophila  
(Aves: Passeriformes)."  
RL Mol. Phylogenet. Evol. 0:0-0 (2004).  
DR EMBL; AY387475; AAR26787.1; -.  
DR EMBL; AY387476; AAR26789.1; -.  
DR EMBL; AY387477; AAR26791.1; -.  
KW Mitochondrion.  
FT NON TER  
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match 28.4%; Score 23; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 7.8e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MPVLPEPPPPV 15  
| | | | |  
DB 1 MPOLNPNPWFPI 12

## RESULT 34

OS 064KD0 PRELIMINARY; PRT; 16 AA.  
AC 064KD0;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE ATPase subunit 8 (Fragment).  
GN Name=ATP8;  
OS Sporophila palustris (marsh seedeater).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256698;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijntmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387473; AAR26783.1; -.
DR EMBL; AY387474; AAR26785.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 35
O64KJ2 PRELIMINARY; PRT; 16 AA.
AC O64KJ2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila nigricollis (yellow-bellied seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=138930;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijntmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387472; AAR26781.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 36
O64KD8 PRELIMINARY; PRT; 16 AA.
AC O64KD8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila minuta (ruddy-breasted seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.

```

```

OX NCBI_TaxID=256697;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijntmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387469; AAR26775.1; -.
DR EMBL; AY387470; AAR26777.1; -.
DR EMBL; AY387471; AAR26779.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 37
O64KE0 PRELIMINARY; PRT; 16 AA.
AC O64KE0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila melanogaster (black-bellied seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256696;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijntmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387468; AAR26773.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match      28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 7.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPVEPPFPV 15
   ||| | | | | |
Db 1 MPQLNPNPWFPI 12

RESULT 38
O64KE2 PRELIMINARY; PRT; 16 AA.
AC O64KE2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila luctuosa (black-and-white seedeater).
OC Mitochondrion.
OC Archosauaria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OX NCBI_TaxID=256695;

```



```

RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387467; AAR26771.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPEVPPFPV 15
DB 1 MPQLNPWFPI 12

RESULT 39
O64KE4 PRELIMINARY; PRT; 16 AA.
AC O64KE4;
DC 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila leucoptera (white-bellied seedeater).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OC NCBI_Taxid=25694;
OX NCBI_Taxid=25694;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;
RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387466; AAR26769.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPEVPPFPV 15
DB 1 MPQLNPWFPI 12

RESULT 40
O64KE8 PRELIMINARY; PRT; 16 AA.
AC O64KE8;
DC 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE ATPase subunit 8 (Fragment).
GN Name=ATP8;
OS Sporophila hypoxantha (tawny-bellied seedeater).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Sporophila.
OC NCBI_Taxid=25693;
OX NCBI_Taxid=25693;
RN [1]
RP SEQUENCE FROM N.A.
RA Lijmaer D.A., Sharpe N.M.M., Tubaro P.L., Loughheed S.C.;

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RT "Molecular phylogenetics and diversification of the genus Sporophila
  (Aves: Passeriformes).";
RL Mol. Phylogenet. Evol. 0:0-0(2004).
DR EMBL; AY387464; AAR26765.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 16 AA; 1936 MW; 0ADD131A3861D99C CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 2; Length 16;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MPVLPEVPPFPV 15
DB 1 MPQLNPWFPI 12

Search completed: June 7, 2005, 23:18:59
Job time : 68 secs

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 59.2 Seconds

(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-6

Perfect score: 62

Sequence: 1 MPQNPYKLPQM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	4	AAE72505
2	62	100.0	11	4	AAE59311
3	62	100.0	11	4	AAE72251
4	62	100.0	11	4	AAE72537
5	62	100.0	11	5	AAO14582
6	62	100.0	11	5	AAE51041
7	62	100.0	11	5	AAE20233
8	62	100.0	11	8	ADN60300
9	62	100.0	11	8	ADN74387
10	62	100.0	12	4	AAE59342
11	60	48.4	8	2	AAE60468
12	30	48.4	11	2	AAE60461
13	30	48.4	11	2	AAE21944
14	30	48.4	11	2	AAE92718
15	30	48.4	11	7	AAE84651
16	29	46.8	15	5	AAW00884
17	29	46.8	15	5	AAE99000
18	29	46.8	15	5	AAE20383
19	29	46.8	15	5	AAE80878
20	29	46.8	15	6	AAE44016
21	28	45.2	7	2	AAE08887
22	28	45.2	9	2	AAE48162
23	28	45.2	9	7	ADK23699
24	28	45.2	10	7	ADK24080
25	28	45.2	10	7	ADK24948

26	26	45.2	11	2	AAE28392
27	27	45.2	12	3	AAE93148
28	28	45.2	12	4	AAE60026
29	28	45.2	12	4	AAE67753
30	28	45.2	12	6	AAE60819
31	28	45.2	12	6	AAE97049
32	28	45.2	12	6	AAE54416
33	28	45.2	12	7	AAE88861
34	28	45.2	12	8	AAE87494
35	28	45.2	12	8	AAE94363
36	28	45.2	14	4	AAE97397
37	28	45.2	15	2	AAE97958
38	28	45.2	18	2	AAE03529
39	28	45.2	18	2	AAE03529
40	28	45.2	18	2	AAE03529
41	28	45.2	18	4	AAE48367
42	28	45.2	18	4	AAE60901
43	28	45.2	18	5	AAE07299
44	28	45.2	18	5	AAE09233
45	28	45.2	18	6	AAE76153
46	28	45.2	18	7	ADT00396
47	27	43.5	6	2	AAE04274
48	27	43.5	8	5	AAE09499
49	27	43.5	10	4	AAE91451
50	27	43.5	11	2	AAE28445
51	27	43.5	11	2	AAE42649
52	27	43.5	11	4	AAE91409
53	27	43.5	11	5	AAE09496
54	27	43.5	12	7	AAE15279
55	27	43.5	12	7	AAE42837
56	27	43.5	15	2	AAE47036
57	27	43.5	15	2	AAE97957
58	27	43.5	17	7	AAE62371
59	26	41.9	8	8	ADK51384
60	26	41.9	8	8	ADK51385
61	26	41.9	9	5	ABE68026
62	26	41.9	9	6	ADK24181
63	26	41.9	9	7	ADK23602
64	26	41.9	9	8	ADK58442
65	26	41.9	9	8	ADK58441
66	26	41.9	9	8	ADK70435
67	26	41.9	9	8	ADK71135
68	26	41.9	9	8	ADK71658
69	26	41.9	9	8	ADK68309
70	26	41.9	9	8	ADK68675
71	26	41.9	9	8	ADK69717
72	26	41.9	9	8	ADK69360
73	26	41.9	9	8	ADK70358
74	26	41.9	9	8	ADK72110
75	26	41.9	9	8	ADK70083
76	26	41.9	9	8	ADK71948
77	26	41.9	9	8	ADK69011
78	26	41.9	9	8	ADK69637
79	26	41.9	9	8	ADK71923
80	26	41.9	10	2	AAE67100
81	26	41.9	10	2	AAE39992
82	26	41.9	10	8	ADK69538
83	26	41.9	10	8	ADK72778
84	26	41.9	10	8	ADK68849
85	26	41.9	10	8	ADK68481
86	26	41.9	10	8	ADK70256
87	26	41.9	10	8	ADK73198
88	26	41.9	10	8	ADK69834
89	26	41.9	10	8	ADK69188
90	26	41.9	10	8	ADK70609
91	26	41.9	10	8	ADK69200
92	26	41.9	10	8	ADK70607
93	26	41.9	10	8	ADK68495
94	26	41.9	10	8	ADK69889
95	26	41.9	10	8	ADK68845
96	26	41.9	10	8	ADK69124
97	26	41.9	10	8	ADK69544
98	26	41.9	10	8	ADK70538

99 26 41.9 10 8 ADQ70255 Cancer re  
100 26 41.9 10 8 ADQ69906 Cancer re

## ALIGNMENTS

## RESULT 1

AAB72505  
ID AAB72505 standard; peptide; 11 AA.

AC AAB72505;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #6.

KW Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR MPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostriin, its

PT constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostriin, or its constituent peptide (e.g. the present peptide), CC to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient

CC Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0;

QY 1 MPQNFYKLPQM 11

DB 1 MPQNFYKLPQM 11

RESULT 2  
AAB59311  
ID AAB59311 standard; peptide; 11 AA.

AC AAB59311;

DT 21-MAR-2001 (first entry)

DE Ewe colostriin peptide fragment A-2.

KW Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR MPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from colostriin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides found in ewe's colostriin. Colostriin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques

CC Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0;

QY 1 MPQNFYKLPQM 11

DB 1 MPQNFYKLPQM 11

## RESULT 3

AAB72251  
ID AAB72251 standard; peptide; 11 AA.

AC AAB72251;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 6.

KW Colostriin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological disorder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.

KW Synthetic.

OS WO20011937-A2.

PN 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI (REGG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostriatin as an immunological  
 PT regulator.  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostriatin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostriatin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 62; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 DB 1 MPQNFYKLPQM 11  
 RESULT 4  
 AAB72537  
 ID AAB72537 standard; peptide; 11 AA.  
 XX  
 AC AAB72537;  
 XX  
 DT 09-MAY-2001 (first entry)  
 DE Colostriatin peptide #6.  
 XX  
 DE Colostriatin peptide #6.  
 XX  
 KW Neuroprotective; neural cell differentiation regulator; colostriatin;  
 KM colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostriatin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostriatin and  
 CC colostriatin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostriatin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 DB 1 MPQNFYKLPQM 11  
 RESULT 5  
 AA014582  
 ID AA014582 standard; peptide; 11 AA.  
 XX  
 AC AA014582;  
 XX  
 DT 27-MAY-2002 (first entry)  
 DE Neural cell regulatory colostriatin peptide 6.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostriatin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 11 /note="Optional C-terminal amide"  
 FT  
 XX  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022777.  
 XX  
 PR 17-AUG-2000; 2000WO-US022777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostriatin, its constituent peptide and/or  
 PT analog..  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostriatin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostriatin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostriatin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 62; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 DB 1 MPQNFYKLPQM 11  
 RESULT 6  
 AAM51041

ID AAM51041 standard; peptide, 11 AA.  
XX  
AC AAM51041;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Colostriin constituent peptide.  
XX  
KW Colostriin; colostrum; immunomodulator; cardiovascular;  
KM blood cell regulator; cytokine inducer; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 11 /note="optional C-terminal amidation"  
FT  
FT  
PN WO200213849-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022775.  
XX  
PR 17-AUG-2000; 2000WO-US022775.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGS-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
DR WPI; 2002-269150/31.  
XX  
PT Modulation of blood cell proliferation in a patient involves use of blood  
PT cell regulator selected from colostriin, its constituent peptide and/or  
PT analog.  
XX  
XX Claim 1, Page 34; 54pp; English.  
XX  
XX The present sequence is that of a colostriin constituent peptide that is  
CC preferred for use as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. Methods are claimed for:  
CC inducing a cytokine in a cell by contact with an immunological regulator,  
CC where the cell is present in a cell culture, a tissue, an organ or an  
CC organism, and the cell is mammalian, including human; modulating an  
CC immune response in a cell by contact with the immunological regulator  
CC under conditions effective to induce a cytokine; modulating an immune  
CC response in a patient by administering an immunological regulator under  
CC conditions effective to induce a cytokine, where the immunological  
CC regulator is administered topically or as part of a dietary supplement,  
CC and where the immune response is specific or non specific, an interferon  
CC response or an antibody response; modulating blood cell proliferation by  
CC contacting blood cells with a blood cell regulator, where the blood cells  
CC are present in a cell culture or an organism, are mammalian or human, and  
CC where the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patient. A claimed  
CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
CC active agent such as the present peptide. Cytokines induced by this  
CC peptide in human leucocyte cultures include interferon-gamma, tumour  
CC necrosis factor-alpha, interleukin-6 and interleukin-10  
XX  
SQ Sequence 11 AA:  
Query Match 100.0%; Score 62; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPQM 11  
| | | | | | | | | |  
DB 1 MPONFYKLPQM 11

RESULT 7  
AAE20233

ID AAE20233 standard; peptide, 11 AA.  
XX  
AC AAE20233;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Colostriin constituent peptide #6.  
XX  
KW Blood cell regulator; colostriin; constituent peptide; oxidative stress;  
KM therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.  
XX  
XX Unidentified.  
XX  
OS  
FH Key Location/Qualifiers  
FT Modified-site 11 /note="Optionally C-terminal amide"  
FT  
FT  
PN WO200213850-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022776.  
XX  
PR 17-AUG-2000; 2000WO-US022776.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2002-269151/31.  
XX  
PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostriin, its  
PT constituent peptide and/or analog.  
XX  
XX Claim 6, Page 25; 51pp; English.  
XX  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostriin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress level  
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
CC organ, or organism; or for treating oxidative damage to the skin of a  
CC patient e.g. animal or human; to modulate oxidative stress during/ after  
CC a premature birth or normal birth, preventing/delaying aging in a  
CC patient; enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostriin constituent peptide  
XX  
SQ Sequence 11 AA:  
Query Match 100.0%; Score 62; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPQM 11  
| | | | | | | | | |  
DB 1 MPONFYKLPQM 11

RESULT 8  
ADN60300  
ID ADN60300 standard; peptide, 11 AA.  
XX

AC ADN60300;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Constituent peptide of colostrinin SEQ ID NO:6.  
 XX  
 KW modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
 KW DNA damage; beta-amyloid; retinoic acid; cytoskeletal; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037851-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033423.  
 XX  
 PR 22-OCT-2002; 2002US-0420369P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (BOLD/) BOLDOGH I.  
 PA (STAN/) STANTON J G.  
 PA (GEOR/) GEORGIADIS J A.  
 PA (HUGH/) HUGHES T K.  
 PA (KRUIZ/) KRUIZEL M.  
 XX  
 PI Bolldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruizel M;  
 XX  
 DR MPI; 2004-365494/34.  
 XX  
 PT Use of colostrinin for e.g. modulating an intracellular signaling  
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 PT a cell.  
 XX  
 PS Claim 6; SEQ ID NO 6; 46pp; English.  
 PS  
 CC The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytoskeletal activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 XX  
 SQ Sequence 11 AA;  
 XX

Query Match 100.0%; Score 62; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11  
 |||||  
 DB 1 MPONFYKLPOM 11

RESULT 9  
 ADS74387  
 ID ADS74387 standard; peptide; 11 AA.  
 XX

AC ADS74387;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Ovine colostrinin peptide.  
 XX  
 KW Colostrum; colostrinin; sheep; peptide purification.  
 XX  
 OS Ovis aries.  
 XX  
 PN WO2004081038-A1.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 10-MAR-2004; 2004WO-GB001014.  
 XX  
 PR 11-MAR-2003; 2003GB-00005552.  
 PR 08-MAR-2004; 2004GB-00005190.  
 XX  
 PA (REGE-), REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA, Polanowski A, Wilusz T, Kruizel M;  
 XX  
 DR MPI; 2004-677519/66.  
 XX  
 PT Recovering peptides such as colostrinin from mammalian colostrum, by  
 PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 PT and precipitate, separating alcohol phase from precipitate, and  
 PT recovering alcohol phase.  
 XX  
 PS Disclosure; SEQ ID NO 2; 41pp; English.  
 PS  
 CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrum using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.  
 XX  
 SQ Sequence 11 AA;  
 XX

Query Match 100.0%; Score 62; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11  
 |||||  
 DB 1 MPONFYKLPOM 11

RESULT 10  
 AAB59342  
 ID AAB59342 standard; peptide; 12 AA.  
 XX  
 AC AAB59342;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment derived sequence #2.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX

XX Ovis sp.  
 OS WO200075173-A2.  
 XX  
 PN 14-DEC-2000.  
 XX  
 PD 02-JUN-2000; 2000WO-GB002128.  
 XX  
 PF 02-JUN-2000; 2000WO-GB002128.  
 XX  
 PR 02-JUN-1999; 99GB-00012852.  
 XX  
 PA (REGS-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 PS Claim 8; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX  
 SQ Sequence 12 AA;  
 Query Match 100.0%; Score 62; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPONFYKLPOM 11  
 Db 2 MPONFYKLPOM 12  
 RESULT 11  
 AAR60468  
 ID AAR60468 standard; peptide; 8 AA.  
 XX  
 AC AAR60468;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-MAR-1995 (first entry)  
 XX  
 DE Antiproliferative peptide to transplantable human B-cell lymphoma.  
 KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;  
 KW inhibit clonal expansion; induce apoptosis; anti-idiotype; IgM lambda;  
 KW inhibit cell proliferation; peptidomimetics; cell surface receptor;  
 KW immunoglobulin superfamily; treatment; neoplasia; identification;  
 KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9418345-A1.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PF 04-FEB-1994; 94WO-US001319.  
 XX  
 PR 05-FEB-1993; 93US-00014426.  
 PR 15-NOV-1993; 93US-00153341.  
 XX  
 PA (AFY-) AFFYMAX TECHNOLOGIES NV.  
 XX

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 XX Renschler MF, Levy R, Bhatt RR, Dower WJ;  
 XX WPI; 1994-279762/34.  
 XX  
 DR Identifying anti-proliferative peptide(s) which specifically bind to  
 PT immunoglobulin super-family species idiotype - esp. to inhibit B-cell  
 PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotype  
 PT therapy.  
 XX  
 PS Claim 7; Page 45; 69pp; English.  
 XX  
 CC AAR60400-73 are peptide ligands which bind to purified IgM lambda  
 CC receptor of the human Burkitt's lymphoma cell line SUP-B8. Peptides  
 CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The  
 CC peptides were identified with the use of filamentous phage libraries  
 CC displaying random peptides. Corresponding synthetic peptides bound  
 CC specifically to this Ig receptor, and blocked the binding of an anti-  
 CC idiotype antibody. The ligands, when conjugated to form dimers or  
 CC tetramers, induced cell death by apoptosis in vitro at nanomolar  
 CC concentrations. This effect was associated with the specific stimulation  
 CC of intracellular protein tyrosine phosphorylation. The peptides of the  
 CC invention can be used individually, as complexes of cross-linked peptides  
 CC or can be conjugated to deliver toxins or radionuclides to neoplastic  
 CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 48.4%; Score 30; DB 2; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPONFYK 7  
 Db 1 MPEDFYR 7  
 RESULT 12  
 AAR60461  
 ID AAR60461 standard; peptide; 8 AA.  
 XX  
 AC AAR60461;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-MAR-1995 (first entry)  
 XX  
 DE Antiproliferative peptide to transplantable human B-cell lymphoma.  
 KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;  
 KW inhibit clonal expansion; induce apoptosis; anti-idiotype; IgM lambda;  
 KW inhibit cell proliferation; peptidomimetics; cell surface receptor;  
 KW immunoglobulin superfamily; treatment; neoplasia; identification;  
 KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9418345-A1.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PF 04-FEB-1994; 94WO-US001319.  
 XX  
 PR 05-FEB-1993; 93US-00014426.  
 PR 15-NOV-1993; 93US-00153341.  
 XX  
 PA (AFY-) AFFYMAX TECHNOLOGIES NV.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 XX Renschler MF, Levy R, Bhatt RR, Dower WJ;  
 XX WPI; 1994-279762/34.  
 DR



XX Identifying anti-proliferative peptide(s) which specifically bind to  
PT immunoglobulin super-family species idotype - esp. to inhibit B-cell  
PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotypic  
PT therapy.  
XX  
XX Claim 7; Page 45; 69pp; English.  
CC AAR60400-73 are peptide ligands which bind to purified IgM lambda  
CC receptor of the human Burkitt's lymphoma cell line SU9-B8. Peptides  
CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The  
CC peptides were identified with the use of filamentous phage libraries  
CC displaying random peptides. Corresponding synthetic peptides bound  
CC specifically to this Ig receptor, and blocked the binding of an anti-  
CC idiotypic antibody. The ligands, when conjugated to form dimers or  
CC tetramers, induced cell death by apoptosis in vitro at nanomolar  
CC concentrations. This effect was associated with the specific stimulation  
CC of intracellular protein tyrosine phosphorylation. The peptides of the  
CC invention can be used individually, as complexes of cross-linked peptides  
CC or can be conjugated to deliver toxins or radionuclides to neoplastic  
CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
XX SQ Sequence 8 AA;  
XX  
XX Query Match 48.4%; Score 30; DB 2; Length 8;  
XX Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
OY 1 PMPNFK 7  
DB 1 MPEDFYR 7  
XX  
XX RESULT 13  
XX AAR21944  
XX ID AAR21944 standard; protein; 11 AA.  
XX  
XX AAR21944;  
XX  
XX 25-JUN-1992 (first entry)  
XX  
XX Substance P [Pro 11].  
XX  
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's; syndrome;  
XX hereditary cerebral haemorrhage.  
XX  
XX OS Synthetic.  
XX  
XX PN WO9202248-A.  
XX  
XX PD 20-FEB-1992.  
XX  
XX PF 27-JUL-1990; 90US-00559173.  
XX  
XX PR 27-JUL-1990; 90US-00559173.  
XX  
XX PA (CHIL-) CHILDRENS MED CENT.  
XX  
XX PI Yankner BA;  
XX  
XX DR WPI; 1992-079804/10.  
XX  
XX PT Treatment of neuronal accumulation of beta-amyloid - using tachykinin  
XX agonists e.g. substance P, physalaemin and neurokinin B, for treating  
XX Alzheimer's disease, downs syndrome, etc.  
XX  
XX PS Claim 10; Page 21; 35pp; English.  
XX  
XX CC The peptide is the tachykinin agonist substance P with a Proline residue  
XX substituted at position 11. The peptide was synthesised by standard solid  
XX phase synthesis. Neuronal accumulation of beta-amyloid may be treated by  
XX administration of tachykinin agonists. The peptide can reduce the

CC neurotoxic effects of a beta-amyloid related polypeptide on cultured  
CC neurons. The peptide and its analogues are useful for controlling  
CC diseases characterised by beta amyloid accumulation in the brain such as  
CC Alzheimer's disease and Down's syndrome. See also AAR21932-75  
XX  
XX SQ Sequence 11 AA;  
XX  
XX Query Match 48.4%; Score 30; DB 2; Length 11;  
XX Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 PMPFKLP 9  
DB 4 PQDFGLP 11  
XX  
XX RESULT 14  
XX AAR92718  
XX ID AAR92718 standard; peptide; 11 AA.  
XX  
XX AAR92718;  
XX  
XX 20-MAR-2003 (revised)  
XX DT 30-APR-1999 (first entry)  
XX  
XX DE Human tachykinin agonist beta-amyloid peptide fragment #64.  
XX  
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;  
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;  
XX hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia..  
XX  
XX OS Homo sapiens.  
XX  
XX PN US5876948-A.  
XX  
XX PD 02-MAR-1999.  
XX  
XX PF 29-JUL-1991; 91US-00737371.  
XX  
XX PR 27-JUL-1990; 90US-00559173.  
XX  
XX PA (CHIL-) CHILDRENS MEDICAL CENT.  
XX  
XX PI Yankner BA;  
XX  
XX DR WPI; 1999-189630/16.  
XX  
XX PT Screening for neurotoxin inhibitors - by testing compounds for their  
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells.  
XX  
XX PS Disclosure; Col 37-38; 28pp; English.  
XX  
XX CC This invention describes a method for screening compounds for inhibiting  
XX a neurotoxin. The method involves incubating tachykinin agonists with  
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be  
XX used for identifying compounds for treating diseases characterised by an  
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,  
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage  
XX with amyloidosis and non-inherited congenital angiodysplasia with cerebral  
XX haemorrhage. AAR92655-W92731 are tachykinin agonists derived from human  
XX beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF  
XX field.)  
XX  
XX SQ Sequence 11 AA;  
XX  
XX Query Match 48.4%; Score 30; DB 2; Length 11;  
XX Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 PMPFKLP 9  
DB 4 PQDFGLP 11

RESULT 15  
ABR84651  
ID ABR84651 standard; peptide; 15 AA.  
XX  
AC ABR84651;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human antigenic SGA-1M peptide fragment #1.  
XX  
KW Human, SGA-1M; cancer; antigen; cytostatic; breast cancer;  
KM ovarian cancer; skin cancer; lymphoid system; thyroid cancer;  
KM pancreatic cancer; stomach cancer; lung cancer.  
XX  
OS Homo sapiens.  
XX  
FN WO2003065873-A2.  
XX  
PD 14-AUG-2003.  
XX  
PF 03-FEB-2003; 2003WO-US002974.  
XX  
PR 01-FEB-2002; 2002US-0353826P.  
XX  
PA (SEAT-) SEATTLE GENETICS INC.  
XX  
PI Petroziello JM, Law C, Wahl AF;  
XX  
DR WPI; 2003-731465/69.  
XX  
PT Diagnosing or staging cancer in a subject by detecting or measuring a SGA  
PT -1M gene product in a sample derived from the subject.  
XX  
PS Example; Page 184; Opp; English.  
XX  
CC The present invention relates to a method of diagnosing or staging cancer  
CC in a subject, which comprises detecting or measuring a SGA-1M gene  
CC product in a sample derived from the subject, where elevated levels of  
CC the SGA-1M gene product compared to a non-cancerous sample or  
CC predetermined standard value for a non-cancerous sample indicates the  
CC presence or advanced stage of cancer in the subject. Also provided is the  
CC human SGA-1M gene, its two open reading frames and the two encoded  
CC proteins. The method is useful for diagnosing or staging cancer in a  
CC subject, and comprises detecting or measuring a SGA-1M gene product in a  
CC sample derived from the subject, where elevated levels of the SGA-1M gene  
CC product compared to a non-cancerous sample or predetermined standard  
CC value for a non-cancerous sample indicates the presence or advanced stage  
CC of cancer. The SGA-1M gene product is also useful for vaccinating a  
CC subject against cancer. It is particularly linked to breast, ovarian,  
CC skin, thyroid, pancreatic, stomach and lung cancer, and cancers of the  
CC lymphoid system. The present sequence is a fragment of the protein of the  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 48.4%; Score 30; DB 7; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MPONFYKLPQ 10  
DB 5 MPETFSNLPR 14  
XX  
RESULT 16  
AAW00884  
ID AAW00884 standard; peptide; 15 AA.  
XX  
AC AAW00884;  
XX  
DT 27-AUG-2003 (revised)  
DT 23-MAY-1997 (first entry)  
XX

XX  
DE Epstein Barr virus EBNA-2 p276-290.  
XX  
KW Adeno-associated virus; vector; liposome; transfection; dendritic cell;  
KM EBV; EBNA-2; adoptive immunotherapy; tumour associated antigen.  
XX  
OS Human herpesvirus 4.  
XX  
FN WO9703703-A1.  
XX  
PD 06-FEB-1997.  
XX  
PF 19-JUL-1996; 96WO-US012012.  
XX  
PR 21-JUL-1995; 95US-0001312P.  
PR 01-NOV-1995; 95US-0007184P.  
PR 01-DEC-1995; 95US-00566286.  
XX  
PA (RHON ) RHONE POULENC RORER PHARM INC.  
XX  
PI Philip R, Lebikowski JS;  
XX  
DR WPI; 1997-145208/13.  
XX  
PT Adeno-associated virus:liposome complexes for transfecting dendritic  
PT cells - for inducing immune response, useful for treating e.g. neoplasia  
PT or infections.  
XX  
PS Example 5; Page 58; 134pp; English.  
XX  
CC Tumour associated antigens (AAW13660-61, AAW0878-903) can be loaded into  
CC dendritic cells and used to induce antitumour immunity. Alternatively,  
CC dendritic cells are transfected with adeno associated virus plasmid  
CC DNA (which includes DNA encoding the tumour associated antigen) complexed  
CC with cationic liposomes. The antigen loaded or transfected dendritic  
CC cells can be used to generate tumour antigen-specific cytotoxic T  
CC lymphocytes for use in adoptive immunotherapy in a patient having the  
CC corresponding tumour. A suitable antigen comprises amino acids 276-290  
CC (AAW00884) of Epstein Barr virus EBNA-2. (Updated on 27-AUG-2003 to  
CC correct OS field.)  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 46.8%; Score 29; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 2 POFYKLPQM 11  
DB 4 PTVFYNIIPM 13  
XX  
RESULT 17  
ABB9900  
ID ABB99000 standard; peptide; 15 AA.  
XX  
AC ABB99000;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02 peptide.  
XX  
KW Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02; cancer;  
KM cytostatic; HIV infection; anti-HIV; enzyme.  
XX  
OS Unidentified.  
XX  
FN CN1363668-A.  
XX  
PD 14-AUG-2002.  
XX  
PF 05-JAN-2001; 2001CN-00105052.  
XX

PR 05-JUN-2001; 2001CN-00105052.  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-751782/82.  
XX  
XX Poly(amide-phosphoenolpyruvate-dependent glycosylphosphate transferase  
PT 9.02 and polynucleotide for coding it.  
XX  
XX Example 5; Page 20 (Disclosure); 33pp; Chinese.  
XX  
XX The present invention relates to phosphoenol pyruvate dependent  
CC glycosylphosphate transferase 9.02 (see ABB98999). The protein can be  
CC used for treating diseases such as cancer and HIV infection. The present  
CC sequence is an N-terminal peptide fragment of the protein, which was used  
CC in an example from the invention  
XX  
XX Sequence 15 AA;  
SQ

Query Match 46.8%; Score 29; DB 5; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
OY 1 MPONFYKLPQ 10  
DB 1 MPANFYQIVQ 10

RESULT 18  
AAE20383  
ID AAE20383 standard; peptide; 15 AA.  
XX  
XX AAE20383;  
XX  
XX 07-AUG-2003 (revised)  
DT 18-JUN-2002 (first entry)  
XX  
XX Epstein-barr virus tumour associated antigen (TNA) peptide epitope #2.  
DE  
XX Gene-delivery compound; single-chain binding polypeptide; SCBP;  
XX nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;  
KW gene therapy; targeted gene delivery; tumour associated antigen; TNA;  
KW epitope.  
XX  
XX Cercopithecine herpesvirus 15.  
OS  
XX WO200200914-A2.  
PN  
XX 03-JAN-2002.  
PD  
XX 25-JUN-2001; 2001WO-US020182.  
PF  
XX 23-JUN-2000; 2000US-0213653P.  
PR  
XX  
XX (HUST/) HUSTON J S.  
PA (WILS/) WILS P.  
PA (QUAN/) QUAN Z.  
PA (LAUR/) LAURENT O.  
PA (MARASCO/) MARASCO W A.  
PA (SCHE/) SCHERMAN D.  
XX  
XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;  
PI WPI; 2002-268789/31.  
DR  
XX  
XX Gene-delivery compound for targeted gene delivery, comprises single-chain  
PT binding polypeptide having effector segment with cysteinyl residue and  
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by  
PT residue.  
XX  
XX Disclosure; Page 28; 96pp; English.

XX  
XX The invention relates to gene-delivery compound comprising a single-chain  
CC binding polypeptide (SCBP) having at least one effector segment having a  
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-  
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery  
CC compound is useful for targeted gene delivery for treating diseases by  
CC gene therapy. The present sequence is Epstein-barr virus tumour  
CC associated antigen (TNA) peptide epitope. TNA may be targeted by the  
CC SCBP of the present invention. (Updated on 07-AUG-2003 to correct OS  
CC field.)  
XX  
XX Sequence 15 AA;  
SQ

Query Match 46.8%; Score 29; DB 5; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 2 PONFYKLPQM 11  
DB 4 PTVFYNIIPM 13

RESULT 19  
ABB08787  
ID ABB08787 standard; peptide; 15 AA.  
XX  
XX ABB08787;  
XX  
XX 22-MAY-2002 (first entry)  
DT  
XX  
XX Human glycosyl-phosphatidyl inositol glycan F10.89 peptide.  
DE  
XX Human; glycosyl-phosphatidyl inositol glycan F10.89;  
XX embryonic development malformation; immunological dysfunction;  
KW hormonal metabolic disturbance.  
KW  
XX Homo sapiens.  
OS  
XX CN1326960-A.  
PN  
XX 19-DEC-2001.  
PD  
XX 05-JUN-2000; 2000CN-00116326.  
PF  
XX 05-JUN-2000; 2000CN-00116326.  
PR  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-206969/27.  
DR  
XX  
XX New polypeptide-glycosyl-phosphatidyl inositol glycan F10.89 and  
PT polynucleotide encoding the polypeptide.  
PT  
XX  
XX Example 5; Page 20 (Disclosure); 35pp; Chinese.  
PS  
XX  
XX The invention relates to human glycosyl-phosphatidyl inositol glycan  
CC F10.89, the polynucleotide encoding this polypeptide and DNA recombinant  
CC processes to produce the polypeptide. The present invention also  
CC discloses the method of applying the polypeptide in treating various  
CC diseases, such as embryonic development malformation, immunological  
CC dysfunction disease and hormonal metabolic disturbance disease. The  
CC present invention also discloses the antagonist for resisting the  
CC polypeptide and its treatment effect. The present invention also  
CC discloses the application of the polynucleotide for encoding glycosyl-  
CC phosphatidyl inositol glycan F10.89. The present sequence is that of the  
CC N-terminal peptide from human glycosyl-phosphatidyl inositol glycan  
CC F10.89, useful in examples of the invention  
XX  
XX Sequence 15 AA;  
SQ

Query Match 46.8%; Score 29; DB 5; Length 15;

Best Local Similarity 71.4%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYKLPM 11  
|:|:|  
Db 9 FVKIPOM 15

## RESULT 20

ABR44016  
ID ABR44016 standard; peptide; 15 AA.

AC ABR44016;

DT 04-AUG-2003 (first entry)

DE E. coli TNase N-terminal fragment.

KM Bacterium; L-cysteine; cystathionine-beta-lyase; drug; cosmetic; food;  
TNase; enzyme.

OS Escherichia coli.

PN EP1298200-A2.

PD 02-APR-2003.

PF 17-SEP-2002; 2002EP-00020588.

PR 28-SEP-2001; 2001JP-00302008.

PA (AJIN) AJINOMOTO CO INC.

PI Takagi H, Wada M, Nakamori S;

DR WPI; 2003-423253/40.

PT New bacterium belonging to genus Escherichia which is modified so that  
cystathionine-beta-lyase activity is reduced/eliminated, useful for  
producing L-cysteine useful in the field of drugs, cosmetics and foods.

PS Example 1; Page 10; 28pp; English.

CC The invention relates to a bacterium belonging to the genus Escherichia  
which has the ability to produce L-cysteine and which is modified so that  
cystathionine-beta-lyase activity is reduced or eliminated. The bacterium  
is useful for producing L-cysteine which is useful in the field of drugs,  
cosmetics and foods. The present sequence represents an E. coli TNase N-  
terminal fragment

SQ Sequence 15 AA;

Query Match 46.8%; Score 29; DB 6; Length 15;

Best Local Similarity 55.6%; Pred. No. 3.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 ONPFYKLPM 11  
|:|:|  
Db 2 ENFKHLPKM 10

## RESULT 21

AA08887  
ID AA08887 standard; protein; 7 AA.

AC AA08887;

DT 19-AUG-1999 (first entry)

DE C. lindemuthianum chitin deacetylase C-terminal fragment.

KM Chitin deacetylase; N-acetyl aminosugar; hypotensive; antibacterial;  
anti-osteoporotic; antitumour; cholesterol reduction; chitin; chitosan;

KM food; animal feed; thickener; blood pressure; treatment; osteoporosis;  
KW gout; hyperurinaemia; Bifidus bacteria.

OS Colletotrichum lindemuthianum.

PN DE19810349-A1.

PD 10-JUN-1999.

PF 10-MAR-1998; 98DE-01010349.

PR 02-DEC-1997; 97JP-00345737.

PA (NORO) NAT FOOD RES INST MIN AGRIC.

PI Hamamatsu S, Hayashi K, Tokuyasu K, Mori Y;

DR WPI; 1999-338951/29.

PT Nucleic acid encoding bacterial chitin deacetylase useful for generating  
chitosan.

PS Example 1; Page 5; 14pp; German.

CC This invention describes a novel protein and its encoding nucleic acid  
deacetylase activity on the N-acetyl group of N-acetyl aminosugars which  
has been isolated from Colletotrichum lindemuthianum. The protein of the  
invention has hypotensive, antibacterial, anti-osteoporotic, antitumour  
and cholesterol reducing activity. The products of the invention can be  
used to convert chitin to chitosan. Chitosan is used in foods or animal  
feeds, particularly as a thickener, and in pharmaceuticals, to reduce  
cholesterol levels or blood pressure, in treatment of gout,  
hyperurinaemia and osteoporosis; for stimulating growth of Bifidus  
bacteria while suppressing Escherichia coli and Clostridium perfringens,  
and as antitumour agent. The protein of the invention is also used to  
produce chitosan oligosaccharides from chitin oligosaccharides and for  
removing N-acetyl from other amino sugars, making it suitable for  
synthesis of new sugar chains

SQ Sequence 7 AA;

Query Match 45.2%; Score 28; DB 2; Length 7;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNFYK 7  
|:|:|  
Db 1 PKNWYK 6

## RESULT 22

AA48162  
ID AA48162 standard; peptide; 9 AA.

AC AA48162;

DT 01-DEC-1999 (first entry)

DE Immunogenic peptide having a human leukocyte antigen binding motif #2773.

KM Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.

OS Synthetic.

OS Homo sapiens.

PN WO945954-A1.

PD 16-SEP-1999.

PF 13-MAR-1998; 98WO-US005039.  
 XX  
 PR 13-MAR-1998; 98WO-US005039.  
 XX  
 PA (EPTM-) EPIMUNE INC.  
 XX  
 PI Sette A, Kubo RT, Sidney J, Cells B, Grey HM, Southwood S;  
 XX WPI, 1999-551214/46.  
 DR  
 XX  
 PT New immunogenic peptides with HLA binding motif, useful in treatment and  
 PT diagnosis of cancers and viral diseases.  
 XX  
 PS Claim 1; Page 140; 150pp; English.  
 XX  
 CC AAY530 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also known  
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 CC than the intact foreign antigen itself, and are particularly important in  
 CC tumour rejection and in fighting viral infections. The peptides are  
 CC therefore useful therapeutically to treat or prevent viral infections and  
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 CC elicit an immune response in individuals susceptible or otherwise at risk  
 CC of viral infection or cancer, or used to treat chronic or acute  
 CC conditions. They are also useful diagnostically, and can be used to  
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 CC patient. The polynucleotides encoding the immunogenic peptides are also  
 CC useful therapeutically and for immunisation as above  
 CC  
 SQ Sequence 9 AA;  
 QY  
 Query Match 45.2%; Score 28; DB 2; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 PONYKL 8  
 2 PONYLTL 8  
 RESULT 23  
 ADK23699  
 ID ADK23699 standard; peptide; 9 AA.  
 AC ADRK23699;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Human 98P4B6 derived motif-bearing CTL peptide epitope #6.  
 XX  
 KW human; 98P4B6; STEAP-2; cancer; breast; colon; lung; kidney; prostate;  
 KW gene therapy; genetic abnormality; transgenic; knockout animal;  
 KW cytostatic; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087306-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010462.  
 XX  
 PR 05-APR-2002; 2002US-0370387P.  
 PR 06-JUN-2002; 2002US-00165044.  
 PR 20-DEC-2002; 2002US-0435480P.  
 XX

PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-Bid PM, Raitano AB, Paris M, Ge W, Jakobovits A;  
 XX  
 DR WPI, 2003-903158/82.  
 XX  
 PT A composition comprising 98P4B6 proteins and nucleic acid molecules for  
 PT detecting, preventing, prognosing and/or treating cancers that express  
 PT 98P4B6 (e.g. pancreatic, prostatic or lung cancer).  
 XX  
 PS Claim 1; Page 143; 616pp; English.  
 XX  
 CC This invention relates to a novel human gene 98P4B6 (also known as STEAP-  
 CC 2, six transmembrane epithelial antigen of prostate-2) located on  
 CC chromosome 7q21 and the encoded protein and variants derived thereof.  
 CC Specifically, it refers to the expression pattern of this gene in adult  
 CC normal tissues and its aberrant over-expression in various cancers  
 CC including breast, colon, lung, kidney and prostate. The present invention  
 CC describes compositions and methods useful for detecting, preventing,  
 CC prognosing and/or treating cancers that express 98P4B6. Furthermore, the  
 CC polynucleotide can be used for gene therapy purposes, for monitoring  
 CC genetic abnormalities and for generating transgenic or 'knockout'  
 CC animals, which can be useful for the development and screening of  
 CC therapeutically useful reagents. The encoded proteins may also be used in  
 CC generating antibodies and vaccines, as well as in identifying ligands and  
 CC cellular constituents that bind to 98P4B6 gene products. Accordingly,  
 CC these compositions exhibit cytostatic activities. This peptide sequence  
 CC is a motif bearing CTL peptide epitope derived from a human 98P4B6  
 CC protein variant of the invention.  
 CC  
 SQ Sequence 9 AA;  
 QY  
 Query Match 45.2%; Score 28; DB 7; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 4 NPYKLP 9  
 3 DPKLP 8  
 RESULT 24  
 ADK24080  
 ID ADK24080 standard; peptide; 10 AA.  
 AC ADRK24080;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Human 98P4B6 derived motif-bearing CTL peptide epitope #387.  
 XX  
 KW human; 98P4B6; STEAP-2; cancer; breast; colon; lung; kidney; prostate;  
 KW gene therapy; genetic abnormality; transgenic; knockout animal;  
 KW cytostatic; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087306-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010462.  
 XX  
 PR 05-APR-2002; 2002US-0370387P.  
 PR 06-JUN-2002; 2002US-00165044.  
 PR 20-DEC-2002; 2002US-0435480P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-Bid PM, Raitano AB, Paris M, Ge W, Jakobovits A;  
 XX  
 DR WPI, 2003-903158/82.  
 XX



DR WPI; 1992-365995/44.  
XX Bradykinin antagonists comprising linked bradykinin antagonist chains -  
PT are for treatment of post-operative pain, asthma and aseptic shock.  
XX  
XX Disclosure; Page 76; 109pp; English.  
XX  
XX The sequence given is a bradykinin receptor antagonist which can form  
CC homo- or heterodimers or higher oligomers. It demonstrates greater  
CC potency and/or duration of action than the parent peptide itself.  
CC Bradykinin receptors antagonists such as this can be used in the  
CC treatment of burns, perioperative pain, migraine and other forms of pain,  
CC shock CNS injury, asthma, rhinitis, premature labour, inflammatory  
CC arthritis, inflammatory bowel disease etc. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 11 AA;  
  
Query Match 45.2%; Score 28; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 PGNFYKL 8  
DB 4 PGNFWL 10  
  
RESULT 27  
AA93148  
ID AA93148 standard; peptide; 12 AA.  
XX  
XX AA93148;  
AC  
XX  
DT 06-DEC-2000 (first entry)  
XX  
XX Rat G-protein coupled receptor protein rGRT022-derived peptide #1.  
DE  
XX G-protein coupled receptor; human; bovine; nervous system disorder; rat;  
XX mouse; somatostatin excretion.  
KW  
XX Rattus sp.  
OS  
XX  
FH Key Location/Qualifiers  
FT Modified-site 12  
FT /note="C-terminal amide"  
XX  
XX WO200029441-A1.  
PN  
XX  
XX 25-MAY-2000.  
PD  
XX  
XX 11-NOV-1999; 99WO-JP006283.  
PP  
XX  
XX 13-NOV-1998; 98JP-00323759.  
PR  
XX 08-MAR-1999; 99JP-00060030.  
PR  
XX 14-APR-1999; 99JP-00106812.  
PR  
XX 14-JUN-1999; 99JP-00166672.  
PR  
XX 04-AUG-1999; 99JP-00221640.  
PR  
XX 14-SEP-1999; 99JP-00259818.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukushima S;  
PI Fujii R, Hosoya M, Kitada C;  
XX  
XX WPI; 2000-387747/33.  
DR  
XX  
XX G protein coupled receptor protein and antibodies to it for treatment and  
PT diagnosis of nerve diseases.  
XX  
XX Example 7; Page 128; 184pp; Japanese.  
PS  
XX  
XX The invention relates to the isolation of novel G-protein coupled  
CC receptor (GPCR) genes and their encoded proteins. This sequence

CC represents a peptide derived from the rat GPCR protein clone rGRT022 and  
CC was used in an acidification rate assay. The DNAs and proteins are used  
CC for the treatment, prevention and diagnosis of disorders of the nervous  
CC system. The proteins and its fragments are also promoters of somatostatin  
CC excretion  
XX  
SQ Sequence 12 AA;  
  
Query Match 45.2%; Score 28; DB 3; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MPGNFYKL 9  
DB 1 MPHSFANLP 9  
  
RESULT 28  
AAB60026  
ID AAB60026 standard; peptide; 12 AA.  
XX  
XX AAB60026;  
AC  
XX  
DT 05-NOV-2001 (first entry)  
XX  
XX  
DE Internalising peptide SEQ ID NO: 41.  
XX  
XX Internalising peptide; transport; apoptosis; arthritis; cancer;  
KW stem cell; cell differentiation; immune response stimulation;  
KW HIV vaccine.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200115511-A2.  
PN  
XX  
XX 08-MAR-2001.  
PD  
XX  
XX 31-AUG-2000; 2000WO-US024034.  
PF  
XX  
XX 01-SEP-1999; 99US-0151980P.  
PR  
XX 13-MAR-2000; 2000US-0188944P.  
PR  
XX  
XX (UVP1-) UNIV PITTSBURGH.  
PA  
XX  
XX Robbins PD, Mi Z, Frizzell R, Glorioso JC, Gambotto A;  
PI  
XX  
XX WPI; 2001-273309/28.  
DR  
XX  
XX Peptides that facilitate uptake and cytoplasmic and/or nuclear transport  
PT of proteins, DNA and viruses, useful, e.g. for facilitating uptake of  
PT antigens in immunogenic compositions.  
XX  
XX Claim 1; Page 122; 129pp; English.  
XX  
XX The present invention provides the sequences of 75 peptides which  
CC facilitate the uptake and transport of viruses, proteins and nucleic  
CC acids. These internalising peptides can be used for transport into the  
CC cytoplasm or the nucleus. They are useful for facilitating uptake into  
CC the cell, inducing apoptosis, for example in the treatment of arthritis  
CC and cancer, to expand a population of stem cells or differentiated cells,  
CC to stimulate cell differentiation, facilitate the integration of AAV into  
CC the genome of a cell, and to stimulate an immune response, for example in  
CC the case of a HIV vaccine. The present sequence is one of the peptides of  
CC the invention  
XX  
SQ Sequence 12 AA;  
  
Query Match 45.2%; Score 28; DB 4; Length 12;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 QNFYKLPM 11  
DB 3 QNFYKLPM 11

Db 4 KNFFWLPEL 12

RESULT 29  
AAG67753  
ID AAG67753 standard; peptide; 12 AA.

AC AAG67753;  
XX  
XX 10-DEC-2001 (first entry)  
XX  
XX Amino acid sequence of synthetic peptide.  
XX  
XX Human; prolactin secretion; hypovarianism; sperm development;  
KW osteoporosis; lactation disorder; hypothyroidism; kidney failure;  
KW menopause; hyperprolactinemia; pituitary tumor; diencephalon tumor;  
KW menstrual disorder; stress; autoimmune disease; prolactinoma; sterility;  
KW impotence; amenorrhea; lactorhea; hyperpituitarism;  
KW Sheehan's syndrome Chaiti-Frommel syndrome; Argonz-del Castillo syndrome;  
KW Liphoma; Forbes-Albright syndrome; spermatogenesis disorder.  
XX  
XX Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX Modified-site 12 /note="amide attached to residue"  
XX  
XX WO200166134-A1.  
XX  
XX 13-SEP-2001.  
XX  
XX 06-MAR-2001; 2001WO-JP001716.  
XX  
XX 06-MAR-2000; 2000JP-00065752.  
XX PR 07-DEC-2000; 2000JP-00378001.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Matsumoto Y, Watanabe T, Hinuma S, Habata Y, Yoshida H;  
XX MPI; 2001-596812/67.  
XX  
XX New polypeptide, useful as a vasotropic, tranquilizing, immunosuppressive  
XX PT and gynecological agent comprises the prolactin secretion regulator.  
XX  
XX PS Example 1; Page 94; 180pp; Japanese.  
XX  
XX CC The specification describes a human polypeptide which is a prolactin  
XX CC secretion regulating agent. The prolactin secretion regulating agent  
XX CC polypeptide and polynucleotide are used for the treatment and prevention  
XX CC of hypovarianism, sperm under development, osteoporosis, menopause,  
XX CC lactation disorders, hypothyroidism, kidney failure, hyperprolactinemia,  
XX CC pituitary tumor, diencephalon tumor, menstrual disorders, stress,  
XX CC autoimmune disease, prolactinoma, sterility, impotence, amenorrhea,  
XX CC lactorhea, hyperpituitarism, Chaiti-Frommel syndrome, Argonz-del Castillo  
XX CC syndrome, Forbes-Albright syndrome, Liphoma, Sheehan's syndrome and  
XX CC spermatogenesis disorders. The present peptide was used in the course of  
XX CC the invention  
XX  
XX SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 4; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
| : | | |  
| : | | |  
DB 1 MPHSFANLP 9

RESULT 30  
ABU60819  
ID ABU60819 standard; peptide; 12 AA.

XX AC ABU60819;  
XX  
XX 06-MAY-2003 (first entry)  
XX  
XX DT Peptide production by gene recombination associated peptide #3.  
XX  
XX DE Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;  
XX KW gene recombination.  
XX KW  
XX OS Homo sapiens.  
XX  
XX PN WO200292829-A1.  
XX  
XX 21-NOV-2002.  
XX  
XX PD 16-MAY-2002; 2002WO-JP004735.  
XX  
XX PF 17-MAY-2001; 2001JP-00147341.  
XX  
XX PR (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX PA Nishimura O, Suenaga M, Ito T, Kitada C;  
XX PI MPI; 2003-129302/12.  
XX  
XX DR Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for  
XX PT subsequent applications by gene recombination technique through tandem  
XX PT repeats to provide precursor protein with specific cleavage sites.  
XX PS Disclosure; Page 52; 87pp; Japanese.  
XX  
XX CC The invention describes a method of producing a peptide comprising the  
XX CC excision of the N and C-terminals of a target peptide with enzymes or  
XX CC chemically through the attached cleavage sites repeated by ligation in a  
XX CC precursor protein. The method is for producing (low-molecular) peptides  
XX CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the  
XX CC gene recombination technique through tandem repeats to provide a  
XX CC precursor protein with specific cleavage sites. With this method, peptide  
XX CC production can be carried out easily to provide large quantities of the  
XX CC required peptides. This is the amino acid sequence of a peptide  
XX CC associated with the peptide production method of the invention  
XX  
XX SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
| : | | |  
| : | | |  
DB 1 MPHSFANLP 9

RESULT 31  
ABP97049  
ID ABP97049 standard; peptide; 12 AA.

AC ABP97049;  
XX  
XX 23-JUN-2003 (first entry)  
XX  
XX DT Human RFRP-3 peptide SEQ ID NO:39.  
XX  
XX DE RFRP-3; prolactin secretion promoter; secretion; prolactin; GPCR;  
XX KW G protein-coupled receptor; gynaecological; osteopathic; cytostatic;  
XX KW immunomodulator; antiinfertility; vasotropic; hypovarianism; menopause;  
XX KW prolactin secretion-related disease; spermatc hypoplasia.  
XX  
XX OS Homo sapiens.  
XX  
XX PI Key Location/Qualifiers  
XX Modified-site 12



/label= amidated

FT XX WO2003018795-A1.  
 XX  
 PD 06-MAR-2003.  
 XX  
 PF 22-AUG-2002; 2002WO-JP008466.  
 XX  
 PR 24-AUG-2001; 2001JP-00254826.  
 XX  
 PA (TAKEDA ) TAKEDA CHEM IND LTD.  
 XX  
 PI Hinuma S, Yoshida H, Habata Y, Hosoya M, Kikada C;  
 XX  
 DR WPI: 2003-269422/26.  
 DR N-PSDB; ACC49304.  
 XX  
 PS Novel RFRP-3 peptides and encoded DNAs, applicable in diagnosis of and  
 PT developing drugs for treating prolactin secretion-related diseases e.g.  
 PT hypovarianism, spermatoc hypoplasia and menopause.  
 XX  
 PS Example; Page 107, 197pp; Japanese.  
 XX  
 CC The present invention describes RFRP-3 peptides. RFRP-3 is a G protein-  
 CC coupled receptor (GPCR) which is a prolactin secretion promoter. RFRP-3  
 CC has gynaecological, osteopathic, cytostatic, immunomodulator, vasotropic  
 CC and antinfertility activities. The RFRP-3 peptides and their encoded  
 CC DNAs can be used in the diagnosis of and developing drugs for treating  
 CC prolactin secretion-related diseases e.g. hypovarianism, spermatoc  
 CC hypoplasia and menopause. The developed drugs are safe with low toxicity.  
 CC The present sequence represents a human RFRP-3 peptide, which is used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;  
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQNFYKLP 9  
 ||:|  
 DB 1 MPHSPANLP 9

RESULT 32  
 ABP54416  
 ID ABP54416 standard; peptide; 12 AA.  
 XX  
 AC ABP54416;  
 XX  
 DT 21-JAN-2003 (first entry)  
 XX  
 DE Human RF amide peptide related sequence SEQ ID NO:3.  
 XX  
 KW RF amide peptide; cytostatic; antinfertility; prolactin-related disease;  
 KW hyperprolactinemia; infertility; Chiari-Frommel syndrome; cancer;  
 KW Forbes-Albright syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246405-A1.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 06-DEC-2001; 2001WO-JP010668.  
 XX  
 PR 07-DEC-2000; 2000JP-00373125.  
 XX  
 PA (TAKEDA ) TAKEDA CHEM IND LTD.  
 XX  
 PI Suenaga M, Yamada T, Nishimura O;  
 XX  
 DR WPI; 2003-018538/01.

DR N-PSDB; ABQ83409.  
 XX  
 PT Producing an RF amide peptide for treating prolactin-related diseases,  
 PT comprises obtaining a fusion protein or peptide using a transformant then  
 PT cleaving the peptide bond in the amino acid side of a cysteine residue.  
 XX  
 PS Claim 6; Page 81; 100pp; Japanese.

CC The present invention describes a method for producing an RF amide  
 CC peptide (I) which can be a partial peptide of a polypeptide selected from  
 CC the amino acid sequences given in ABP5442 to ABP54427, by cleaving a  
 CC peptide bond in the amino acid side of the cysteine residue of a fusion  
 CC protein or polypeptide linked to the N-terminal of a protein or  
 CC polypeptide with cysteine at its N-terminal and optionally an oxidisable  
 CC methionine residue. (I) has cytostatic and antinfertility activities.  
 CC The method can be used for producing a peptide which is used for  
 CC preventing or treating prolactin-related diseases, e.g.  
 CC hyperprolactinemia, infertility, Chiari-Frommel syndrome, Forbes-Albright  
 CC syndrome and cancer. The method is used for large-scale industrial  
 CC production of the peptide. The present sequence represents a specifically  
 CC claimed peptide from the present invention  
 XX  
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;  
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQNFYKLP 9  
 ||:|  
 DB 1 MPHSPANLP 9

RESULT 33  
 ADA88861  
 ID ADA88861 standard; peptide; 12 AA.  
 XX  
 AC ADA88861;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Internalised peptide pep35 SEQ ID NO:41.  
 XX  
 KW internalising peptide; cytostatic; antiinflammatory; immunomodulator;  
 KW antiarthritic; cytoplasmic transport; nuclear transport;  
 KW peptide-cargo complex; apoptosis; arthritic; tumour; differentiation;  
 KW immune response; vaccine; inflammation; necrosis; transplantation;  
 KW cystic fibrosis; lung inflammation; gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003068942-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 12-FEB-2003; 2003WO-US004632.  
 XX  
 PR 13-FEB-2002; 2002US-00075869.  
 XX  
 PA (UVP1-) UNIV PITTSBURGH.  
 XX  
 PI Robbins PD, Mi Z, Fritzel R, Glorioso JC, Gambotto A, Mai JC;  
 XX  
 DR WPI; 2003-697526/66.  
 XX  
 PT New internalising peptides, useful for facilitating the delivery, uptake  
 PT and cytoplasmic and/or nuclear transport of proteins, DNA or viruses into  
 PT a target cell, for inducing apoptosis in arthritic or tumor cells, or in  
 PT gene therapy.  
 XX  
 PS Example 3; Page 19; 171pp; English.  
 XX  
 CC The present invention describes an internalising peptide (I) comprising

CC any one of 14 fully defined amino acid sequences (designated P1-P14, see  
CC ADA8896 to ADA8906, and ADA8917 to ADA8919). (1) has cytosolic,  
CC anti-inflammatory, immunomodulator and anticholinergic activities. The  
CC internalising peptides are useful for facilitating the delivery, uptake  
CC and cytoplasmic and/or nuclear transport of cargo, e.g. proteins, DNA or  
CC viruses, into a target cell. The internalising peptides and peptide-cargo  
CC complexes from the present invention are also useful for inducing  
CC apoptosis in cells (e.g. arthritic cells or tumour cells), expanding a  
CC population of stem cell or differentiated cells, stimulating the  
CC differentiation of a population of stem cells, facilitating the  
CC integration of adeno-associated virus DNA into the genome of a cell,  
CC stimulating or eliciting an immune response in a subject, facilitating  
CC the delivery of immunogens (e.g. vaccines), inhibiting the inflammatory  
CC process, protecting tissue from apoptosis or necrosis during tissue  
CC isolation prior to transplantation, facilitating transfer of proteins and  
CC peptides to the lung for the treatment of cystic fibrosis or lung  
CC inflammation, or in gene therapy. The present sequence represents a  
CC peptide used in the exemplification of the present invention.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 7; Length 12;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 QNFYKLPQM 11  
: ||: ||:  
DB 4 KNFVWLPPEL 12

RESULT 34

ADJ87494  
ID ADJ87494 standard; peptide; 12 AA.

AC ADJ87494;

DT 06-MAY-2004 (first entry)

DE RFRP C-terminal peptide SEQ ID NO.13.

XX RFRP: myopathy; behavioural abnormality; RFRP: receptor protein OT7T022;  
XX neuroprotective; ophthalmological; cardiac; haemostatic;  
XX immunostimulant; nephroprotective; anabolic; anorectic; antidepressant;  
XX tranquiliser; anticonvulsant; nootropic; muscular; adrenal dysfunction;  
XX twitching; aggressive behaviour; abnormal gait; hyperthermia;  
XX leukopenia; thrombopenia; increased voluntary behaviour;  
XX muscle depression; neurasthenia; eye disease; kidney disease; myasthenia;  
XX heart disease; blood disorder; appetite loss; obesity; depression;  
XX anxiety; epilepsy; emotional disorder.

OS Unidentified.

PN WO2004014414-A1.

PD 19-FEB-2004.

PF 07-AUG-2003; 2003WO-JP010078.

PR 09-AUG-2002; 2002JP-00232684.

PA (TAKE ) TAKEDA CHEM IND LTD.

PI Kasuga H, Hinuma S, Miyashita H, Matsuoaka K;

PS WPI; 2004-191658/18.

XX The invention describes an isolated G-protein-coupled receptor (MrgC11)  
XX polypeptide (1) comprising a sequence of 322 amino acids fully defined in  
XX the specification. (1) is useful for identifying a compound that can be  
XX used to alter pain perception in a mammal, involves contacting test  
XX compounds with at least a portion of (1), identifying the test compounds  
XX that form complexes with (1), measuring the effect of the test compounds  
XX identified in above step, in an animal model of pain, and identifying  
XX test compounds that alter pain perception in the animal model as useful

CC The invention relates to novel compounds for treatment and prevention of

CC diseases including myopathy and behavioural abnormalities contain RFRP or  
CC receptor protein OT7T022 or their partial peptides or DNA encoding them.  
CC A compound of the invention has neuroprotective, ophthalmological,  
CC cardiac, haemostatic, immunostimulant, nephroprotective, anabolic,  
CC anorectic, antidepressant, tranquiliser, anticonvulsant, nootropic, and  
CC muscular-gen. activity. The compounds are useful for prevention,  
CC treatment, diagnosis and investigation of diseases including myopathy,  
CC adrenal dysfunction, twitching, aggressive behaviour, abnormal gait,  
CC hyperthermia, leukopenia, thrombopenia, increased voluntary behaviour,  
CC muscle depression, neurasthenia, eye disease, kidney disease, myasthenia,  
CC heart disease, blood disorders, appetite loss, obesity, depression,  
CC anxiety, epilepsy and emotional disorders. The present sequence is used  
CC in the exemplification of the invention.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 8; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPQNFYKLP 9  
: ||: ||:  
DB 1 MPHSPANLP 9

RESULT 35

ADQ94363  
ID ADQ94363 standard; peptide; 12 AA.

AC ADQ94363;

DT 23-SEP-2004 (first entry)

DE MrgC11 ligand screen related RFRP-1 peptide.

XX analgesic; G-protein-coupled receptor; MrgC11; pain perception; pain;  
XX animal model; structure based ligand identification; diagnostic marker;  
XX sensory perception; chronic pain; allodynia; hyperalgesia; glaucoma;  
XX MrgC11 ligand screen.

OS Unidentified.

PN US2004121410-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00327387.

PR 20-DEC-2002; 2002US-00327387.

PA (ANDE/) ANDERSON D J.

PA (DONG/) DONG X.

PA (ZYLK/) ZYLKA M.

PA (HANS/) HAN S.

PA (SIMO/) SIMON M.

PI Anderson DJ, Dong X, Zylka M, Han S, Simon M;

PS WPI; 2004-505997/48.

XX Novel G-protein coupled receptor called MrgC11 polypeptide, useful for  
XX identifying agents that alter pain perception in mammal.

XX Example 2; Page 29; 40pp; English.

XX The invention describes an isolated G-protein-coupled receptor (MrgC11)  
XX polypeptide (1) comprising a sequence of 322 amino acids fully defined in  
XX the specification. (1) is useful for identifying a compound that can be  
XX used to alter pain perception in a mammal, involves contacting test  
XX compounds with at least a portion of (1), identifying the test compounds  
XX that form complexes with (1), measuring the effect of the test compounds  
XX identified in above step, in an animal model of pain, and identifying  
XX test compounds that alter pain perception in the animal model as useful

CC in altering pain perception in a mammal, where (I) is a native Mrgc11  
CC polypeptide. The test compounds identified in the above method enhance or  
CC decrease the perception of pain. The test compounds are chosen from  
CC peptides, peptide mimetics, antibodies, small organic molecules and small  
CC inorganic molecules, preferably binding peptides. The peptides are anchored to a  
CC solid support by specifically binding an immobilised antibody. The test  
CC compounds are contained in a cellular extract prepared from cells known  
CC to express (I) or from dorsal root ganglion cells. (I) is useful for  
CC identifying a compound that binds (I), and for identifying agonist or  
CC antagonist of (I). (I) is useful as an antigen to raise polyclonal or  
CC monoclonal antibodies, as a therapeutic target, target for structure  
CC based ligand identification, and as a diagnostic marker for diagnosing  
CC changes in sensory perception, in patients suffering from disease such as  
CC chronic pain, allodynia, hyperalgesia and glaucoma. This is the amino  
CC acid sequence of a peptide used in a screening of potential mouse G-  
CC protein-coupled receptor Mrgc11 ligands.

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 8; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPONFYKLP 9  
| | | | |  
DB 1 MPHSFANLP 9

RESULT 36

AAM97397  
ID AAM97397 standard; peptide; 14 AA.

AAM97397;

24-JAN-2002 (first entry)

Human peptide #672 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KM complement related protein; cytochrome; kinase; cytokine; interferon;  
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KM multifactorial disease; autoimmune disease; infection;  
KM nervous system disease.

XX Homo sapiens.

OS WO200147944-A2.

PN 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

PF 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M,

XX WPI, 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.

PS Disclosure; Page 3815; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,

CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinases, cytokines,  
CC interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms

SQ Sequence 14 AA;

Query Match 45.2%; Score 28; DB 4; Length 14;  
Best Local Similarity 71.4%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PONFYKL 8  
| | | | |  
DB 4 PONSXYKL 10

RESULT 37

AAR97958  
ID AAR97958 standard; peptide; 15 AA.

AAR97958;

16-AUG-1996 (first entry)

Japan cedar pollen mature allergen Cry j II amino acids 436-450.

XX Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
KM Sugi pollinosis; diagnosis; treatment.

XX Cryptomeria japonica.

PN JP08047392-A.

PD 20-FEB-1996.

XX 07-NOV-1994; 94JP-00297840.

PR 05-NOV-1993; 93JP-00276773.

PR 26-MAY-1994; 94JP-00134868.

PA (MEIP) MEIJI MILK PROD CO LTD.

XX WPI; 1996-166249/17.

XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of  
PT specified 460 aminoacid protein.

PS Disclosure; Fig 5; 17pp; Japanese.

XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of  
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
CC peptides of it are useful in the diagnosis, prevention and treatment of  
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant  
CC regions of the allergen were identified using the overlapping peptides of  
CC the full epitope derived from a Cry j II antigen-specific T cell line.  
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460  
XX amino acid allergen are the most allergenic of the 90 peptides tested

SQ Sequence 15 AA;

Query Match 45.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

OY 1 MFQNFYKLPQ 10  
 ||| : |||  
 DB 5 MFOEY--PQ 12

## RESULT 38

AAW03529  
 ID AAW03529 standard; peptide; 18 AA.

XX AAW03529;

DT 17-FEB-1997 (first entry)

DE Transcriptional activation motif from human Oct-2 protein.

XX Chimaeric protein; transcription activation; cleavage;

KW transcription repression; gene therapy; therapeutic protein; phenotype;

KM prophylactic protein; gene expression.

OS Homo sapiens.

PN WO9620951-A1.

PD 11-JUL-1996.

PF 29-DEC-1995; 95WO-US016982.

PR 29-DEC-1994; 94US-00366083.

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

PI Pomerantz JL, Sharp PA, Pabo CO;

DR WPI; 1996-33938/33.

PT New chimaeric protein contg. two or more DNA binding domains - opt. also

PT domain that activates or represses transcription or cleaves target DNA,

XX and DNA encoding them, useful in gene therapy.

PS Example 4; Page 18; 74pp; English.

CC New chimaeric proteins which selectively bind DNA with Kd 10(-8) or

CC better, comprise at least one composite DNA-binding region comprising a

CC continuous polypeptide chain of 2 or more component polypeptide domains,

CC at least 2 of these being mutually heterologous and additionally may also

CC comprise at least one transcription activating or repressing domain (TAD

CC or TRD), or a DNA cleaving domain (DCD), these domains being able to bind

CC to DNA sequences linked to the target DNA sequence. Genes encoding such

CC proteins are useful in gene therapy to correct/compensate for abnormal

CC gene expression, to direct expression of therapeutic/prophylactic

CC proteins or RNA and generally to modify cell phenotype. The chimaeric

CC proteins are used to express, repress or cleave the target. This

CC transcription activating domain was derived from the human Oct-2 protein

XX SQ Sequence 18 AA;

DT 18-JUN-1999 (first entry)

DE Activation domain of human CTF.

KW Chimeric; transcription activator; DNA-binding domain; cytotoxicity;

KW proliferation; immune response; inflammatory response; clotting; p65;

XX hormonal regulation; activation domain; human.

OS Homo sapiens.

PN WO9910508-A1.

PD 04-MAR-1999.

PF 27-AUG-1997; 97WO-US015219.

PR 27-AUG-1997; 97WO-US015219.

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

PI Sridaran N;

DR WPI, 1999-190623/16.

PT Nucleic acid encoding chimeric transcription activator protein - which

PT activates transcription of a gene in a cell.

PS Disclosure; Page 21; 90pp; English.

CC The invention relates to a nucleic acid encoding a chimeric transcription

CC activator protein which activates transcription of a gene to which the

CC chimeric transcription activator protein is targeted. The nucleic acid

CC contains at least one composite transcription activation domain

CC comprising a continuous polypeptide region containing two or more

CC heterologous and do not occur in nature in the same gene product, and at

CC least one additional domain comprising a DNA-binding domain. The chimeric

CC proteins can be used to inhibit a transcriptional regulation protein or

CC inhibit the translation of an inhibitor of a cellular pathway. The

CC proteins can involve homing, cytotoxicity, proliferation, immune

CC response, inflammatory response, clotting or dissolving of clots,

CC hormonal regulation etc. By using the chimeric constructs, the production

CC of a specific protein is increased by stimulating expression of the

CC endogenous gene encoding the protein, with the absence of an immune

CC reaction against the protein, thereby resulting in a more efficient

XX SQ Sequence 18 AA;

DT 20-APR-2001 (first entry)

DE Human CTF protein activation domain motif.

KW Fusion protein; transcription factor; ligand binding domain; OCA-B; OAD;

KW transcription activation domain; gene therapy; therapeutic protein;

KW B cell specific transcriptional co-activator; cytokine; interleukin;

XX erythropoietin; tissue plasminogen activator; clotting factor; CTF.

OS Homo sapiens.

XX AAB48367

ID AAB48367 standard; peptide; 18 AA.

XX AAB48367;

PN WO20078951-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 16-JUN-2000; 2000MO-US016620.  
 XX  
 PR 18-JUN-1999; 99US-0140289P.  
 XX  
 PA (ARIA-) ARIAD GENE THERAPEUTICS INC.  
 XX  
 PI Natesan S;  
 XX  
 DR WPI; 2001-102722/11.  
 XX  
 PT New recombinant nucleic acid encoding chimeric transcription activator,  
 PT useful to effect transcription of target genes in transgenic cells or  
 PT organisms, comprising ligand binding domain and OCA-B activation domain.  
 XX  
 PS Disclosure; Page 16; 55pp; English.  
 XX  
 CC The invention relates to a recombinant nucleic acid (I) encoding a fusion  
 CC protein (chimeric transcription factor) that comprises a ligand binding  
 CC domain and a transcription activation domain which contains all or a part  
 CC of an OCA-B (a B cell specific transcriptional co-activator) activation  
 CC domain (OAB). (I) is useful for rendering a cell capable of expressing a  
 CC target gene in a ligand-dependent manner. The method involves transducing  
 CC a cell in vitro or in vivo, with (I) which encodes the fusion protein  
 CC that stimulates, in a ligand dependent manner, the transcription of a  
 CC target gene operably linked to a transcription control sequence  
 CC recognized by the fusion protein. (I) and vectors, virus and cells  
 CC containing (I) are useful for rendering a host organism capable of  
 CC regulating expression of a target gene such as a therapeutic protein,  
 CC antisense sequence or ribozyme of interest. The therapeutic proteins such  
 CC as cytokines (interleukin-2, IL-4, IL-12) when expressed can involve  
 CC homing, cytotoxicity, proliferation, immune response, inflammatory  
 CC response, clotting or dissolving of clots or hormonal regulation etc.,  
 CC and thus are useful in gene therapy techniques. The method is useful for  
 CC increasing the efficacy of many gene therapy strategies by substantially  
 CC elevating the expression of a therapeutic target gene allowing expression  
 CC to reach therapeutically effective levels. Transcription factors encoded  
 CC by (I) are also useful in the large scale production of recombinant  
 CC proteins such as erythropoietin, tissue plasminogen activator, clotting  
 CC factors, antibodies etc. Also, the factors encoded by (I) are useful in a  
 CC range of biological experiments in which precise control over a target  
 CC gene is desired. The present sequence represents an activation domain  
 CC peptide motif from human CTF  
 XX  
 SQ Sequence 18 AA;  
 Query Match 45.2%; Score 28; DB 4; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 NPYKLPQ 10  
 ||:||||  
 Db 1 NFIQLPQ 7

Search completed: June 7, 2005, 23:10:53  
 Job time : 62.2 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 15 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-6  
Perfect score: 62  
Sequence: 1 MPQNRXKLPQM 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCROS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	4	US-09-641-803-6
2	30	48.4	8	1	US-08-014-426-53
3	30	48.4	8	1	US-08-014-426-60
4	30	48.4	8	5	PCT-US94-01319-53
5	30	48.4	8	5	PCT-US94-01319-60
6	30	48.4	11	2	US-07-737-371E-64
7	29	46.8	15	4	US-09-000-003A-11
8	28	46.2	18	3	US-08-920-610-4
9	28	46.2	18	3	US-09-140-149-2
10	28	46.2	18	3	US-08-672-213-4
11	28	46.2	18	3	US-08-973-131-31
12	28	46.2	18	4	US-09-615-917-2
13	27	45.5	15	4	US-08-480-190-271
14	27	45.5	15	4	US-08-488-379-271
15	27	45.5	15	4	US-08-475-399A-271
16	27	43.5	15	4	US-08-077-255A-271
17	27	43.5	15	5	PCT-US93-07545-271
18	26	41.9	10	2	US-08-934-222-93
19	26	41.9	10	2	US-08-933-402-93
20	26	41.9	10	2	US-09-207-621-93
21	26	41.9	10	2	US-08-532-818-93
22	26	41.9	10	3	US-09-231-797-93
23	26	41.9	10	3	US-08-934-224-93
24	26	41.9	10	3	US-08-933-843-93
25	26	41.9	10	3	US-08-934-223-93
26	26	41.9	10	3	US-09-413-492-93
27	26	41.9	11	2	US-08-704-655-18

28	41.9	11	4	US-09-920-174-3	Sequence 3, Appl
29	41.9	11	4	US-09-920-195A-3	Sequence 3, Appl
30	41.9	16	3	US-08-462-436-22	Sequence 22, Appl
31	41.9	16	3	US-08-465-275-22	Sequence 22, Appl
32	41.9	16	4	US-08-640-877-22	Sequence 22, Appl
33	41.9	16	4	US-09-799-576A-22	Sequence 22, Appl
34	41.9	16	4	US-09-799-540-22	Sequence 22, Appl
35	40.3	8	2	US-08-765-061-9	Sequence 2, Appl
36	40.3	8	3	US-09-514-739-2	Sequence 2, Appl
37	40.3	10	1	US-07-954-213-4	Sequence 4, Appl
38	40.3	10	2	US-08-765-061-7	Sequence 7, Appl
39	40.3	11	2	US-07-737-371E-39	Sequence 39, Appl
40	40.3	11	2	US-07-737-371E-40	Sequence 40, Appl
41	40.3	11	4	US-09-579-883B-12	Sequence 12, Appl
42	40.3	12	1	US-08-275-983B-17	Sequence 17, Appl
43	40.3	12	3	US-08-794-002-10	Sequence 10, Appl
44	40.3	12	3	US-08-854-039B-10	Sequence 10, Appl
45	40.3	12	4	US-08-765-702B-10	Sequence 10, Appl
46	40.3	15	2	US-08-637-418-9	Sequence 9, Appl
47	40.3	15	2	US-08-637-418-10	Sequence 10, Appl
48	40.3	16	1	US-07-954-213-12	Sequence 12, Appl
49	40.3	16	3	US-07-861-458C-134	Sequence 134, Appl
50	40.3	5	4	US-09-608-892-36	Sequence 36, Appl
51	38.7	7	2	US-08-968-676-69	Sequence 69, Appl
52	38.7	7	4	US-09-261-894A-69	Sequence 69, Appl
53	38.7	8	4	US-09-266-764-26	Sequence 26, Appl
54	38.7	8	4	US-09-239-043D-52	Sequence 52, Appl
55	38.7	8	4	US-09-239-043D-823	Sequence 823, Appl
56	38.7	8	4	US-09-239-043D-1597	Sequence 1597, Appl
57	38.7	9	1	US-08-024-253-18	Sequence 18, Appl
58	38.7	9	2	US-08-629-291A-27	Sequence 27, Appl
59	38.7	9	2	US-08-658-335B-27	Sequence 27, Appl
60	38.7	9	3	US-08-159-339A-367	Sequence 367, Appl
61	38.7	9	3	US-07-987-264-6	Sequence 6, Appl
62	38.7	9	3	US-09-492-543-73	Sequence 73, Appl
63	38.7	9	3	US-09-492-543-101	Sequence 101, Appl
64	38.7	9	4	US-09-406-640-27	Sequence 27, Appl
65	38.7	9	4	US-09-239-043D-47	Sequence 47, Appl
66	38.7	9	4	US-09-239-043D-803	Sequence 803, Appl
67	38.7	9	4	US-09-239-043D-1591	Sequence 1591, Appl
68	38.7	9	4	US-09-239-043D-1842	Sequence 1842, Appl
69	38.7	9	4	US-09-971-020A-20	Sequence 20, Appl
70	38.7	9	4	US-09-971-020A-22	Sequence 22, Appl
71	38.7	10	4	US-09-239-043D-1194	Sequence 1194, Appl
72	38.7	10	4	US-09-239-043D-2291	Sequence 2291, Appl
73	38.7	11	2	US-07-737-371E-20	Sequence 20, Appl
74	38.7	11	2	US-07-737-371E-21	Sequence 21, Appl
75	38.7	11	2	US-07-737-371E-22	Sequence 22, Appl
76	38.7	11	2	US-07-737-371E-23	Sequence 23, Appl
77	38.7	11	2	US-07-737-371E-24	Sequence 24, Appl
78	38.7	11	2	US-07-737-371E-27	Sequence 27, Appl
79	38.7	11	2	US-07-737-371E-37	Sequence 37, Appl
80	38.7	11	2	US-07-737-371E-55	Sequence 55, Appl
81	38.7	11	2	US-07-737-371E-65	Sequence 65, Appl
82	38.7	11	4	US-09-239-043D-107	Sequence 107, Appl
83	38.7	11	4	US-09-239-043D-957	Sequence 957, Appl
84	38.7	11	4	US-09-239-043D-1676	Sequence 1676, Appl
85	38.7	11	6	5441935-8	Patent No. 5441935
86	38.7	12	2	US-08-811-492-145	Sequence 145, Appl
87	38.7	12	2	US-08-811-492-147	Sequence 147, Appl
88	38.7	12	2	US-08-811-492-147	Sequence 147, Appl
89	38.7	13	4	US-09-927-734C-10	Sequence 10, Appl
90	38.7	13	4	US-08-637-418-19	Sequence 19, Appl
91	38.7	15	2	US-08-637-418-20	Sequence 20, Appl
92	38.7	15	3	US-08-101-624-19	Sequence 19, Appl
93	38.7	15	3	US-08-596-257A-10	Sequence 10, Appl
94	38.7	15	3	US-08-479-744A-19	Sequence 19, Appl
95	38.7	15	3	US-08-860-339-10	Sequence 10, Appl
96	38.7	15	3	US-08-280-757B-19	Sequence 19, Appl
97	38.7	15	3	US-09-227-357-539	Sequence 539, Appl
98	38.7	15	4	US-09-370-644B-10	Sequence 10, Appl
99	38.7	15	4	US-09-425-762-19	Sequence 19, Appl
100	38.7	15	4	US-09-573-629-10	Sequence 10, Appl





RESULT 4  
PCT-US94-01319-53  
Sequence 53, Application PC/TUS9401319  
GENERAL INFORMATION:  
APPLICANT: Renschler, Markus F.  
APPLICANT: Levy, Ronald  
APPLICANT: Bharti, Ramesh  
APPLICANT: Dower, William  
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE  
TITLE OF INVENTION: PEPTIDES  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01319  
FILING DATE: 04-FEB-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,426  
FILING DATE: 05-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 5490A-204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
PCT-US94-01319-53  
Query Match 48.4%; Score 30; DB 5; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 0; Indels 0;  
Qy 1 MPONFYK 7  
Db 1 MPEDFYR 7  
RESULT 5  
PCT-US94-01319-60  
Sequence 60, Application PC/TUS9401319  
GENERAL INFORMATION:  
APPLICANT: Renschler, Markus F.  
APPLICANT: Levy, Ronald  
APPLICANT: Bharti, Ramesh  
APPLICANT: Dower, William  
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE  
TITLE OF INVENTION: PEPTIDES  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto

STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01319  
FILING DATE: 04-FEB-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,426  
FILING DATE: 05-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 5490A-204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
PCT-US94-01319-60  
Query Match 48.4%; Score 30; DB 5; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 0; Indels 0;  
Qy 1 MPONFYK 7  
Db 1 MPEDFYR 7  
RESULT 6  
US-07-737-371E-64  
Sequence 64, Application US/07737371E  
Patent No. 5876948  
GENERAL INFORMATION:  
APPLICANT: Yankner, Bruce A.  
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,371E  
FILING DATE: 29-JUL-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/559,172  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00108/028002

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-64

Query Match 48.4%; Score 30; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 29;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PNFYKLP 9  
|||:  
Db 4 PQFFGLP 11

RESULT 7  
US-09-000-003A-11  
Sequence 11, Application US/09000003A  
Patent No. 6652850  
GENERAL INFORMATION:  
APPLICANT: Philip, Ramla  
Lebkowski, Jane S.  
TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND  
THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE  
SPECIFIC IMMUNITY  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Alexis Barron, Esq.  
STREET: Suite 2600 Aramark Tower, 1101 Market Street  
CITY: Philadelphia  
STATE: PA  
COUNTRY: United States of America  
ZIP: 19107  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/000,003A  
FILING DATE: 15-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12012  
FILING DATE: 19-JUL-1996  
APPLICATION NUMBER: US 60/001,312  
FILING DATE: 21-JUL-1995  
APPLICATION NUMBER: US 60/007,184  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: US 08/566,286  
FILING DATE: 01-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barron, Alexis  
REGISTRATION NUMBER: 22,702  
REFERENCE/DOCKET NUMBER: 20,846-K USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 923-4466  
TELEFAX: (215) 923-2189  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: N-terminal  
FRAGMENT TYPE: N-terminal  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-000-003A-11

Query Match 46.8%; Score 29; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 62;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PNFYKLPQM 11  
|||:  
Db 4 PTVFYNIIPM 13

RESULT 8  
US-08-920-610-4  
Sequence 4, Application US/08920610  
Patent No. 6015709  
GENERAL INFORMATION:  
APPLICANT: Natesan, Sridaran  
TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS AND  
COMPOSITIONS AND USES RELATED THERETO  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FOLEY, HONG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/920,610  
FILING DATE: 27-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: APV-006.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-920-610-4  
Query Match 45.2%; Score 28; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1,1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NPFYKLPQ 10  
|||:  
Db 1 NPLGLPQ 7

RESULT 9  
US-09-140-149-2  
Sequence 2, Application US/09140149  
Patent No. 6117680  
GENERAL INFORMATION:  
APPLICANT: Natesan, Sridaran  
APPLICANT: Gilman, Michael Z  
TITLE OF INVENTION: No. 6117680e1 Compositions and Methods for Regulation of  
FILE REFERENCE: 363C  
CURRENT APPLICATION NUMBER: US/09/140,149  
FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 08/918,401

EARLIER FILING DATE: 1997-08-26  
EARLIER APPLICATION NUMBER: 08/920,610  
EARLIER FILING DATE: 1997-08-27  
EARLIER APPLICATION NUMBER: 09/126,009  
EARLIER FILING DATE: 1998-07-29  
EARLIER APPLICATION NUMBER: PCT/US97/15219  
EARLIER FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-140-149-2

Query Match 45.2%; Score 28; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10  
Db 1 NFKLPQ 7

RESULT 10  
US-08-672-213-4  
Sequence 4, Application US/08672213  
Patent No. 6306649

GENERAL INFORMATION:  
APPLICANT: GILMAN, Michael Z.  
APPLICANT: NATESAN, Sridaran  
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
TITLE OF INVENTION: FACTORS IN GENE THERAPY  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139-4234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,213  
FILING DATE: 27-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,553  
FILING DATE: 27-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,614  
FILING DATE: 29-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BERSTEIN, David L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: ARIAD 3468  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-0208

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-672-213-4

Query Match 45.2%; Score 28; DB 3; Length 18;

Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10  
Db 1 NFKLPQ 7

RESULT 11  
US-08-973-131-31  
Sequence 31, Application US/08973131  
Patent No. 6326166

GENERAL INFORMATION:  
APPLICANT: Pomerantz, Joel L.  
APPLICANT: Pado, Carl O.  
TITLE OF INVENTION: Chimeric DNA-binding proteins  
FILE REFERENCE: APV-022.02  
CURRENT APPLICATION NUMBER: US/08/973,131  
CURRENT FILING DATE: 1998-03-16  
EARLIER APPLICATION NUMBER: PCT/US95/16982  
EARLIER FILING DATE: 1995-12-29  
EARLIER APPLICATION NUMBER: 08/366,083  
EARLIER FILING DATE: 1994-12-29  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 18  
TYPE: PRT  
ORGANISM: human  
US-08-973-131-31

Query Match 45.2%; Score 28; DB 3; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFKLPQ 10  
Db 1 NFKLPQ 7

RESULT 12  
US-09-615-917-2  
Sequence 2, Application US/09615917  
Patent No. 6479653

GENERAL INFORMATION:  
APPLICANT: Natesan, Sridaran  
APPLICANT: Gilman, Michael Z.  
TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of  
TITLE OF INVENTION: Transcription  
FILE REFERENCE: 363C continuation  
CURRENT APPLICATION NUMBER: US/09/615,917  
CURRENT FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 08/918,401  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 08/920,610  
PRIOR FILING DATE: 1997-08-27  
PRIOR APPLICATION NUMBER: 09/126,009  
PRIOR FILING DATE: 1998-07-29  
PRIOR APPLICATION NUMBER: 09/140,149  
PRIOR FILING DATE: 1998-08-26  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-615-917-2

Query Match 45.2%; Score 28; DB 4; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NFKLPO 10  
|||  
DB 1 NFKLPO 7

## RESULT 13

US-08-480-190-271  
; Sequence 271, Application US/08480190  
; Patent No. 5827516  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,190  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 271:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-480-190-271

Query Match 43.5%; Score 27; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NFKLPO 10  
|||  
DB 2 NFYSPO 8

## RESULT 14

US-08-488-379-271  
; Sequence 271, Application US/08488379  
; Patent No. 5880103  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-488-379-271

Query Match 43.5%; Score 27; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NFKLPO 10  
|||  
DB 2 NFYSPO 8

## RESULT 15

US-08-475-399A-271  
; Sequence 271, Application US/08475399A  
; Patent No. 6509033  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chicz, Roman M.  
; APPLICANT: Vignali, Dario A.A.  
; APPLICANT: Hedley, Mary L.  
; APPLICANT: Stern, Lawrence J.  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 276  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/06/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-271

Query Match  
Best Local Similarity 43.5%; Score 27; DB 4; Length 15;  
Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10  
DB 2 NRYSPQ 8

RESULT 16  
US-08-077-255A-271  
Sequence 271, Application US/08077255A  
Patent No. 6696061  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906

TELEX: 200154  
INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-077-255A-271

Query Match  
Best Local Similarity 43.5%; Score 27; DB 4; Length 15;  
Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10  
DB 2 NRYSPQ 8

RESULT 17  
PCT-US93-07545-271  
Sequence 271, Application PC/TUS9307545  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 271:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-271

Query Match  
Best Local Similarity 43.5%; Score 27; DB 5; Length 15;  
Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NRYKLPQ 10  
DB 2 NRYSPQ 8

RESULT 18  
US-08-934-222-93  
Sequence 93, Application US/08934222  
Patent No. 5926896  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,222  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-222-93  
Query Match Score 26; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 PONFYKLP 9  
DB 2 PNNLDKLP 9  
RESULT 19  
US-08-933-402-93  
Sequence 93, Application US/08933402  
Patent No. 5948887  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA

ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-93  
Query Match Score 26; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 PONFYKLP 9  
DB 2 PNNLDKLP 9  
RESULT 20  
US-09-207-621-93  
Sequence 93, Application US/09207621  
Patent No. 5952465  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/207,621  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-207-621-93

Query Match 41.9%; Score 26; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PNNFYKLP 9  
Db 2 PNNLDKLP 9

RESULT 21  
US-08-532-818-93  
Sequence 93, Application US/08532818  
Patent No. 5965698  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-93

Query Match 41.9%; Score 26; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 PNNFYKLP 9  
Db 2 PNNLDKLP 9

Db 2 PNNLDKLP 9

RESULT 22  
US-09-231-797-93  
Sequence 93, Application US/09231797  
Patent No. 6084066  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/231,797  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-231-797-93

Query Match 41.9%; Score 26; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PNNFYKLP 9  
Db 2 PNNLDKLP 9

RESULT 23  
US-08-934-224-93  
Sequence 93, Application US/08934224  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW

CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-224-93

Query Match 41.9%; Score 26; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKLP 9  
| | | | |  
Db 2 PNNLDKLP 9

RESULT 24  
US-08-933-843-93  
Sequence 93, Application US/08933843  
Patent No. 6111069  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,843  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-843-93

Query Match 41.9%; Score 26; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKLP 9  
| | | | |  
Db 2 PNNLDKLP 9

RESULT 25  
US-08-934-223-93  
Sequence 93, Application US/08934223  
Patent No. 6147189  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,223  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-223-93



Query Match 41.9%; Score 26; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNNFYKLP 9  
DB 2 PNNLDKLP 9

RESULT 26  
US-09-413-492-93  
; Sequence 93, Application US/09413492  
; Patent No. 6258550  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjmatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/413,492  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Iacason, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-413-492-93

Query Match 41.9%; Score 26; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNNFYKLP 9  
DB 2 PNNLDKLP 9

RESULT 27  
US-08-704-655-18  
; Sequence 18, Application US/08704655  
; Patent No. 5869453  
; GENERAL INFORMATION:  
; APPLICANT: Moss, Denis J.  
; APPLICANT: Burrows, Scott R.

APPLICANT: Khanna, Rajiv  
APPLICANT: Kerr, Vebberly M.  
APPLICANT: Burrows, Jacqueline M.  
APPLICANT: Sunbrier, Andreas  
TITLE OF INVENTION: Cytotoxic T Cell Epitopes  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,655  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU95/00140  
FILING DATE: 16-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (712) 789-2679  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-704-655-18

Query Match 41.9%; Score 26; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11  
DB 3 FYNIPPM 9

RESULT 28  
US-09-920-174-3  
; Sequence 3, Application US/09920174  
; Patent No. 6699477  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.  
; APPLICANT: MOSS, DENIS J.  
; APPLICANT: BURROWS, SCOTT R.  
; TITLE OF INVENTION: EBV CTL EPITOPES  
; FILE REFERENCE: FBRC:008USC2  
; CURRENT APPLICATION NUMBER: US/09/920,174  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 09/920,175  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 09/194,450  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-09-920-174-3

Query Match 41.9%; Score 26; DB 4; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPOM 11  
DB 3 FYNIPPM 9

RESULT 29  
US-09-920-195A-3  
Sequence 3, Application US/09920195A  
Patent No. 6703024  
GENERAL INFORMATION:  
APPLICANT: KHANNA, RAJIV  
APPLICANT: KERR, BEVERLEY M.  
APPLICANT: MISKO, THOR S.  
APPLICANT: MOSS, DENIS J.  
APPLICANT: BURROWS, SCOTT R.  
TITLE OF INVENTION: EBV CTL EPITOPES  
FILE REFERENCE: FBRC:008USC1  
CURRENT APPLICATION NUMBER: US/09/920,195A  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 09/194,450  
PRIOR FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-920-195A-3

Query Match 41.9%; Score 26; DB 4; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPOM 11  
DB 3 FYNIPPM 9

RESULT 30  
US-08-462-436-22  
Sequence 22, Application US/08462436  
Patent No. 6001823  
GENERAL INFORMATION:  
APPLICANT: HULTGREN, SCOTT  
TITLE OF INVENTION: A NEW METHOD FOR THE TREATMENT AND  
TITLE OF INVENTION: PROPHYLAXIS OF BACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,436

FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13455  
FILING DATE: 18-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,035  
FILING DATE: 18-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: HULTGREN-1C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-436-22

Query Match 41.9%; Score 26; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
DB 9 QDHYKMP 15

RESULT 31  
US-08-465-275-22  
Sequence 22, Application US/08465275  
Patent No. 6153396  
GENERAL INFORMATION:  
APPLICANT: HULTGREN, SCOTT  
APPLICANT: KUEHN, META  
APPLICANT: XU, Zheng  
APPLICANT: OGG, Derek  
APPLICANT: HARRIS, Mark  
APPLICANT: LEPISTO, Matci  
APPLICANT: KILBERG, Jan  
APPLICANT: JONES, Charles H.  
TITLE OF INVENTION: TREATMENT OR PROPHYLAXIS OF DISEASES  
TITLE OF INVENTION: CAUSED BY PILUS-FORMING BACTERIA  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,275  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,035  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-275-22

Query Match 41.9%; Score 26; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|  
DB 9 QDHYKMP 15

RESULT 32  
US-08-640-877-22  
Sequence 22, Application US/08640877  
Patent No. 6420127  
GENERAL INFORMATION:  
APPLICANT: HULJGREN, Scott  
APPLICANT: KUEHN, Meta  
APPLICANT: XU, Zheng  
APPLICANT: OGG, Derek  
APPLICANT: HARRIS, Mark  
APPLICANT: LEPISTO, Matti  
APPLICANT: JONES, Charles H.  
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 2213-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/640,877  
FILING DATE: 10-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-640-877-22

Query Match 41.9%; Score 26; DB 4; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|  
DB 9 QDHYKMP 15

RESULT 33  
US-09-799-576A-22  
Sequence 22, Application US/09799576A  
Patent No. 6548255  
GENERAL INFORMATION:  
APPLICANT: HULJGREN, Scott  
APPLICANT: KUEHN, Meta  
APPLICANT: XU, Zheng  
APPLICANT: OGG, Derek  
APPLICANT: HARRIS, Mark  
APPLICANT: LEPISTO, Matti  
APPLICANT: JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 2213-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,576A  
FILING DATE: 07-Mar-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/640,877  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: WO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-164  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-799-576A-22

Query Match 41.9%; Score 26; DB 4; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|  
DB 9 QDHYKMP 15

```
RESULT 34
US-09-799-540-22
; Sequence 22, Application US/09799540
; Patent No. 6596504
; GENERAL INFORMATION:
; APPLICANT: HULTIGREN, Scott
; APPLICANT: KUEHN, Meta
; APPLICANT: XU, Zheng
; APPLICANT: OGG, Derek
; APPLICANT: HARRIS, Mark
; APPLICANT: LEPISTO, Matti
; APPLICANT: KTHLBERG, Jan
; APPLICANT: JONES, Charles H.
; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/799,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,877
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 016921-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-799-540-22

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9
|:|:|:|
DB 9 QDHYKWP 15

RESULT 35
US-08-765-061-9
; Sequence 9, Application US/08765061
; Patent No. 5935796
; GENERAL INFORMATION:
; APPLICANT: FOSANG, AMANDA J
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: RELATING TO THE PROTEOLYCAN PROTEINS OF CARTILAGE
; TITLE OF INVENTION: BREAKDOWN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRIFFITH HACK
; STREET: 509 ST KILDA ROAD
```

```
; CITY: MELBOURNE
; STATE: VICTORIA
; COUNTRY: AUSTRALIA
; ZIP: 3004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,061
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM6668
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTER, VIVIAN B
; REFERENCE/DOCKET NUMBER: PP4262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +61 3 9243 8300
; TELEFAX: +61 3 9 243 8333/4
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-765-061-9

Query Match 40.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONEY 6
|:|:|:|
DB 2 IPENPF 7

RESULT 36
US-09-514-739-2
; Sequence 2, Application US/09514739
; Patent No. 6379946
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Tenor, Jennifer L
; APPLICANT: Cliche, Todd A
; APPLICANT: Petell, James K.
; APPLICANT: Strickland, James A
; APPLICANT: Orr, Gregory L
; APPLICANT: Faily, Raymond
; APPLICANT: Binstlim, Scott
; TITLE OF INVENTION: INSECTICIDAL PROTEIN TOXINS FROM XENORHABDUS
; FILE REFERENCE: 50585A
; CURRENT APPLICATION NUMBER: US/09/514,739
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: 09/072,264
; EARLIER FILING DATE: 1998-05-04
; EARLIER APPLICATION NUMBER: 60/045,641
; EARLIER FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenorhabdus Wi
; US-09-514-739-2
```

Query Match 40.3%; Score 25; DB 3; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
| | | | |  
Db 2 QNFYRYP 8

## RESULT 37

US-07-954-213-4  
; Sequence 4, Application US/07954213  
; Patent No. 5387504  
; GENERAL INFORMATION:  
; APPLICANT: Mumford, Richard A.  
; APPLICANT: Lark, Michael W.  
; APPLICANT: Bayne, Ellen B.K.  
; APPLICANT: Hoerner, Lori A.  
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM  
; TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 E. Lincoln Avenue  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/07/954,213  
; APPLICATION NUMBER: US/07/954,213  
; FILING DATE: 19920930  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wallen, John W.III  
; REGISTRATION NUMBER: 35,403  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-954-213-4

Query Match 40.3%; Score 25; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6  
| | | | |  
Db 2 IPENFF 7

## RESULT 38

US-08-765-061-7  
; Sequence 7, Application US/08765061  
; Patent No. 5935796  
; GENERAL INFORMATION:  
; APPLICANT: POSANG, AMANDA J  
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS  
; TITLE OF INVENTION: RELATING TO THE PROTEOLYCAN PROTEINS OF CARTILAGE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: GRIFFITH HACK  
STREET: 509 ST KILDA ROAD  
CITY: MELBOURNE  
STATE: VICTORIA  
COUNTRY: AUSTRALIA  
ZIP: 3004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,061  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PM6668  
FILING DATE: 07-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SANTER, VIVIEN B  
REFERENCE/DOCKET NUMBER: FP4262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: +61 3 9243 8300  
TELEFAX: +61 3 9 243 8333/4  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: C-terminal  
US-08-765-061-7

Query Match 40.3%; Score 25; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6  
| | | | |  
Db 2 IPENFF 7

## RESULT 39

US-07-737-371E-39  
; Sequence 39, Application US/07737371E  
; Patent No. 5876948  
; GENERAL INFORMATION:  
; APPLICANT: Yankner, Bruce A.  
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/737,371E  
; FILING DATE: 29-JUL-1991  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/559,172  
; FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29, 066  
REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-39

Query Match 40.3%; Score 25; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 P0NFYKL 8  
|||  
Db 4 P0CFYPL 10

RESULT 40  
US-07-737-371E-40  
Sequence 40, Application US/07737371E  
Patent No. 5876948  
GENERAL INFORMATION:  
APPLICANT: Yankner, Bruce A.  
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,371E  
FILING DATE: 29-JUL-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/559,172  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29, 066  
REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-40

Query Match 40.3%; Score 25; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 P0NFYKL 8  
|||  
Db 4 P0CFYPL 10

Search completed: June 7, 2005, 23:23:17  
Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 49.5 Seconds  
(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-6  
Perfect score: 62  
Sequence: 1 MPQNYKLPQM 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	11	14	US-10-281-652-6
2	62	100.0	11	16	US-10-691-157-6
3	62	100.0	11	17	US-10-691-330-6
4	29	46.8	10	14	US-10-062-710-83
5	29	46.8	15	9	US-09-888-721-10
6	28	45.2	12	14	US-10-075-869-41
7	28	45.2	12	15	US-10-366-493-41
8	28	45.2	12	15	US-10-432-585-3
9	28	45.2	12	16	US-10-719-587-39
10	28	45.2	12	16	US-10-477-712B-7
11	28	45.2	12	16	US-10-487-634-39

12	45.2	12	17	US-10-926-893-41	Sequence 41, Appl	
13	28	45.2	18	10	US-09-852-370-31	Sequence 31, Appl
14	28	45.2	18	14	US-10-002-244-4	Sequence 4, Appl
15	27	43.5	12	16	US-10-649-873-111	Sequence 111, App
16	26	41.9	9	17	US-10-014-340-803	Sequence 803, App
17	26	41.9	9	14	US-10-845-391-53	Sequence 53, Appl
18	26	41.9	11	9	US-09-920-174-3	Sequence 3, Appl
19	26	41.9	11	17	US-09-920-195A-3	Sequence 3, Appl
20	26	41.9	15	14	US-10-125-869A-43	Sequence 43, Appl
21	26	41.9	15	14	US-10-125-869A-119	Sequence 119, App
22	26	41.9	15	15	US-10-462-262-267	Sequence 267, App
23	26	41.9	15	15	US-10-462-262-343	Sequence 343, App
24	26	41.9	16	9	US-09-799-576A-22	Sequence 22, Appl
25	26	41.9	16	9	US-09-799-540-22	Sequence 22, Appl
26	26	41.9	16	9	US-09-799-608-22	Sequence 22, Appl
27	26	41.9	16	10	US-09-798-932-22	Sequence 22, Appl
28	26	41.9	16	10	US-09-799-680-22	Sequence 22, Appl
29	26	41.9	17	10	US-09-745-078A-21	Sequence 21, Appl
30	26	41.9	17	10	US-09-962-756-1205	Sequence 1205, App
31	26	41.9	17	10	US-09-962-756-1757	Sequence 1757, App
32	26	41.9	17	10	US-09-962-756-1911	Sequence 1911, App
33	26	41.9	17	14	US-10-374-624-21	Sequence 21, Appl
34	26	41.9	17	15	US-10-253-471-1205	Sequence 1205, App
35	26	41.9	17	15	US-10-253-471-1757	Sequence 1757, App
36	26	41.9	17	15	US-10-253-493-1205	Sequence 1205, App
37	26	41.9	17	15	US-10-253-493-1757	Sequence 1757, App
38	26	41.9	17	15	US-10-253-493-1911	Sequence 1911, App
39	26	41.9	17	15	US-10-253-493-1911	Sequence 1911, App
40	26	41.9	18	10	US-09-745-078A-20	Sequence 20, Appl
41	26	41.9	18	14	US-09-943-944E-140	Sequence 140, App
42	26	40.3	5	11	US-09-756-283A-42	Sequence 42, Appl
43	26	40.3	8	9	US-09-756-283A-58	Sequence 58, Appl
44	26	40.3	8	9	US-09-756-283A-90	Sequence 90, Appl
45	26	40.3	8	9	US-09-756-283A-96	Sequence 96, Appl
46	26	40.3	8	13	US-10-078-968-2	Sequence 2, Appl
47	26	40.3	8	17	US-10-931-697-2	Sequence 2, Appl
48	26	40.3	8	17	US-10-684-346-31	Sequence 31, Appl
49	26	40.3	9	15	US-10-245-871-107	Sequence 107, App
50	26	40.3	9	15	US-10-253-286-107	Sequence 107, App
51	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
52	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
53	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
54	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
55	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
56	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
57	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
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59	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
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61	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
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64	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
65	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
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77	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
78	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
79	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
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81	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
82	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
83	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl
84	26	40.3	9	17	US-10-823-253-6	Sequence 6, Appl

85	24	38.7	6	17	US-10-808-187-2401	Sequence 2401, Ap
86	24	38.7	7	10	US-09-261-894-69	Sequence 69, Appl
87	24	38.7	8	15	US-10-408-133-26	Sequence 26, Appl
88	24	38.7	8	17	US-10-654-601-52	Sequence 52, Appl
89	24	38.7	8	17	US-10-654-601-823	Sequence 823, Appl
90	24	38.7	8	17	US-10-654-601-1597	Sequence 1597, Ap
91	24	38.7	9	8	US-08-344-824-331	Sequence 331, Appl
92	24	38.7	9	8	US-09-749-831-6	Sequence 6, Appl1
93	24	38.7	9	9	US-09-835-948-73	Sequence 73, Appl
94	24	38.7	9	9	US-09-835-948-101	Sequence 101, Appl
95	24	38.7	9	14	US-10-172-587-27	Sequence 27, Appl
96	24	38.7	9	14	US-10-172-587-73	Sequence 73, Appl
97	24	38.7	9	14	US-10-172-587-101	Sequence 101, Appl
98	24	38.7	9	15	US-10-428-335-92	Sequence 92, Appl
99	24	38.7	9	15	US-10-428-335-133	Sequence 133, Appl
100	24	38.7	9	16	US-10-469-125-6	Sequence 6, Appl1

## ALIGNMENTS

## RESULT 1

US-10-281-652-6  
; Sequence 6, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-6

Query Match 100.0%; Score 62; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00038;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11  
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Db 1 MPONFYKLPOM 11

RESULT 2  
US-10-691-157-6  
; Sequence 6, Application US/10691157  
; Publication No. US20040266681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265.00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-6

Query Match 100.0%; Score 62; DB 16; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00038;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFYKLPOM 11  
| | | | | | | | | | | | |  
Db 1 MPONFYKLPOM 11

RESULT 3  
US-10-691-330-6  
; Sequence 6, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Krusel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265.00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-6

Query Match 100.0%; Score 62; DB 17; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00038;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPONFYKLPOM 11

RESULT 4  
US-10-062-710-83  
; Sequence 83, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank O.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Pai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes



FILE OF INVENTION: Via Peptide Vaccines  
FILE REFERENCE: 3781-001-27  
CURRENT APPLICATION NUMBER: US/10/062,710  
CURRENT FILING DATE: 2002-02-05  
PRIOR APPLICATION NUMBER: US 60/310,498  
PRIOR FILING DATE: 2001-08-08  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 83  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HIV CTL-Epitopes  
US-10-062-710-83

Query Match 46.8%; Score 29; DB 14; Length 10;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYKL 8  
DB 1 PDNFYKL 7

RESULT 5  
US-09-888-721-10  
Sequence 10, Application US/09888721  
Patent No. US2002013290A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Wils, Pierre  
APPLICANT: Zhu, Quan  
APPLICANT: Laurent, Olivier  
APPLICANT: Marasco, Wayne A.  
APPLICANT: Schertman, Daniel  
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
FILE REFERENCE: 23611-A USA  
CURRENT APPLICATION NUMBER: US/09/888,721  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: 60/213,653  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Epstein-Barr Virus  
US-09-888-721-10

Query Match 46.8%; Score 29; DB 9; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PQNFYKL 11  
DB 4 PTFYFNIPPM 13

RESULT 6  
US-10-075-869-41  
Sequence 41, Application US/10075869  
Publication No. US20030104622A1  
GENERAL INFORMATION:  
APPLICANT: Robbins, Paul D.  
APPLICANT: Mi, Zhibao  
APPLICANT: Frizzeil, Raymond  
APPLICANT: Glorioso, Joseph C.  
APPLICANT: Gambotto, Andrea  
TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT  
FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT  
TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES

FILE REFERENCE: AP32573-AAA 072396,0237  
CURRENT APPLICATION NUMBER: US/10/075,869  
CURRENT FILING DATE: 2002-02-13  
PRIOR APPLICATION NUMBER: 60/151,980  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: 60/188,944  
PRIOR FILING DATE: 2000-03-13  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 41  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: random peptide library  
US-10-075-869-41

Query Match 45.2%; Score 28; DB 14; Length 12;  
Best Local Similarity 44.4%; Pred. No. 3.7e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKL 11  
DB 4 KNFFWLPEL 12

RESULT 7  
US-10-366-493-41  
Sequence 41, Application US/10366493  
Publication No. US20030219826A1  
GENERAL INFORMATION:  
APPLICANT: Robbins, Paul D.  
APPLICANT: Mi, Zhibao  
APPLICANT: Frizzeil, Raymond  
APPLICANT: Glorioso, Joseph C.  
APPLICANT: Gambotto, Andrea  
APPLICANT: Mai, Jeffrey C.  
TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND CYTOPLASMIC  
TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES  
FILE REFERENCE: AP32573-A-A-A-A 072396,0246  
CURRENT APPLICATION NUMBER: US/10/366,493  
CURRENT FILING DATE: 2003-02-12  
PRIOR APPLICATION NUMBER: 10/075,869  
PRIOR FILING DATE: 2002-02-13  
PRIOR APPLICATION NUMBER: 09/653,182  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: 60/188,944  
PRIOR FILING DATE: 2000-03-13  
PRIOR APPLICATION NUMBER: 60/151,980  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 41  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pep 35  
US-10-366-493-41

Query Match 45.2%; Score 28; DB 15; Length 12;  
Best Local Similarity 44.4%; Pred. No. 3.7e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKL 11  
DB 4 KNFFWLPEL 12

RESULT 8  
US-10-432-585-3  
Sequence 3, Application US/10432585

; Publication No. US20040029215A1  
; GENERAL INFORMATION:  
; APPLICANT: SUENAGA, Masato  
; APPLICANT: YAMADA, Takao  
; APPLICANT: NISHIMURA, Osamu  
; TITLE OF INVENTION: Method of Production for RFRP  
; FILE REFERENCE: 2829 USOP  
; CURRENT APPLICATION NUMBER: US/10/432,585  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: JP 2000-373125  
; PRIOR FILING DATE: 2000-12-07  
; NUMBER OF SEQ ID NOS: 30  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Human  
US-10-432-585-3

Query Match 45.2%; Score 28; DB 15; Length 12;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
||:|  
Db 1 MPHSFANLP 9

RESULT 9  
US-10-719-587-39  
; Sequence 39, Application US/10719587  
; Publication No. US20040132073A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: Novel G protein-coupled receptor protein, its DNA and ligand ther  
; FILE REFERENCE: 2368USOP-CIP  
; CURRENT APPLICATION NUMBER: US/10/719,587  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 09/831,758  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: PCT/JP99/06283  
; PRIOR FILING DATE: 1999-11-11  
; PRIOR APPLICATION NUMBER: JP 10-323759  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: JP 11-060030  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: JP 11-106812  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: JP 11-166672  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: JP 11-221640  
; PRIOR FILING DATE: 1999-08-04  
; PRIOR APPLICATION NUMBER: JP 11-259818  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 39  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form  
US-10-719-587-39

Query Match 45.2%; Score 28; DB 16; Length 12;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
||:|  
Db 1 MPHSFANLP 9

RESULT 10  
US-10-477-712B-7

; Sequence 7, Application US/10477712B  
; Publication No. US20040185525A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: A Method for Producing A Peptide  
; FILE REFERENCE: OKA-0213  
; CURRENT APPLICATION NUMBER: US/10/477,712B  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: JP 2001-147341  
; PRIOR FILING DATE: 2001-05-17  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Human  
US-10-477-712B-7

Query Match 45.2%; Score 28; DB 16; Length 12;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
||:|  
Db 1 MPHSFANLP 9

RESULT 11  
US-10-487-634-39  
; Sequence 39, Application US/10487634  
; Publication No. US20040241165A1  
; GENERAL INFORMATION:  
; APPLICANT: HINUMA, Shuji  
; APPLICANT: YOSHIDA, Hiroaki  
; APPLICANT: HABAHA, Yugo  
; APPLICANT: HOSOYA, Masaki  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: Novel RFRP-3 And Its DNA  
; FILE REFERENCE: 2944USOP  
; CURRENT APPLICATION NUMBER: US/10/487,634  
; CURRENT FILING DATE: 2004-02-24  
; PRIOR APPLICATION NUMBER: PCT/JP02/08466  
; PRIOR FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: JP 2001-254826  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 39  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form  
US-10-487-634-39

Query Match 45.2%; Score 28; DB 16; Length 12;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9  
||:|  
Db 1 MPHSFANLP 9

RESULT 12  
US-10-925-893-41  
; Sequence 41, Application US/10928893  
; Publication No. US20050074884A1  
; GENERAL INFORMATION:  
; APPLICANT: Robbins, Paul D.  
; APPLICANT: Mi, Zhibao  
; APPLICANT: Fritzell, Raymond  
; APPLICANT: Giorio, Joseph C.  
; APPLICANT: Gambotto, Andrea  
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND CYTOPLASMIC

```
/ TITLE OF INVENTION: NUCLEAR TRANSPORT
/ TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
/ FILE REFERENCE: AP32573-AAA8 072396, 0269
/ CURRENT APPLICATION NUMBER: US/10/926,893
/ CURRENT FILING DATE: 2004-08-26
/ PRIOR APPLICATION NUMBER: 60/151,980
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: 60/188,944
/ PRIOR FILING DATE: 2000-03-13
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: random peptide library
US-10-926-893-41
```

```
Query Match          45.2%; Score 28; DB 17; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 QNFYKLPQM 11
        |||:||||
DB      4 KNFPLPEL 12
```

```
RESULT 13
US-09-852-370-31
/ Sequence 31, Application US/09852370
/ Publication No. US20030126624A1
/ GENERAL INFORMATION:
/ APPLICANT: Pomerantz, Joel L.
/ APPLICANT: Sharp, Phillip A.
/ TITLE OF INVENTION: Chimeric DNA-binding proteins
/ FILE REFERENCE: APV-023, 02
/ CURRENT APPLICATION NUMBER: US/09/852,370
/ CURRENT FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 08/973,131
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: PCT/US95/16982
/ PRIOR FILING DATE: 1995-12-29
/ PRIOR APPLICATION NUMBER: 08/366,083
/ PRIOR FILING DATE: 1994-12-29
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: human
US-09-852-370-31
```

```
Query Match          45.2%; Score 28; DB 10; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NFKLPQ 10
        |||:||||
DB      1 NFKLPQ 7
```

```
RESULT 14
US-10-002-244-4
/ Sequence 4, Application US/10002244
/ Publication No. US20030143731A1
/ GENERAL INFORMATION:
/ APPLICANT: ARIAD Gene Therapeutics, Inc.
/ TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
/ FILE REFERENCE: 346B USC1
/ CURRENT APPLICATION NUMBER: US/10/002,244
/ CURRENT FILING DATE: 2002-01-29
```

```
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapien
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (1)..(18)
/ OTHER INFORMATION: glutamine rich region of Oct-2
US-10-002-244-4
```

```
Query Match          45.2%; Score 28; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NFKLPQ 10
        |||:||||
DB      1 NFKLPQ 7
```

```
RESULT 15
US-10-649-873-111
/ Sequence 111, Application US/10649873
/ Publication No. US20040171552A1
/ GENERAL INFORMATION:
/ APPLICANT: Biokine Therapeutics Ltd.
/ APPLICANT: Peled, Amnon
/ APPLICANT: Bizenberg, Orly
/ APPLICANT: Valzel-Obayon, Dalit
/ TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
/ FILE REFERENCE: 26732
/ CURRENT APPLICATION NUMBER: US/10/649,873
/ CURRENT FILING DATE: 2003-08-28
/ NUMBER OF SEQ ID NOS: 157
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 111
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-649-873-111
```

```
Query Match          43.5%; Score 27; DB 16; Length 12;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NFKLPQ 10
        |||:||||
DB      4 NSYSLPQ 10
```

```
RESULT 16
US-10-014-340-803
/ Sequence 803, Application US/10014340
/ Publication No. US20030064411A1
/ GENERAL INFORMATION:
/ APPLICANT: Heratch, et al
/ TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
/ FILE REFERENCE: 9195-078
/ CURRENT APPLICATION NUMBER: US/10/014,340
/ CURRENT FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 823
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 803
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-014-340-803
```

Query Match 41.9%; Score 26; DB 14; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONEFKL 8  
|:|:|  
DB 2 PENFFLL 9

RESULT 17  
US-10-845-391-53

; Sequence 53, Application US/10845391  
; Publication No. US2005003483A1  
; GENERAL INFORMATION:  
; APPLICANT: Hildebrand, William  
; APPLICANT: Hickman, Heather  
; TITLE OF INVENTION: COMPARATIVE LIGAND MAPPING FROM MHC CLASS I POSITIVE CELLS  
; FILE REFERENCE: 6680.058  
; CURRENT APPLICATION NUMBER: US/10/845,391  
; CURRENT FILING DATE: 2004-05-13  
; PRIOR APPLICATION NUMBER: 60/469,995  
; PRIOR FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: 60/518,132  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: 09/974,366  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 60/240,143  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 60/299,452  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/327,907  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-845-391-53

Query Match 41.9%; Score 26; DB 17; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PONEFKL 8  
|:|:|  
DB 3 PENFFLL 9

RESULT 18  
US-09-920-174-3

; Sequence 3, Application US/09920174  
; Patent No. US20020150590A1  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.  
; APPLICANT: MOSS, DENIS J.  
; APPLICANT: BURROWS, SCOTT R.  
; TITLE OF INVENTION: EBV CTL EPITOPES  
; FILE REFERENCE: FBRC:008USC2  
; CURRENT APPLICATION NUMBER: US/09/920,174  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 09/920,175  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 09/194,450  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-920-174-3

Query Match 41.9%; Score 26; DB 9; Length 11;  
Best Local Similarity 57.1%; Pred. No. 7.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11  
|:|:|  
DB 3 FYNIPPM 9

RESULT 19  
US-09-920-195A-3  
; Sequence 3, Application US/09920195A  
; Publication No. US20030175300A1  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.  
; APPLICANT: MOSS, DENIS J.  
; APPLICANT: BURROWS, SCOTT R.  
; TITLE OF INVENTION: EBV CTL EPITOPES  
; FILE REFERENCE: FBRC:008USC1  
; CURRENT APPLICATION NUMBER: US/09/920,195A  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 09/194,450  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-920-195A-3

Query Match 41.9%; Score 26; DB 10; Length 11;  
Best Local Similarity 57.1%; Pred. No. 7.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPQM 11  
|:|:|  
DB 3 FYNIPPM 9

RESULT 20  
US-10-752-380-3  
; Sequence 3, Application US/10752380  
; Publication No. US20050084498A1  
; GENERAL INFORMATION:  
; APPLICANT: KHANNA, RAJIV  
; APPLICANT: KERR, BEVERLEY M.  
; APPLICANT: MISKO, IHOR S.  
; APPLICANT: MOSS, DENIS J.  
; APPLICANT: BURROWS, SCOTT R.  
; TITLE OF INVENTION: EBV CTL EPITOPES  
; FILE REFERENCE: FBRC:008  
; CURRENT APPLICATION NUMBER: US/10/752,380  
; CURRENT FILING DATE: 2004-01-06  
; PRIOR APPLICATION NUMBER: US/09/194,450  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3

```
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-752-380-3
```

```
Query Match          41.9%; Score 26; DB 17; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 FYKLPQM 11
      ||:|
DB      3 FYNIRPM 9
```

```
RESULT 21
US-10-125-869A-43
; Sequence 43, Application US/10125869A
; Publication No. US2003019671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ranschoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-43
```

```
Query Match          41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 NPYKLP 9
      ||:|
DB      5 NFWQLP 10
```

```
RESULT 22
US-10-125-869A-119
; Sequence 119, Application US/10125869A
; Publication No. US2003019671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ranschoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-119
```

```
Query Match          41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 NPYKLP 9
      ||:|
DB      5 NFWQLP 10
```

```
RESULT 23
US-10-462-262-267
; Sequence 267, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin binding polypeptide
US-10-462-262-267
```

```
Query Match          41.9%; Score 26; DB 15; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 NPYKLP 9
      ||:|
DB      5 NFWQLP 10
```

```
RESULT 24
US-10-462-262-343
; Sequence 343, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin binding polypeptide
US-10-462-262-343
```

Query Match 41.9%; Score 26; DB 15; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFFYKLP 9  
|:|:|  
Db 5 NFWOLP 10

## RESULT 25

US-09-799-576A-22

; Sequence 22, Application US/09799576A  
; Patent No. US20020034774A1  
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/799,576A

FILING DATE: 07-Mar-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/640,877

FILING DATE: 10-OCT-1996

APPLICATION NUMBER: WO PCT/US94/13455

FILING DATE: 18-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Rea, Teresa Stanek

REGISTRATION NUMBER: 30,427

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-799-576A-22

Query Match 41.9%; Score 26; DB 9; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|  
Db 9 QDHYKMP 15

## RESULT 26

US-09-799-540-22

; Sequence 22, Application US/09799540  
; Patent No. US20020045199A1  
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

APPLICANT: JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/799,540

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/640,877

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Rea, Teresa Stanek

REGISTRATION NUMBER: 30,427

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-799-540-22

Query Match 41.9%; Score 26; DB 9; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|  
Db 9 QDHYKMP 15

## RESULT 27

US-09-799-608-22

; Sequence 22, Application US/09799608  
; Patent No. US20020146428A1  
; GENERAL INFORMATION:

APPLICANT: HULTGREN, Scott

KUEHN, Meta

XU, Zheng

OGG, Derek

HARRIS, Mark

LEPISTO, Matti

KILBERG, Jan

JONES, Charles H.

TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,608  
FILING DATE: 07-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/640,877  
FILING DATE: <Unknown>  
APPLICATION NUMBER: NO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6201  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-799-608-22

Query Match 41.9%; Score 26; DB 9; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|:  
DB 9 QDHYKMP 15

RESULT 28  
US-09-798-932-22  
Sequence 22, Application US/09798932  
Publication No. US20030198992A1  
GENERAL INFORMATION:  
APPLICANT: HULTGREN, Scott  
KUEHN, Meta  
XU, Zheng  
OGG, Derek  
HARRIS, Mark  
LEPISTO, Matti  
KILBERG, Jan  
JONES, Charles H.  
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/798,932  
FILING DATE: 01-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/640,877  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: NO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-798-932-22

Query Match 41.9%; Score 26; DB 10; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QNFYKLP 9  
|:|:|:  
DB 9 QDHYKMP 15

RESULT 29  
US-09-799-680-22  
Sequence 22, Application US/09799680  
Publication No. US20030224468A1  
GENERAL INFORMATION:  
APPLICANT: HULTGREN, Scott  
KUEHN, Meta  
XU, Zheng  
OGG, Derek  
HARRIS, Mark  
LEPISTO, Matti  
KILBERG, Jan  
JONES, Charles H.  
TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS  
FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL INFECTIONS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,680  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/640,877

FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: WO PCT/US94/13455  
FILING DATE: 18-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 016921-122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-799-680-22

Query Match 41.9%; Score 26; DB 10; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 QNFYKLP 9  
| : | : |  
Db 9 QDHYKMP 15

RESULT 30  
US-09-745-078A-21  
Sequence 21, Application US/09745078A  
Publication No. US2003050434A1  
GENERAL INFORMATION:  
APPLICANT: Garth J. S. COOPER  
APPLICANT: Christina M. BUCHANAN  
TITLE OF INVENTION: PEPTIDE  
FILE REFERENCE: 441842000100  
CURRENT APPLICATION NUMBER: US/09/745,078A  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: NZ336359  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: PCT/NZ00/00102  
PRIOR FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Analog of human preptin  
US-09-745-078A-21

Query Match 41.9%; Score 26; DB 10; Length 17;  
Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MPQNFYKLP 9  
| : | : |  
Db 9 LPDQNFYKLP 17

RESULT 31  
US-09-962-756-1205  
Sequence 1205, Application US/09962756  
Publication No. US20030195147A1  
GENERAL INFORMATION:  
APPLICANT: PILIUTIA, RENUKA  
APPLICANT: BRISSETTE, RENEE  
APPLICANT: BLUME, ARTHUR J.  
APPLICANT: SCHAEFER, LAUGE  
APPLICANT: BRANDT, JAKOB  
APPLICANT: GOLDSTEIN, NEIL I.

APPLICANT: SPETZLER, JANE  
APPLICANT: OSTERGAARD, SOREN  
APPLICANT: HANSEN, PER HERTZ  
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
FILE REFERENCE: 1878-4051US1  
CURRENT APPLICATION NUMBER: US/09/962,756  
CURRENT FILING DATE: 2001-09-24  
PRIOR APPLICATION NUMBER: 09/538,038  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 09/146,127  
PRIOR FILING DATE: 1998-09-02  
NUMBER OF SEQ ID NOS: 2227  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1205  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-962-756-1205

Query Match 41.9%; Score 26; DB 10; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PQNFY 6  
| : | : |  
Db 3 PSNFY 7

RESULT 32  
US-09-962-756-1757  
Sequence 1757, Application US/09962756  
Publication No. US20030195147A1  
GENERAL INFORMATION:  
APPLICANT: PILIUTIA, RENUKA  
APPLICANT: BRISSETTE, RENEE  
APPLICANT: BLUME, ARTHUR J.  
APPLICANT: SCHAEFER, LAUGE  
APPLICANT: BRANDT, JAKOB  
APPLICANT: GOLDSTEIN, NEIL I.  
APPLICANT: SPETZLER, JANE  
APPLICANT: OSTERGAARD, SOREN  
APPLICANT: HANSEN, PER HERTZ  
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
FILE REFERENCE: 1878-4051US1  
CURRENT APPLICATION NUMBER: US/09/962,756  
CURRENT FILING DATE: 2001-09-24  
PRIOR APPLICATION NUMBER: 09/538,038  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 09/146,127  
PRIOR FILING DATE: 1998-09-02  
NUMBER OF SEQ ID NOS: 2227  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1757  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-962-756-1757

Query Match 41.9%; Score 26; DB 10; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PQNFY 6  
| : | : |  
Db 3 PSNFY 7



```
RESULT 33
US-09-962-756-1911
; Sequence 1911, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAEFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1911

Query Match      41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PONFY 6
        | |||
Db      3 PSNPFY 7

RESULT 34
US-10-374-624-21
; Sequence 21, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: GARTH J. S. COOPER
; APPLICANT: CHRISTINA M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-21

Query Match      41.9%; Score 26; DB 14; Length 17;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 MPONFYKLP 9
        : ||| : |
Db      9 LPDNFPRYP 17

RESULT 35
US-10-253-471-1205
; Sequence 1205, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1205
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1205

Query Match      41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 PONFY 6
        | |||
Db      3 PSNPFY 7

RESULT 36
US-10-253-471-1757
; Sequence 1757, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLOTTA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1757
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1757

Query Match      41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PONFY 6
```

Db 3 PSNFY 7

RESULT 37  
US-10-253-471-1911  
; Sequence 1911, Application US/10253471  
; Publication No. US20030236190A1  
; GENERAL INFORMATION:  
; APPLICANT: PILITUTLA, RENUKA et al.  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4057  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: 09/962,756  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1911  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-253-471-1911

Query Match 41.9%; Score 26; DB 15; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 PSNFY 6  
Db 3 PSNFY 7

RESULT 38  
US-10-253-493-1205  
; Sequence 1205, Application US/10253493  
; Publication No. US20040023887A1  
; GENERAL INFORMATION:  
; APPLICANT: PILITUTLA, RENUKA et al.  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4056  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: 09/962,756  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1205  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-253-493-1205

Query Match 41.9%; Score 26; DB 15; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 PSNFY 6  
Db 3 PSNFY 7

Db 3 PSNFY 7

RESULT 39  
US-10-253-493-1757  
; Sequence 1757, Application US/10253493  
; Publication No. US20040023887A1  
; GENERAL INFORMATION:  
; APPLICANT: PILITUTLA, RENUKA et al.  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4056  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: 09/962,756  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1757  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-253-493-1757

Query Match 41.9%; Score 26; DB 15; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 PSNFY 6  
Db 3 PSNFY 7

RESULT 40  
US-10-253-493-1911  
; Sequence 1911, Application US/10253493  
; Publication No. US20040023887A1  
; GENERAL INFORMATION:  
; APPLICANT: PILITUTLA, RENUKA et al.  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4056  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: 09/962,756  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1911  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-253-493-1911

Query Match 41.9%; Score 26; DB 15; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 PSNFY 6  
Db 3 PSNFY 7

Search completed: June 7, 2005, 23:31:38  
Job time : 50.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 10.2 Seconds  
(without alignments)  
103.763 Million cell updates/sec

Title: US-10-691-157-6  
Perfect score: 62  
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	40.3	17	2	hydroxyproline-ric
2	38.7	12	2	T-cell receptor al
3	38.7	13	2	T-cell receptor al
4	37.1	11	1	substance P - quin
5	37.1	11	1	substance P - hore
6	37.1	11	2	substance P - chic
7	35.5	11	2	phytaeamin - frog
8	35.5	11	2	ranatachytin A -
9	35.5	11	2	benzoyl-CoA ligase
10	35.5	15	2	benzoyl-CoA ligase
11	33.9	9	2	Ig heavy chain CRD
12	33.9	9	2	PC0270
13	33.9	12	2	PC0228
14	32.3	7	2	B44787
15	32.3	11	2	S07203
16	32.3	11	4	IS2708
17	32.3	12	2	A09985
18	32.3	12	2	S57570
19	32.3	12	2	S74144
20	32.3	12	2	S07436
21	32.3	16	2	T37075
22	30.6	10	2	C39398
23	30.6	11	2	S23373
24	30.6	11	2	S23305
25	30.6	13	2	S47358
26	30.6	15	2	S51735
27	30.6	15	2	B49655
28	30.6	15	2	PA0008
29	30.6	15	2	A36279

30	19	30.6	16	2	PH1778	T cell receptor al
31	19	30.6	16	2	B49255	T-cell receptor be
32	19	30.6	16	2	F49039	T-cell receptor be
33	19	30.6	16	2	S22040	cob protein - comm
34	19	30.6	18	2	S23971	alpha-macroglobulin
35	18	29.0	6	2	S11556	hydrogensulfite re
36	18	29.0	8	2	I49404	prealbumin - weste
37	18	29.0	8	2	B24749	neuropeptide B - b
38	18	29.0	11	2	B60409	substance P-like p
39	18	29.0	11	2	B60409	substance P-like p
40	18	29.0	11	2	S23308	substance P - rain
41	18	29.0	13	2	S01119	photosystem II pro
42	18	29.0	13	4	I70076	glycophorin B/glyc
43	18	29.0	14	2	PL0152	metal-binding prot
44	18	29.0	14	2	B20872	alpha-2-macroglobu
45	18	29.0	14	2	PT0294	Ig heavy chain CRD
46	18	29.0	14	2	S58862	botulinum neurotox
47	18	29.0	14	2	S58866	botulinum neurotox
48	18	29.0	14	2	B36079	hypothetical prote
49	18	29.0	15	2	S08209	hypothetical prote
50	18	29.0	15	2	A56049	hypothetical prote
51	18	29.0	15	2	I86335	urinary tract ston
52	18	29.0	16	2	S65520	hypothetical TBL/M
53	18	29.0	18	2	PN0149	phospholipase A2 (
54	18	29.0	18	2	A24749	beta-glucanase 13 -
55	17.5	28.2	11	2	PC2330	neuropeptide A - b
56	17	27.4	6	2	A37765	cyclooligooligosac
57	17	27.4	6	2	A43129	hypothetical prote
58	17	27.4	9	2	DS8503	neuropeptide GNFR
59	17	27.4	11	2	S53436	translation elonga
60	17	27.4	13	2	S29488	beta-D-galactosida
61	17	27.4	14	2	H64008	GRP-binding protei
62	17	27.4	14	2	PA0101	hypothetical prote
63	17	27.4	14	2	S29486	protein QP200020 -
64	17	27.4	15	2	PA0088	GRP-binding protei
65	17	27.4	15	2	C36198	T-cell receptor be
66	17	27.4	15	2	PO0073	T-cell receptor be
67	17	27.4	16	2	A24039	crystal protein, 2
68	17	27.4	16	2	C39509	mannose-specific 1
69	17	27.4	16	2	I46275	hemoglobin beta-x
70	17	27.4	17	2	I78870	gene R81 protein -
71	17	27.4	18	2	S29264	ovohemerythrin - d
72	17	27.4	18	2	A60915	enkephalin-degradi
73	17	27.4	18	2	B44995	alkanol monooxygen
74	17	27.4	18	2	S09722	2S albumin small c
75	17	27.4	18	2	A30541	F7-I fibritial prot
76	17	27.4	18	2	I51427	hemoglobin alpha c
77	16	25.8	8	2	S16324	hypothetical prote
78	16	25.8	9	2	C36730	hutu protein - Kle
79	16	25.8	9	2	PT0285	Ig heavy chain CRD
80	16	25.8	9	2	PT0080	60K Ca binding pro
81	16	25.8	10	2	B61033	ranatachytin B -
82	16	25.8	11	2	S68392	H+-transporting tw
83	16	25.8	11	2	F33098	214K exoantigen (v
84	16	25.8	11	2	A38590	transforming prote
85	16	25.8	11	2	S33300	probable substance
86	16	25.8	12	2	B45691	probable minor cap
87	16	25.8	12	2	PA0047	protein QH10045 -
88	16	25.8	13	2	A59387	VCM-1 5'UTR bindi
89	16	25.8	13	2	S21152	tryptophan-11n-reia
90	16	25.8	14	2	A60840	somatostatin I - B
91	16	25.8	14	2	C60414	somatostatin I - B
92	16	25.8	14	2	B60842	somatostatin I - B
93	16	25.8	14	2	S00172	somatostatin I - B
94	16	25.8	14	2	PL0142	carbon-monoxide de
95	16	25.8	14	2	PT0254	Ig heavy chain CRD
96	16	25.8	14	2	US0272	hypothetical 1.5K
97	16	25.8	14	2	PC4382	dehydrin 4.5K poly
98	16	25.8	15	2	I52734	gene-C-Ki- ras prot
99	16	25.8	15	2	PH1762	T cell receptor su
100	16	25.8	15	2	D46743	corneal keratan su

## ALIGNMENTS

## RESULT 1

hydroxyproline-rich protein - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata

C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S57991

R:Goomachig, S.; Valerio-Leptec, M.; Szczylowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Sesbania rostrata genes ent

A:Reference number: S57991

C:Accession: S57991

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <GO>

A:Cross-References: UNIPROT:Q41400; EMBL:Z48673; NID:g899484; PID:g899485

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 40.3%; Score 25; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9  
DB 3 PHYXXSP 10

## RESULT 2

PH1454  
T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004

C:Accession: PH1454

R:Caanova, J.L.; Marinton, F.; Gournier, H.; Barra, C.; Penetier, C.; Regnault, A.; Ko

J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1454

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Experimental source: cytolitic T-lymphocyte

C:Keywords: receptor; T-cell

Query Match 38.7%; Score 24; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ONFY 6  
DB 7 ONFY 10

## RESULT 3

PH0787  
T-cell receptor alpha chain (F8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PH0787

R:Caanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-I

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0787

A:Molecule type: mRNA

A:Residues: 1-13 <CAS>

A:Cross-References: EMBL:X60891

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 38.7%; Score 24; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ONFY 6  
DB 8 ONFY 11

## RESULT 4

A60654  
substance P - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; MUID:90044685; PMID:2478925

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MUR>

A:Cross-References: UNIPROT:P01290

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYKLP 8  
DB 4 PQQFRL 10

## RESULT 5

SPHO  
substance P - horse

C:Species: Equus caballus (domestic horse)

C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C:Accession: A01558

R:Studer, R.O.; Tzeczak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

A:Cross-References: UNIPROT:P01290

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYKLP 8  
DB 4 PQQFRL 10

## RESULT 6

UN0023  
substance P - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C:Accession: UN0023

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neukinin A from chicken small intestine.

A:Reference number: UN0023; MUID:88204263; PMID:2452461

A:Accession: UN0023

A.Molecule type: protein

A.Residues: 1-11 <CON>

A.Cross-references: UNIPROT:P19850

C.Superfamily: substance P precursor

C.Keywords: amidated carboxyl end; tachykinin

F.11/Modified site: amidated carboxyl end (Met) #status predicted

#### Query Match

Best Local Similarity 37.1%; Score 23; DB 2; Length 11;  
Pred. No. 3.1e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 4; Conservative 1;

QY 2 PONFYKL 8

DB 4 PQQFFGL 10

#### RESULT 7

S07201 physalaemin - frog (Physalaemus fuscumaculatus)

C.Species: Physalaemus fuscumaculatus

C.Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004

C.Accession: S07201

R.Erpsamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A.Title: Structure and pharmacological actions of physalaemin, the main active polypepti

A.Reference number: S07201; MUID:66076612; PMID:5657249

A.Accession: S07201

A.Molecule type: protein

A.Residues: 1-11 <ERS>

A.Cross-references: UNIPROT:P08615

C.Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F.11/Modified site: amidated carboxyl end (Met) #status experimental

#### Query Match

Best Local Similarity 35.5%; Score 22; DB 2; Length 11;  
Pred. No. 4.8e+02; Mismatches 3; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 2 PONFYKL 8

DB 4 PMKRYGL 10

#### RESULT 8

A61033 ranachykinin A - bullfrog

C.Species: Rana catesbeiana (bullfrog)

C.Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C.Accession: A61033; J00426

R.Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A.Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A.Reference number: A61033

A.Accession: A61033

A.Molecule type: protein

A.Residues: 1-11 <KAN>

A.Cross-references: UNIPROT:P22688

R.Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A.Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A.Reference number: J00426; MUID:91254337; PMID:2043143

A.Accession: J00426

A.Molecule type: protein

A.Residues: 1-11 <KOZ>

C.Superfamily: unassigned animal peptides

C.Keywords: amidated carboxyl end; neuropeptide

F.11/Modified site: amidated carboxyl end (Met) #status experimental

#### Query Match

Best Local Similarity 35.5%; Score 22; DB 2; Length 11;  
Pred. No. 4.8e+02; Mismatches 3; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 2 PONFYKL 8

DB 4 PDRFYGL 10

#### RESULT 9

D61033 ranachykinin D - bullfrog

C.Species: Rana catesbeiana (bullfrog)

C.Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Aug-2004

C.Accession: D61033; J00429

R.Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A.Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A.Reference number: A61033

A.Accession: D61033

A.Molecule type: protein

A.Residues: 1-11 <KAN>

A.Cross-references: UNIPROT:P22691

R.Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A.Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte

A.Reference number: J00426; MUID:91254337; PMID:2043143

A.Accession: J00429

A.Molecule type: protein

A.Residues: 1-11 <KOZ>

C.Keywords: amidated carboxyl end; neuropeptide

F.11/Modified site: amidated carboxyl end (Met) #status experimental

#### Query Match

Best Local Similarity 35.5%; Score 22; DB 2; Length 11;  
Pred. No. 4.8e+02; Mismatches 3; Conservative 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

QY 2 PONFY 6

DB 4 PERFY 8

#### RESULT 10

A48372

benzoyl-CoA ligase - Methanospirillum hungatei (fragment)

C.Species: Methanospirillum hungatei

C.Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C.Accession: A48372

R.Auburger, G.; Winter, J.

Appl. Microbiol. Biotechnol. 37, 789-795, 1992

A.Title: Purification and characterization of benzoyl-CoA ligase from a syntrophic, benz

A.Reference number: A48372; MUID:93040109; PMID:1369492

A.Accession: A48372

A.Status: preliminary

A.Molecule type: protein

A.Residues: 1-15 <ADB>

A.Cross-references: UNIPROT:Q9UWM1

A.Note: sequence extracted from NCBI Backbone (NCBI:118357)

#### Query Match

Best Local Similarity 35.5%; Score 22; DB 2; Length 15;  
Pred. No. 6.7e+02; Mismatches 3; Conservative 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

QY 2 PONFY 6

DB 5 PERFY 9

#### RESULT 11

A39892

P element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)

C.Species: Drosophila melanogaster

C.Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Feb-1997

C.Accession: A39892

R.Nitaseaka, E.; Mukai, T.; Yamazaki, T.

Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987

A.Title: Repressor of P elements in Drosophila melanogaster: cytotype determination by a

A.Reference number: A39892

A:Accession: A39892  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-8 <NT>  
C:Genetics:  
A:Gene: FlyBase:FBgn0003055  
A:Cross-references: FlyBase:FBgn0003055

Query Match 33.9%; Score 21; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5  
|:|:  
Db 1 IPKNF 5

## RESULT 12

PT0270  
Ig heavy chain CRD3 region (clone 3-100) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0270  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0270  
A:Molecule type: DNA  
A:Residues: 1-9 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterodimer; immunoglobulin

Query Match 33.9%; Score 21; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6  
|:|:  
Db 1 QNFY 4

## RESULT 13

B60228  
Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)  
N:Alternate names: membrane protein B29  
C:Species: Mus musculus (house mouse)  
C:Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Mar-1998  
C:Accession: B60228; B39398  
R:Hombach, J.; Lottspeich, F.; Reith, M.  
Eur. J. Immunol. 20, 2795-2799, 1990  
A:Title: Identification of the genes encoding the IgM-alpha and Ig-beta components of th  
A:Reference number: A60228; MUID:91099432; PMID:2269334  
A:Accession: B60228  
A:Molecule type: protein  
A:Residues: 1-12 <HOM>  
R:Cambell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
A:Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g  
A:Reference number: A39398; MUID:91219496; PMID:2023945  
C:Accession: B39398  
A:Molecule type: protein  
A:Residues: 'XX', 3-10 <CAM>  
C:Keywords: membrane protein

Query Match 33.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 8.2e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 9  
|:|:  
Db 4 LPLNFQGSP 12

## RESULT 14

B44787  
Calliphoramide II - bluebottle fly (Calliphora vomitoria)  
C:Species: Calliphora vomitoria  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: B44787  
R:Dive, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thore  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A:Reference number: A41978; MUID:92196111; PMID:1549595  
A:Accession: B44787  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <DUV>  
A:Cross-references: UNIPROT:P41866  
C:Keywords: amidated carboxyl end; neuropeptide  
F:7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYK 7  
|:|:  
Db 1 PDNFWR 6

## RESULT 15

S07203  
Uperolein - frog (Uperoleia marmorata)  
C:Species: Uperoleia marmorata  
C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
C:Accession: S07203  
R:Anastasi, A.; Erganer, V.; Edean, R.  
Experientia 31, 394-395, 1975  
A:Title: Structure of uperolein, a physalemin-like endecapeptide occurring in the skin  
A:Reference number: S07203; MUID:75131227; PMID:1120493  
A:Accession: S07203  
A:Molecule type: protein  
A:Residues: 1-11 <ANA>  
C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin  
F:1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental  
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8  
|:|:  
Db 4 PNAFYGL 10

## RESULT 16

I52708  
ELAV-like neuronal protein 1, truncated splice form - human  
N:Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen  
C:Species: Homo sapiens (man)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: I52708  
R:Seikido, Y.; Bader, S.A.; Cardone, D.P.; Johnson, B.E.; Minna, J.D.  
Cancer Res. 54, 4988-4992, 1994  
A:Title: Molecular analysis of the Hnd gene encoding a paraneoplastic encephalomyelitis  
A:Reference number: I52708; MUID:94349312; PMID:8065866  
C:Accession: I52708  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-11 <SEK>  
A:Cross-references: UNIPROT:O16234; GB:S73887; NID:9688242; PIDN:AA014142.1; PID:9426184  
C:Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.  
A:Gene: GDB: ELAVL4; HUD; PNEW



A:Cross-references: GDB:141875; OMIM:168360  
A:Map position: 1p36-1p36  
C:Keywords: alternative splicing

Query Match 32.3%; Score 20; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPONFYKL 8  
| | | |  
| | | |  
DB 3 MPRRIKL 10

## RESULT 17

A09985  
gamma-crystallin - haddock (fragments)  
C:Species: Melanogrammus aeglefinus (haddock)  
C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 18-Jun-1993  
C:Accession: A09985  
R: Croft, L.R.  
Biochim. Biophys. Acta 295, 174-177, 1973  
A:Title: Amino and carboxy terminal sequence of gamma-crystallin, from haddock lens.  
A:Reference number: A09985; MUID:73088761; PMID:4685070  
A:Accession: A09985  
A:Molecule type: protein  
A:Residues: 1-12 <CRO>

Query Match 32.3%; Score 20; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FYKLPMQ 11  
| | | | |  
| | | | |  
DB 5 FYITIDM 11

## RESULT 18

S57570  
T cell receptor V-J junctional alpha chain region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S57570  
R: Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.  
submitted to the EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified  
A:Reference number: S57494  
A:Accession: S57570  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <BUR>  
A:Cross-references: EMBL:Z49954; NID:9887488; PIDN:CAA90225.1; PID:9887489  
C:Keywords: T-cell receptor

Query Match 32.3%; Score 20; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYF 6  
| | | |  
| | | |  
DB 6 PNOFY 10

## RESULT 19

S74144  
aggrecan - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C:Accession: S74144  
R: Bonassar, L.U.; Stimm, J.L.; Peguio, C.G.; Frank, E.H.; Moore, V.L.; Lark, M.W.; Sandy  
Arch. Biochem. Biophys. 333, 359-367, 1996  
A:Title: Activation and inhibition of endogenous matrix metalloproteinases in articular  
A:Reference number: S74144; MUID:96404934; PMID:8809074  
A:Accession: S74144

A:Molecule type: mRNA  
A:Residues: 1-12 <BON>  
A:Experimental source: cartilage  
C:Keywords: cartilage; glycoprotein

Query Match 32.3%; Score 20; DB 2; Length 12;  
Best Local Similarity 33.3%; Pred. No. 1.3e+03;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPONFY 6  
| | | |  
| | | |  
DB 4 IPESFP 9

## RESULT 20

S07436  
tachykinin - African tree frog (Kassina maculata)  
N:Alternate names: hylambatin  
C:Species: Kassina maculata  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004  
C:Accession: S07436  
R: Yasunaga, T.; Nakajima, T.; Brepamer, G.F.; Brepamer, V.  
Biomed. Res. 2, 613-617, 1981  
A:Title: New tachykinins, Glu12, Pro5-kassinin (hylambates-kassinin) and hylambatin, in  
A:Reference number: S07436  
A:Accession: S07436  
A:Molecule type: protein  
A:Residues: 1-12 <YAS>  
A:Cross-references: UNIPROT:P08614  
A:Experimental source: skin  
A:Note: the source is designated as Hylambates maculatus  
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 32.3%; Score 20; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONYF 6  
| | | |  
| | | |  
DB 5 PDRFY 9

## RESULT 21

T37075  
hypothetical protein SCU30.08 - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37075  
R: Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1999  
A:Reference number: Z21621  
A:Accession: T37075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <SAN>  
A:Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070; SCOEDB:SCU30.08  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SCU30.08

Query Match 32.3%; Score 20; DB 2; Length 16;  
Best Local Similarity 44.4%; Pred. No. 1.7e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPONFYKLP 9  
| | | | |  
| | | | |  
DB 7 MPRSAIGLP 15

## RESULT 22

C39398  
Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 20-Mar-1998  
 C:Accession: C39398  
 R:Campbell, K.S.; Hager, B.J.; Friedrich, R.J.; Gambler, J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
 A:Title: IGM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g  
 A:Reference number: A39398; MUID:91219496; PMID:2023945  
 A:Accession: C39398  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <CAM>

Query Match 30.6%; Score 19; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQNPF 5  
 |||  
 Db 4 LPNPF 8

## RESULT 23

S23373  
 T-cell receptor alpha chain J region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C:Accession: S23373  
 R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmar  
 Eur. J. Immunol. 21, 2749-2754, 1991  
 A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rhe  
 A:Reference number: S23364; MUID:92037820; PMID:1657615  
 A:Accession: S23373  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-11 <PLU>  
 A:Cross-references: EMBL:X58168  
 C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYKL 8  
 |||  
 Db 3 PSNYDKV 9

## RESULT 24

S23306  
 substance P - Atlantic cod  
 C:Species: Gadus morhua (Atlantic cod)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004  
 C:Accession: S23306  
 R:Jensen, J.; Conlon, J.M.  
 Eur. J. Biochem. 206, 659-664, 1992  
 A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod  
 A:Reference number: S23186; MUID:92298992; PMID:1376687  
 A:Accession: S23306  
 A:Molecule type: protein  
 A:Residues: 1-11 <JEN>  
 A:Cross-references: UNIPROT:P28498  
 A:Experimental source: brain  
 C:Function:  
 A:Description: may play a physiological role in the regulation of cardiovascular and gas  
 A:Note: substance P is derived by post-translational processing of preprotachykinin A  
 C:Keywords: neuropeptide; amidated carboxyl end; tachykinin  
 F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 30.6%; Score 19; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQNFYKL 8

Db 4 PQQFYGL 10  
 |||

## RESULT 25

S47358  
 T-cell antigen receptor VJ junction beta chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S47358  
 R:Lehner, P.J.  
 submitted to the EMBL Data Library, August 1994  
 A:Description: Human HLA-A\*0201 restricted recognition of influenza A is dominated by T c  
 A:Reference number: S47355  
 A:Accession: S47358  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <LEH>  
 A:Cross-references: EMBL:Z35682; NID:9527453; PIDN:CAA84751.1; PID:9527454  
 C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5  
 |||  
 Db 10 PQHF 13

## RESULT 26

S51735  
 T-cell receptor beta-chain joining region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999  
 C:Accession: S51735  
 R:Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.  
 submitted to the EMBL Data Library, November 1993  
 A:Reference number: S51732  
 A:Accession: S51735  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <DUR>  
 A:Cross-references: EMBL:Z28344; NID:9607122; PIDN:CAA82198.1; PID:9607123  
 C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5  
 |||  
 Db 12 PQHF 15

## RESULT 27

B49655  
 T-cell-receptor beta chain variable region, TCR V beta (clone SF-2) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
 C:Accession: B49655  
 R:Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993  
 A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni  
 A:Reference number: B49655; MUID:94068553; PMID:8248215  
 A:Accession: B49655  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-15 <GRO>  
 A:Experimental source: knee joint, synovial fluid lymphocytes  
 A:Note: sequence extracted from NCBI backbone (NCBIP:1140446)  
 C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5  
 ||:|  
 Db 11 PQHF 14

## RESULT 28

PA0008

lectin B2 - Psophocarpus scandens (fragment)

C:Species: Psophocarpus scandens

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C:Accession: PA0008

R:Kortt, A.A.

Phytochemistry 27, 2847-2855, 1988

A:Title: Isolation and characterization of the lectins from the seeds of Psophocarpus sc

A:Reference number: PA0005

A:Accession: PA0008

A:Molecule type: protein

A:Residues: 1-15 &lt;KOR&gt;

A:Cross-references: UNIPROT:P22585

A:Experimental source: seed

C:Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can be

C:Keywords: lectin

Query Match 30.6%; Score 19; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NPYKLQ 10  
 ||:|  
 Db 7 NPNKFEQ 13

## RESULT 29

A36279

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C:Species: Lumbricus terrestris (common earthworm)

C:Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004

C:Accession: A36279

R:Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990

A:Title: Purification and characterization of a chemoattractant from electric shock-indu

smates.

A:Reference number: A36279; PMID:90256800; PMID:2160465

A:Accession: A36279

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 &lt;DIA&gt;

A:Cross-references: UNIPROT:O44335

Query Match 30.6%; Score 19; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PGNFKLP 9  
 ||:|  
 Db 5 PPGFTYLP 12

## RESULT 30

PH1778

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C:Accession: PH1778

R:Porcellli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; PMID:93301585; PMID:8391057

A:Accession: PH1778  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <POR>

Query Match 30.6%; Score 19; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NPYKL 8  
 ||:|  
 Db 10 NDYKL 14

## RESULT 31

E49255

T-cell receptor beta chain V-D-J-C region (V beta 17, J beta 1.5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C:Accession: E49255

R:Rothenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; PMID:92164737; PMID:1311263

A:Accession: E49255

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 &lt;ROS&gt;

A:Note: sequence extracted from NCBI backbone (NCBI:90726)

C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5  
 ||:|  
 Db 12 PQHF 15

## RESULT 32

F49039

T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C:Accession: F49039

R:Rothenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; PMID:92164737; PMID:1311263

A:Accession: F49039

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 &lt;ROS&gt;

A:Note: sequence extracted from NCBI backbone (NCBI:90716)

C:Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PGNF 5  
 ||:|  
 Db 12 PQHF 15

## RESULT 33

S22040

cbb protein - common sunflower

C:Species: Helianthus annuus (common sunflower)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S22040

R:Koehler, R.H.

submitted to the EMBL Data Library, October 1991

A:Reference number: S22040  
A:Accession: S22040  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <KOE>  
A:Cross-references: UNIPROT:Q34699; EMBL:X62592; NID:g12990; PID:g12991

Query Match 30.6%; Score 19; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NPY 6  
|||  
Db 3 NPY 5

## RESULT 34

S23971  
alpha-macroglobulin proteinase inhibitor - common octopus

C:Species: Octopus vulgaris (common octopus)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S23971  
R:Hoegersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Engnild, J.J.  
Biochem. J. 285, 521-527, 1992  
A:Title: Purification and characterization of an alpha-macroglobulin proteinase inhibitor  
A:Reference number: S23971; MUID:92344633; PMID:1379044  
A:Accession: S23971  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <THO>  
A:Cross-references: UNIPROT:E30800

Query Match 30.6%; Score 19; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NPY 6  
|||  
Db 12 NPY 14

## RESULT 35

S11556

hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)

N:Alternate names: bisulfite reductase; desulfosulfidn  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C:Accession: S11556  
R:Faque, G.; Iino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.J.G.; I  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfosulfidn) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817  
A:Accession: S11556  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
A:Keywords: oxidoreductase

Query Match 29.0%; Score 18; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 POFYK 7  
|||  
Db 1 PEFYK 6

## RESULT 36

I49404

prealbumin - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49404

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hegen, M.D.; Takahashi, N.; Maesaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I49404

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <RSS>

A:Cross-references: UNIPROT:Q62527; EMBL:U05689; NID:g497008; PIDN:AAB60461.1; PID:g6428

Query Match 29.0%; Score 18; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 POF 4  
|||  
Db 6 POF 8

## RESULT 37

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 09-Jul-2004

C:Accession: B24749

R:Yang, H.Y.T.; Fratka, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b

A:Reference number: A94074; MUID:86067985; PMID:3865193

A:Accession: B24749

A:Molecule type: protein

A:Residues: 1-8 <YAN>

A:Cross-references: UNIPROT:P15507

C:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide

Query Match 29.0%; Score 18; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 POF 5  
|||  
Db 5 POF 8

## RESULT 38

B60409

substance P-like peptide I - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 16-Aug-2004

C:Accession: B60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 329-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: B60409

A:Molecule type: protein

A:Residues: 1-11 <SIM>

A:Cross-references: UNIPROT:P42989

C:Keywords: amidated carboxyl end; pyroglutamic acid

F11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 29.0%; Score 18; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 2.8e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 POFYKL 8  
|||  
Db 4 PDEFGL 10

## RESULT 39

F60409

Substance P-like peptide II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 16-Aug-2004

C:Accession: F60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: F60409

A:Molecule type: protein

A:Residues: 1-11 &lt;SIM&gt;

A:Cross-references: UNIPROT:P42990

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Met) #status experimental

## Query Match

29.0%; Score 18; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKL 8

DB 4 PNEFFGL 10

## RESULT 40

S23308

Substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004

C:Accession: S23308

R:Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod

A:Reference number: S23186; MUID:92298992; PMID:1376687

A:Accession: S23308

A:Molecule type: protein

A:Residues: 1-11 &lt;JEN&gt;

A:Cross-references: UNIPROT:P28499

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas

A&gt;Note: Substance P is derived by post-translational processing of preprotachykinin A

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

## Query Match

29.0%; Score 18; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PGNFYKL 8

DB 4 PNEFFGL 10

Search completed: June 7, 2005, 23:20:41  
Job time : 11.2 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 48.4 Seconds

(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-6

Perfect score: 62

Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	41.9	15	1	SODM_ENTAB
2	40.3	17	2	O49225
3	40.3	17	2	O41400
4	38.7	11	1	TKNA_RANRI
5	38.7	13	2	O6LDM2
6	37.1	11	1	TKN2_UPERU
7	37.1	11	1	TKNA_CAVPO
8	37.1	11	1	TKNA_CHICK
9	37.1	11	1	TKNA_HORSE
10	37.1	13	1	SODM_ARTDA
11	35.5	11	1	TKNA_RANCA
12	35.5	11	1	TKND_RANCA
13	35.5	11	1	TKN_PHYFU
14	35.5	14	2	O9MJ03
15	35.5	15	1	GTEI_PSEVO
16	35.5	15	2	O9UWMI
17	35.5	17	2	O9UCA4
18	33.9	10	2	O6K6C9
19	33.9	10	2	O9XBH3
20	33.9	13	2	O9OXV4
21	33.9	15	2	O9TOX7
22	33.9	15	2	O71GTO
23	33.9	16	1	BRB_BASAL
24	33.9	17	2	O6R9P0
25	33.9	17	2	O6R9P2
26	33.9	17	2	O6R9P2
27	33.9	17	2	O6R9P2
28	33.9	17	2	O6R9P4
29	33.9	17	2	O6R9P8
30	33.9	18	2	O9RGRI
31	33.9	18	2	O9RGRI

32	20	32.3	7	1	P41866	calliphora
33	20	32.3	9	1	P16223	locusta mtg
34	20	32.3	11	1	P82026	uperoleia i
35	20	32.3	11	1	P08612	uperoleia r
36	20	32.3	11	2	O16234	homo sapien
37	20	32.3	11	2	O9PF22	mycoplasma
38	20	32.3	12	1	P08614	kaesina mac
39	20	32.3	12	2	O53579	rhodobacter
40	20	32.3	13	2	O9THR8	hyopais sp
41	20	32.3	13	2	O9TKG6	lambda anta
42	20	32.3	13	2	O8J322	ficedula al
43	20	32.3	14	2	O7PE81	anophelis g
44	20	32.3	14	2	O71G78	andrena bro
45	20	32.3	15	2	O71G78	andrena ref
46	20	32.3	15	2	O9TOQ9	bos taurus
47	20	32.3	15	2	O9TR40	bos taurus
48	20	32.3	15	2	O71GVO	andrena teg
49	20	32.3	15	2	O71H02	andrena inc
50	20	32.3	15	2	O71H38	andrena aur
51	20	32.3	15	2	O53580	rhodobacter
52	20	32.3	15	2	O9R472	bacillus in
53	20	32.3	16	2	O6Y662	mycoplasma
54	20	32.3	17	2	O7RY15	neurospora
55	20	32.3	17	2	O9QUY6	rattus sp.
56	20	32.3	18	2	O8SKY0	cuscuta ref
57	19	30.6	8	2	O9HC00	homo sapien
58	19	30.6	8	2	O45615	bacillus su
59	19	30.6	9	2	O67605	squash leaf
60	19	30.6	9	2	O67606	gadus morhu
61	19	30.6	11	2	TKNA_GADMO	
62	19	30.6	11	2	O9URGI	tomato leaf
63	19	30.6	11	2	O80G99	pinus pinas
64	19	30.6	13	1	UN02_PINDS	
65	19	30.6	13	2	O71A29	pinus pinas
66	19	30.6	13	2	O9T4K3	hyopais sp
67	19	30.6	13	2	O9T4K4	hyopais sp
68	19	30.6	13	2	O9T4K5	hyopais sp
69	19	30.6	13	2	O9T4K6	hyopais sp
70	19	30.6	13	2	O9THS2	hyopais sp
71	19	30.6	13	2	O9THS3	hyopais sp
72	19	30.6	14	2	O71GY0	andrena ofe
73	19	30.6	15	1	LEC2_PSO5C	psophocarpu
74	19	30.6	15	1	LG29_VIGUS	vigna ungui
75	19	30.6	15	1	SODM_STRGR	streptomyce
76	19	30.6	15	2	O7RE88	plasmodium
77	19	30.6	15	2	O7R8B9	plasmodium
78	19	30.6	16	2	O7R8B9	plasmodium
79	19	30.6	16	2	O34639	helianthus
80	19	30.6	16	2	O38671	bacterioph
81	19	30.6	17	2	O13376	homo sapien
82	19	30.6	17	2	O7RM54	plasmodium
83	19	30.6	17	2	O9XSG1	bos taurus
84	19	30.6	17	2	O9PRU8	gallus galli
85	19	30.6	18	1	A2M_OCTVU	octopus vuli
86	19	30.6	18	1	SODM_MYCHA	mycobacteri
87	19	30.6	18	2	O97773	ceratophtec
88	19	30.6	18	2	O7RH77	sus scrofa
89	19	30.6	18	2	O9ZG42	chlamydia t
90	19	30.6	18	2	O7TNW8	mus musculu
91	19	30.6	18	2	O7TNW8	rattus norv
92	19	29.0	8	1	NEMB_BOVIN	bos taurus
93	18	29.0	8	2	O61D47	homo sapien
94	18	29.0	8	2	O62527	mus epretus
95	18	29.0	9	2	O94VG2	varanus ind
96	18	29.0	9	2	O9S8J8	oryza sativ
97	18	29.0	10	2	O9H121	homo sapien
98	18	29.0	11	1	TKN5_PSEGU	pseudophrym
99	18	29.0	11	1	TKN5_PSEGU	pseudophrym
100	18	29.0	11	1	TKNA_ONCMY	oncothychnu

## ALIGNMENTS

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RESULT 1
SODM_ENTAE STANDARD; PRT; 15 AA.
AC P22799;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
CN Name=soda;
OS Enterobacter aerogenes (Enterobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes."
RL Agric. Biol. Chem. 55:101-108(1991).
CC -1- FUNCTION: Destructs radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR PIR, P06015; P0615.
DR InterPro, IPR001189; SODismutase.
DR Pfam, PF00081; Sod_Fe_N; 1.
DR PROSITE, PS00088; SOD_NM; PARTIAL.
KW Direct protein sequencing; Iron; Metal-binding; Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202B642 CRC64;

Query Match 41.9%; Score 26; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLPQM 11
DB 2 YELPOL 7

RESULT 2
O49225 PRELIMINARY; PRT; 17 AA.
AC O49225;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (Fragment).
CN Name=hrgp;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=94211912; PubMed=8159793; DOI=10.1104/pp.104.2.793;
RA Hong J.C., Chong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs."
RT Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RA Mahalingam R., Knop H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF047052; AAC03558.1; -.
FT NON_TER 1

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SQ SEQUENCE 17 AA; 2149 MW; 285E5B74515A2222 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9
DB 4 PHYXYKSP 11

RESULT 3
Q41400 PRELIMINARY; PRT; 17 AA.
ID Q41400;
AC Q41400;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Geornachtig S., Valerio-Lepintec M., Szczylowski K., Van Montagu M.,
RA Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Azorhizobium caulinodans infection."
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL, Z48673; CAA88592.1; -.
DR PIR, S57991; S57991.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 40.3%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PONYKLP 9
DB 3 PHYXYKSP 10

RESULT 4
TKNA_RANRI STANDARD; PRT; 11 AA.
ID TKNA_RANRI
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranakinin (Substance-P-related peptide).
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Iovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda."
RL J. Neurochem. 57:2086-2091(1991).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.

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DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match
Best Local Similarity 38.7%; Score 24; DB 1; Length 11;
Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 5
O6LDM2 PRELIMINARY; PRT; 13 AA.
ID O6LDM2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=90036723; PubMed=2509433;
RA Hoshino T., Kose K.;
RT "Cloning and nucleotide sequence of brac, the structural gene for the
RT leucine-, isoleucine-, and valine-binding protein of Pseudomonas
RT aeruginosa PAO."
RL J. Bacteriol. 171:6300-6306(1989).
DR EMBL; M31071; AA08431.1; -.
KW Hypothetical protein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1648 MW; F275BF6289E3B51 CRC64;

Query Match
Best Local Similarity 38.7%; Score 24; DB 2; Length 13;
Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPONTYKLPOW 11
DB 1 MPEITHYLOQL 11

RESULT 6
TKN2 UPERU STANDARD; PRT; 11 AA.
ID TKN2 UPERU STANDARD; PRT; 11 AA.
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rugosauperolein II (lives, thirphysalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC Tissue=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and Bombesin-like peptides in the skin of the Australian
RT lepodactylid frog Uperoleia rugosa."

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RL Chem. Pharm. Bull. 28:689-695(1980).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyroglutamate carboxylic acid; Tachykinin.
FT MOD_RES 11
FT MOD_RES 11
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1270 MW; 3293693B59D1A327 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 7
TKNA CAVPO STANDARD; PRT; 11 AA.
ID TKNA CAVPO STANDARD; PRT; 11 AA.
AC P67932; P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Substance P.
GN Name=TAC1; Synonyms=NKA, NKNA, TAC2;
OS Bavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC Tissue=Small intestine;
RX MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P."
RL Neuropeptides 14:105-110(1989).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD_RES 11
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1349 MW; 3E75FE3C9D6C67 CRC64;

Query Match
Best Local Similarity 37.1%; Score 23; DB 1; Length 11;
Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONTYKL 8
DB 4 PRTFYL 10

RESULT 8
TKNA CHICK STANDARD; PRT; 11 AA.
ID TKNA CHICK STANDARD; PRT; 11 AA.

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AC P19850;
DR 01-FEB-1991 (Rel. 17, Created)
DR 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P. (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3] substance P and neurokinin A from chicken small intestine.";
RU Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amikation: Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD_RES 11 Methionine amide.
FT SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;
SQ
Query Match 37.1%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQPFYKL 8
DB 4 PQPFYKL 10

RESULT 9
TKNA HORSE STANDARD; PRT; 11 AA.
AC P67933; P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Substance P.
GN Name=TAC1; Synonyms=NKA, NKNA, TAC2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
RT intestine.";
RU Helv. Chim. Acta 56:860-866(1973).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amikation: Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW Tachykinin.
FT MOD_RES 11 Methionine amide.
FT SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;
SQ

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SQ SEQUENCE 11 AA; 1349 MW; 3E57FE3C9D6C6C7 CRC64;
Query Match 37.1%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQPFYKL 8
DB 4 PQPFYKL 10

RESULT 10
SODM ARTDA STANDARD; PRT; 13 AA.
ID SODM_ARTDA
AC P83289;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1) (Fragment).
OS Arthropods; Arthropoda; Insecta; Arthropoda; Arthropoda;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;
OC Orbiliales; Orbiliaceae; mitosporic Orbiliaceae; Arthropods;
OX NCBI_TaxID=74499;
RN [1]
RP SEQUENCE.
RC STRAIN=072;
RA Zhao M., Zhang K.;
RL Submitted (FEB-2002) to Swiss-Prot.
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese or iron ion per subunit (By
CC similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro: IPR001189; SODismutase.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KW Direct protein sequencing; Iron; Manganese; Metal-binding;
KW Oxidoreductase.
FT NON_TER 13
FT SEQUENCE 13 AA; 1515 MW; 69949202E642672B CRC64;
SQ
Query Match 37.1%; Score 23; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLPM 11
DB 2 YKLPM 7

RESULT 11
TKNA RANCA STANDARD; PRT; 11 AA.
ID TKNA_RANCA
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranatatesbeina A (RTK A).
OS Rana catesbeiana (Bull Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RU Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.

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CC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506; DOI=10.1016/0167-0115(93)90016-2;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
Intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR InterPro: IPR008215; Tachykinin.  
DR Pfam: PF02202; Tachykinin; 1.  
DR SMART: SM00203; TK; 1.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD\_RES 11 Methionine amide.  
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;  
  
Query Match 35.5%; Score 22; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 PONTYKL 8  
DB 4 PNTFYGL 10  
  
RESULT 12  
TXND\_RANCA STANDARD; PRT; 11 AA.  
AC P22691;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ranachykinin D (RTK D).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBT\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
brain and intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR PROSITE: PS00267; TACHYKININ; FALSE\_NEG.  
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD\_RES 11 Methionine amide.  
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;  
  
Query Match 35.5%; Score 22; DB 1; Length 11;

Best Local Similarity 60.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 PONTY 6  
DB 4 PERFY 8  
  
RESULT 13  
TKN\_PHYFU STANDARD; PRT; 11 AA.  
AC P08615;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Physalaemin.  
OS Physalaemus fuscumaculatus (Neotropical frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Leptodactylidae;  
OC Lepodactylinae; Physalaemus.  
OX NCBT\_TaxID=8378;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=66076612; PubMed=5857249;  
RA Erppamer V., Anaestasi A., Bertaccini G., Col J.M.;  
RT "Structure and pharmacological actions of physalaemin, the main active  
RT polypeptide of the skin of Physalaemus fuscumaculatus.";  
RL Experientia 20:489-490(1964).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR Pfam: PF02202; Tachykinin; 1.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD\_RES 11 Methionine amide.  
FT MOD\_RES 11 Pyrrolidone carboxylic acid.  
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C3457 CRC64;  
  
Query Match 35.5%; Score 22; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 PONTYKL 8  
DB 4 PNTFYGL 10  
  
RESULT 14  
Q9MW03 PRELIMINARY; PRT; 14 AA.  
AC Q9MW03;  
DT 01-OCT-2000 (TRMBLrel. 15, Created)  
DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)  
DE Cytochrome b (Fragment).  
GN Name=Cytb;  
OS Podospira curvicolle.  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospira.  
OX NCBT\_TaxID=48157;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;  
RA Saguez C., Lecellier G., Koll F.;

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RT "Intronic GIV-YIG endonuclease gene in the mitochondrial genome of
RT Padozpora curvicolia: evidence for mobility."
RL Nucleic Acids Res. 28:1299-1306 (2000).
DR EMBL: AJ249985; CAB72449.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Mitochondrion.
FT NON TER 1 1
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1603 MW; 2972D7731A723B43 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
Db 7 WTLPSM 13

RESULT 15
GREL_PSEUDO STANDARD; PRT; 15 AA.
AC P8299;
DT 05-JUL-2004 (rel. 44, Created)
DT 05-JUL-2004 (rel. 44, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
OS Pseudomonas sp. (strain ML).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=95619;
RN [1]
RP LOCATION, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND SUBCELLULAR
RX MEDLINE=21896940; PubMed=11900268; DOI=10.1016/S0923-2508(01)01293-1;
RA Santos P.M., Mignogna G., Heipieper H.J., Zennaro E.;
RT "Occurrence and properties of glutathione S-transferases in phenol-
RT degrading Pseudomonas strains."
RL Res. Microbiol. 153:89-98 (2002).
CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Monomer and homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GST superfamily.
DR GO: GO:0005737; C:cytoplasm; NAS.
DR GO: GO:0004364; F:glutathione transferase activity; NAS.
DR GO: GO:0008152; P:metabolism; IC.
KW Direct protein sequencing; Transferase.
FT NON TER 15 15
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1817 MW; 0E2A0FC5F55CBAC2 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 10
Db 7 FYHSPQ 12

RESULT 16
GQUWMI PRELIMINARY; PRT; 15 AA.
AC Q9UWMI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Benzoyl-CoA ligase (Fragment).
OS Methanospirillum hungatei.
RL Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales;

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OC Methanospirillaceae; Methanospirillum.
OX NCBI_TaxID=2203;
RN [1]
RP SEQUENCE.
RX MEDLINE=93040109; PubMed=1369492;
RA Auburger G., Winter J.;
RL Appl. Microbiol. Biotechnol. 37:789-795 (1992).
DR PIR: A48372; A48372.
SQ SEQUENCE 15 AA; 1880 MW; D2972EF3E690AC5C CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PGNFY 6
Db 5 PEEFY 9

RESULT 17
Q9UCA4 PRELIMINARY; PRT; 17 AA.
AC Q9UCA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tumor necrosis factor inhibitor I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Suzuki J., Tomizawa S., Arai H., Seki Y., Maruyama K., Kurome T.;
RT "Purification of two types of TNF inhibitors in the urine of the
RT patient with chronic glomerulonephritis."
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
SQ SEQUENCE 17 AA; 1903 MW; D418485E6981B28 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 17;
Best Local Similarity 55.6%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PGNFY 10
Db 5 PQGXYHPQ 13

RESULT 18
Q6KC69 PRELIMINARY; PRT; 10 AA.
AC Q6KC69;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative glutamine synthetase (Fragment).
OS Eucaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; rosids;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Eucalyptus.
OX NCBI_TaxID=71271;
RN [1]
RP SEQUENCE FROM N.A.
RA Pelosi A.;
RT "Molecular and genetic studies into the formation of lateral roots in
RT Eucalyptus and Arabidopsis."
RL Thesis (2002), Department of Biological Sciences, Monash University,
RL Melbourne, Australia.
RN [2]
RP SEQUENCE FROM N.A.
RA Hamill J.D.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: A0697760; CAG30778.1; -.

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FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1218 MW; CS19C76AA339C05D CRC64;

Query Match  
 Best Local Similarity 33.9%; Score 21; DB 2; Length 10;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 POFYKLP 9  
 DB 1 POFYKLP 8

## RESULT 19

Q9XBH3 PRELIMINARY; PRT; 10 AA.

AC Q9XBH3;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Celf-like protein (Fragment).

OS Name=celf;  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI\_TaxId=1396;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10987;  
 RA MEDLINE=99231848; PubMed=10217496;  
 RA Oksend O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;  
 RT "Genome organization is not conserved between *Bacillus cereus* and  
 RT *Bacillus subtilis*."  
 RL Microbiology 145:621-631(1999).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10987;  
 RA Hegna I.K.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ000394; CAB40625.1; -.

FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match  
 Best Local Similarity 33.9%; Score 21; DB 2; Length 10;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPONFYKL 8  
 DB 1 LPOFPCV 8

## RESULT 20

Q9QVLA PRELIMINARY; PRT; 13 AA.

AC Q9QVLA;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE 90 kDa advanced glycosylation ENDPRODUCT binding protein  
 DE (Fragment).

OS Rattus sp.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10118;

RN [1]  
 RP SEQUENCE.

RX MEDLINE=9134142; PubMed=1651976;  
 RA Yang Z., Makita Z., Horii Y., Brunelle S., Cerami A., Sehajpal P.,

RA Suchanichitran M., Vlasara H.;  
 RT "Two novel rat liver membrane proteins that bind advanced  
 RT glycosylation endproducts: relationship to macrophage receptor for  
 RT glucose-modified proteins."  
 RL J. Exp. Med. 174:515-524(1991).

FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1466 MW; 349B02BECFCE9A87 CRC64;

Query Match  
 Best Local Similarity 33.9%; Score 21; DB 2; Length 13;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLPOM 11  
 DB 4 KLPDM 8

## RESULT 21

Q9TOX7 PRELIMINARY; PRT; 15 AA.

AC Q9TOX7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Cartilage oligomeric matrix protein (Fragment).

OS Bos taurus (Bovine).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.

RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=95046341; PubMed=7957930; DOI=10.1016/0014-5793(94)01134-6;  
 RA Dicesare P., Hauser N., Lehman D., Pasumarti S., Paulsson M.;  
 RT "Cartilage oligomeric matrix protein (COMP) is an abundant component  
 RT of tendon."  
 RL FEBS Lett. 354:237-240(1994).

SQ SEQUENCE 15 AA; 1689 MW; D709168394B5861C CRC64;  
 Query Match  
 Best Local Similarity 33.9%; Score 21; DB 2; Length 15;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYKLPOM 11  
 DB 1 FYEGPBL 7

## RESULT 22

Q71GTO PRELIMINARY; PRT; 15 AA.

AC Q71GTO;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit I.

OS Andrea aff. manifeesta LLU-2002.  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Andrenidae; Andreninae; Andrena.

OC NCBI\_TaxId=205242;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Larkin L.L., Neff J.L., Simpson B.B.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF504374; AA007719.1; -.  
 DR GO:GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.

SQ SEQUENCE 15 AA; 1840 MW; 118B961922A39B59 CRC64;

Query Match  
 Best Local Similarity 33.9%; Score 21; DB 2; Length 15;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MNHSPNIP1M 11

# RESULT 23

BRB\_BASAL STANDARD; PRT; 16 AA.  
 AC P83187;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Beta-barubin (Fragment).  
 OS Basella alba (Malabar spinach) (Ceylon spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Basellaceae; Basella.  
 OC NCBI\_TaxID=3589;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=21547763; PubMed=11688973; DOI=10.1006/brc.2001.5822;  
 RA Wang H., Ng T.B.;  
 RT "Novel antifungal peptides from ceylon spinach seeds.";  
 RL Biochem. Biophys. Res. Commun. 288:765-770(2001).  
 CC -I- FUNCTION: Possesses antifungal activity against B.cinerea,  
 M.arachidicola and F.oxysporum but not C.comatus and R.solani.  
 CC Inhibits HIV-1 reverse transcriptase and cell-free translation.  
 CC GO: GO:0050832; P:defense response to fungi; IDA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IDA.  
 DR Direct protein sequencing; Fungicide.  
 KW NON TER  
 FT SEQUENCE 16 AA; 1952 MW; 2899FE4FC181682C CRC64;  
 SQ

Query Match 33.9%; Score 21; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PONEFK 7  
 Db 6 PSKPYE 11

# RESULT 24

Q6R9P0 PRELIMINARY; PRT; 17 AA.  
 AC Q6R9P0;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=Mcpnl;  
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Trachypithecus.  
 OC NCBI\_TaxID=54180;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain  
 size.";  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506354; AAS88719.1; -.  
 FT NON TER  
 SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKLPQ 10  
 Db 13 YLPPQ 17

# RESULT 25

Q6R9P1 PRELIMINARY; PRT; 17 AA.  
 AC Q6R9P1;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=Mcpnl;  
 OS Trachypithecus phayrei (Phayre's leaf monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Trachypithecus.  
 OC NCBI\_TaxID=61618;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain  
 size.";  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506354; AAS88718.1; -.  
 FT NON TER  
 SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKLPQ 10  
 Db 13 YLPPQ 17

# RESULT 26

Q6R9P2 PRELIMINARY; PRT; 17 AA.  
 AC Q6R9P2;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=Mcpnl;  
 OS Pygathrix nemaeus (Dove langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OC NCBI\_TaxID=54133;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain  
 size.";  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506354; AAS88717.1; -.  
 FT NON TER  
 SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10  
 |  
 |  
 |  
 |  
 Db 13 YLPPQ 17

## RESULT 27

Q6R9P3 PRELIMINARY; PRT; 17 AA.

AC Q6R9P3; 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=McpH1;  
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OC NCBI\_TaxID=61621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain size."  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506353; AAS8716.1; --  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 1931 MW; DC63AF1C7785B5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10  
 |  
 |  
 |  
 |  
 Db 13 YLPPQ 17

## RESULT 28

Q6R9P4 PRELIMINARY; PRT; 17 AA.

AC Q6R9P4; 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=McpH1;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecidae; Macaca.  
 OC NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain size."  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506352; AAS8715.1; --

FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 1931 MW; DC63AF1C7785B5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10  
 |  
 |  
 |  
 |  
 Db 13 YLPPQ 17

## RESULT 29

Q6R9P8 PRELIMINARY; PRT; 17 AA.

AC Q6R9P8; 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Microcephalin (Fragment).  
 GN Name=McpH1;  
 OS Erythrocebus patas (Red guenon) (Cercopithecus patas).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Erythrocebus.  
 OC NCBI\_TaxID=9538;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
 RA Wang Y.Q., Su B.;  
 RT "Molecular evolution of microcephalin, a gene determining human brain size."  
 RL Hum. Mol. Genet. 13:1131-1137(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Su B.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506348; AAS8711.1; --  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 1945 MW; DC63AF1C77F2E5B CRC64;

Query Match 33.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10  
 |  
 |  
 |  
 |  
 Db 13 YLPPQ 17

## RESULT 30

Q6R9R1 PRELIMINARY; PRT; 18 AA.

AC Q6R9R1; 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Adhesin (Fragment).  
 GN Name=fnaB;  
 OS Bordetella parapertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OC NCBI\_TaxID=519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=8234;  
 RX MEDLINE=20290246; PubMed=10832649;  
 RA Jacob-Pudissson F., Kehoe B., Willery E., Reveneau N., Loch C.,  
 Reiman D.A.;  
 RT "Molecular characterization of Bordetella bronchiseptica filamentous hemagglutinin and its secretion machinery."  
 RL Microbiology 146:1211-1221(2000).  
 DR EMBL; AF11798; AAF21948.1; --

FT NON TER 18 18  
SQ SEQUENCE 18 AA; 2135 MW; F129A793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 8e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFONFYKL 8  
| | | | |  
1 MNTNLYRL 8

RESULT 31  
Q9RGR2 PRELIMINARY; PRT; 18 AA.

ID Q9RGR2  
AC Q9RGR2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Adhesin (Fragment).  
GN Name=fnab;  
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
OX NCBI\_TaxID=518;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RB50;  
RX MEDLINE=20290246; PubMed=10832649;  
RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,  
RA Relhan D.A.;

RT "Molecular characterization of Bordetella bronchiseptica filamentous  
hemagglutinin and its secretion machinery.";  
RL Microbiology 146:1211-1221(2000).  
DR EMBL, AF11797; AAF21947.1; -.

FT NON TER 18 18  
SQ SEQUENCE 18 AA; 2151 MW; F139E793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 8e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFONFYKL 8  
| | | | |  
1 MNTNLYRL 8

RESULT 32  
FARB\_CALVO STANDARD; PRT; 7 AA.

ID FARB\_CALVO  
AC P41866;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Calliphoridae 11.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;

RT "Isolation, structure, and activity of Phe-Met-Arg-Phe-NH2  
neuropeptides (designated calliphoramides) from the blowfly Calliphora  
vomitoria.";  
RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
family.

DR PIR, B44787, B44787.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 926 MW; 69D40659C44AB700 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 POFNFK 7  
| | | | |  
1 PDNFKR 6

RESULT 33  
TKL1\_LOCOMI STANDARD; PRT; 9 AA.

ID TKL1\_LOCOMI  
AC P16223;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Locustatachykinin I (TK-I).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=90184489; PubMed=2111766; DOI=10.1016/0014-5793(90)80601-E;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RT "Locustatachykinin I and II, two novel insect neuropeptides with  
homology to peptides of the vertebrate tachykinin family.";  
RL FEBS Lett. 261:397-401(1990).

CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the  
oviduct and foregut.

CC -1- SUBCELLULAR LOCATION: Secreted.  
DR PIR, S08265; ECDQIM.  
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 939 MW; 2389C6B59C865A7 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 POFNFK 6  
| | | | |  
2 PSGFY 6

RESULT 34  
TKN1\_UPEIN STANDARD; PRT; 11 AA.

ID TKN1\_UPEIN  
AC P82026;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Uperin 1.1.  
OS Uperoleia inundata (loodplain toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=104953;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
RA Adams G.W., Severini C.;

RT "Novel uperin peptides from the dorsal glands of the australian  
loodplain toadlet Uperoleia inundata.";  
RT Aust. J. Chem. 49:475-484(1996).



CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=1208; METHOD=FAB; RANGE=1-11; NOTE=Ref.1.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro: IPR002040; Tachy\_Neurokinin.  
 DR Pfam: PF02202; Tachykinin\_1.  
 DR PROSITE: PS00267; TACHYKININ, 1.  
 KW Neuropeptide; Amphibian defense peptide; Direct protein sequencing;  
 KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
 FT MOD RES 1 1 Methionine amide.  
 FT MOD RES 11 11 Pyrrolidone carboxylic acid.  
 SQ SEQUENCE 11 AA; 1226 MW; 3293693B59CDD457 CRC64;

Query Match  
 Best Local Similarity 32.3%; Score 20; DB 1; Length 11;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQQFYKL 8  
 DB 4 PNAFYGL 10

RESULT 35  
 TRK1\_UPERU STANDARD; PRT; 11 AA.  
 ID TKN1\_UPERU  
 AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OC NCBI\_Taxid=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75131227; PubMed=1120493;  
 RA Anastasi A., Exsperner V., Endean R.;  
 RT "Structure of uperolein, a physalaemin-like endopeptide occurring in  
 RT the skin of Uperoleia rugosa and Uperoleia marmorata.";  
 RL Experientia 31:394-395(1975).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro: IPR002040; Tachy\_Neurokinin.  
 DR InterPro: IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin\_1.  
 DR SMART; SM00203; TK, 1.  
 DR PROSITE; PS00267; TACHYKININ, 1.  
 KW Neuropeptide; Amphibian defense peptide; Direct protein sequencing;  
 KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
 FT MOD RES 1 1 Methionine amide.  
 FT MOD RES 11 11 Pyrrolidone carboxylic acid.  
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3B59CDD457 CRC64;

Query Match  
 Best Local Similarity 32.3%; Score 20; DB 1; Length 11;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQQFYKL 8  
 DB 4 PNAFYGL 10

RESULT 36  
 ID Q16234 PRELIMINARY; PRT; 11 AA.  
 AC Q16234;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hud protein.  
 GN Name=Hud;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94349312; PubMed=8069866;  
 RA Sekido Y., Bader S.A., Cardone D.P., Johnson B.E., Mina J.D.;  
 RT "Molecular analysis of the Hud gene encoding a paraneoplastic  
 RT oncofetal antigen in human lung cancer cell lines.";  
 RL Cancer Res 54:4988-4992(1994).  
 DR EMBL; S73867; AAD14142.1; -.  
 DR PIR; I52708; I52708.  
 SQ SEQUENCE 11 AA; 1289 MW; 2EDCE20E204415A7 CRC64;

Query Match  
 Best Local Similarity 32.3%; Score 20; DB 2; Length 11;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPQFYKL 8  
 DB 3 MPRRLKL 10

RESULT 37  
 ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.  
 AC Q9RFZ2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Fructose biphosphate aldolase (Fragment).  
 GN Name=fba;  
 OS Mycoplasma mycoides (subsp. capri).  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OC NCBI\_Taxid=40477;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PG3;  
 RX MEDLINE=20193983; PubMed=10727835; DOI=10.1016/S0378-1135(99)00204-7;  
 RA Thiaucourt F., Lorenzon S., David A., Breaud A.;  
 RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing  
 RT of a putative membrane protein gene.";  
 RL Vet. Microbiol. 72:251-268(2000).  
 DR EMBL; AF162998; AAF15255.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match  
 Best Local Similarity 32.3%; Score 20; DB 2; Length 11;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPQFYKL 7  
 DB 1 MPKLYHK 7

RESULT 38  
 TRK2\_KASMA STANDARD; PRT; 12 AA.  
 ID TKN2\_KASMA  
 AC P08614;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Hylambatin.  
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hylaroliidae;  
 CC Kassina.  
 OX NCBI\_TaxID=8414;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erespamer G.F., Erespamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (Hylambates-kassinin) and  
 RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
 RT maculatus.";  
 RL Biomed. Res. 2:613-617(1981).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR, S07436; S07436.  
 DR InterPro, IPR02040; Tachy\_Neurokinin.  
 DR Pfam, PF02202; Tachykinin; 1.  
 DR PROSITE, PS00267; TACHYKININ; 1.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
 KW Neuropeptide; Tachykinin.  
 FT MOD\_RES 12 12 Methionine amide.  
 SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PONY 6  
 |||  
 Db 5 PDIFY 9

RESULT 39  
 Q53579 PRELIMINARY; PRT; 12 AA.  
 AC Q53579;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Light-harvesting complex I alpha polypeptide (Fragment).  
 GN Name=puFA;  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 CC Rhodospirillaceae; Rhodospirillum.  
 OX NCBI\_TaxID=1061;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92234963; PubMed=1569029;  
 RA Richter P., Brand M., Drews G.;  
 RT "Characterization of LHI- and LHI+ Rhodospirillum rubrum puFA  
 RT mutants.";  
 RL J. Bacteriol. 174:3030-3041(1992).  
 DR EMBL, S97551; AAC60405.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1627 MW; 0F92FEBA8A70532B CRC64;

Query Match 32.3%; Score 20; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 |||  
 Db 4 FYKI 7

RESULT 40  
 Q9THR8 PRELIMINARY; PRT; 13 AA.  
 ID Q9THR8  
 AC Q9THR8;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE PbsH (Fragment).  
 DR Name=pbsH;  
 GN Name=pbsH;  
 OS Bryopsis sp. A.  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;  
 CC Bryopsidaceae; Bryopsis.  
 OX NCBI\_TaxID=103784;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Krellwitz E.C., Kowalik K.V., Manos P.S.;  
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, AF170413; AAD56858.1; -.  
 DR GO, GO:0009507; Chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1785 MW; 3F9A1C3E247D0323 CRC64;

Query Match 32.3%; Score 20; DB 2; Length 13;  
 Best Local Similarity 42.9%; Pred. No. 8.7e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPONYK 7  
 |||  
 Db 1 MPXYWK 7

Search completed: June 7, 2005, 23:19:02  
 Job time : 51.4 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPEPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	4	AA872506
2	81	100.0	15	4	AA859312
3	81	100.0	15	4	AA872252
4	81	100.0	15	4	AA872538
5	81	100.0	15	5	AA014583
6	81	100.0	15	5	AAW51042
7	81	100.0	15	5	AAE20234
8	81	100.0	15	5	ADN60301
9	81	100.0	15	8	AD574388
10	81	100.0	16	4	AA859343
11	38	46.9	14	4	AA806249
12	38	46.9	15	8	ADJ38585
13	38	46.9	18	2	AAW47567
14	38	46.9	18	2	AAW47571
15	38	46.9	18	2	AAW47577
16	38	46.9	18	2	AAW47550
17	38	46.9	18	2	AAW03738
18	38	46.9	18	2	AAW03721
19	38	46.9	18	3	AA852880
20	38	46.9	18	3	AA852886
21	38	46.9	18	3	AA852876
22	38	46.9	18	3	AA852885
23	37	45.7	18	5	ABG72860
24	37	45.7	18	2	AAW05469
25	37	45.7	18	2	AAW37677

26	37	45.7	18	2	AAW38909	AAW38909 Peptide r
27	37	45.7	18	2	AAW47562	AAW47562 Extendin a
28	37	45.7	18	2	AAW03733	AAW03733 Extendin a
29	37	45.7	18	7	ADB49303	ADB49303 Novel KW
30	36	44.4	10	2	AA807284	AA807284 Smooth mu
31	36	44.4	14	4	AA879174	AA879174 Peptide d
32	36	44.4	15	4	AA879166	AA879166 Synthetic
33	36	44.4	18	2	AAW47569	AAW47569 Extendin a
34	36	44.4	18	2	AAW47552	AAW47552 Extendin a
35	36	44.4	18	2	AAW47564	AAW47564 Extendin a
36	36	44.4	18	2	AAW03740	AAW03740 Extendin a
37	36	44.4	18	2	AAW03742	AAW03742 Extendin a
38	36	44.4	18	2	AAW03735	AAW03735 Extendin a
39	36	44.4	18	2	AAW52878	AAW52878 Extendin a
40	36	44.4	18	3	AAW52873	AAW52873 Extendin
41	36	44.4	18	3	AAW52877	AAW52877 Extendin
42	36	44.4	18	8	ADK50264	ADK50264 Human car
43	36	44.4	18	8	ADK49142	ADK49142 Human car
44	35	43.2	10	2	AAW47943	AAW47943 AE101 ana
45	35	43.2	10	4	AAU09138	AAU09138 Ena/VASP
46	35	43.2	12	2	AAW48084	AAW48084 AE101 ser
47	35	43.2	13	2	AAW38053	AAW38053 Peptide r
48	35	43.2	13	7	ADB49201	ADB49201 Biotinyl a
49	35	43.2	15	1	AAW10189	AAW10189 Sequence
50	35	43.2	15	1	AAW70999	AAW70999 Sequence
51	35	43.2	15	1	AAW80033	AAW80033 Beta-huma
52	35	43.2	15	1	AAW91840	AAW91840 Analogue
53	35	43.2	15	2	AAW39024	AAW39024 Peptide r
54	35	43.2	15	2	AAW38952	AAW38952 Peptide r
55	35	43.2	15	2	AAW37268	AAW37268 Peptide d
56	35	43.2	15	2	AAW69452	AAW69452 HCG antiq
57	35	43.2	15	2	AAW93437	AAW93437 Human hcg
58	35	43.2	15	3	AAW87482	AAW87482 Human cho
59	35	43.2	15	3	AAW20559	AAW20559 Human cho
60	35	43.2	15	4	AAU01142	AAU01142 Structure
61	35	43.2	15	4	AAW48388	AAW48388 Human cho
62	35	43.2	15	4	AAU02840	AAU02840 Human cho
63	35	43.2	15	4	AAW04124	AAW04124 Peptide f
64	35	43.2	16	2	AAW47923	AAW47923 Mammalian
65	35	43.2	16	4	AAW73469	AAW73469 Mammalian
66	35	43.2	16	8	ADW12046	ADW12046 Mammalian
67	35	43.2	16	8	ADW38264	ADW38264 Mammalian
68	35	43.2	17	6	AAW83411	AAW83411 G protein
69	34	42.0	5	2	AAW37157	AAW37157 EVH1 lig
70	34	42.0	5	4	AAW79177	AAW79177 Amino aci
71	34	42.0	5	4	AAU09140	AAU09140 Ena/VASP
72	34	42.0	6	2	AAW17762	AAW17762 Zyxine VA
73	34	42.0	6	2	AAW31441	AAW31441 Transcrip
74	34	42.0	9	2	AAW47926	AAW47926 Human MHC
75	34	42.0	10	4	AAU09144	AAU09144 Ena/VASP
76	34	42.0	10	2	AAW47942	AAW47942 AE101 ana
77	34	42.0	13	2	AAW38008	AAW38008 WW domain
78	34	42.0	14	4	AAW83035	AAW83035 Human Sma
79	34	42.0	15	2	AAW02172	AAW02172 Peptide w
80	34	42.0	15	2	AAW38059	AAW38059 Peptide w
81	34	42.0	15	2	AAW39006	AAW39006 Peptide r
82	34	42.0	15	2	AAW38942	AAW38942 Peptide r
83	34	42.0	15	5	AAW25358	AAW25358 Abi SH3 d
84	34	42.0	15	5	AAW59535	AAW59535 Human rib
85	34	42.0	15	7	ADB49249	ADB49249 Biotinyl a
86	34	42.0	16	2	AAW76284	AAW76284 GAr78B84
87	34	42.0	16	2	AAW82834	AAW82834 Mutated P
88	34	42.0	16	2	AAW82832	AAW82832 PY motif
89	34	42.0	16	2	AAW82832	AAW82832 MUC1 muta
90	34	42.0	16	3	AAW65944	AAW65944 MUC1 muta
91	34	42.0	17	5	AAW66086	AAW66086 Amino aci
92	34	42.0	17	4	AAW83313	AAW83313 LRP5 prot
93	33	40.7	7	4	AAW72512	AAW72512 Colostri
94	33	40.7	7	4	AAW59315	AAW59315 Ewe colos
95	33	40.7	7	4	AAW72259	AAW72259 Colostri
96	33	40.7	7	4	AAW72544	AAW72544 Colostri
97	33	40.7	7	5	AAW14590	AAW14590 Human rib
98	33	40.7	7	5	AAW51048	AAW51048 Neutral ce
99	33	40.7	7	5	AAW20241	AAW20241 Colostri

99 33 40.7 7 8 ADN60308  
100 33 40.7 7 8 ADS74391

Adn60308 Constitue  
Ads74391 Ovine col

## ALIGNMENTS

RESULT 1  
AAB72506  
ID AAB72506 standard; peptide; 15 AA.

XX AAB72506;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #7.

XX Dermatalogical; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022665.

XX 17-AUG-1999; 99US-0149310P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell  
PT with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations.

XX Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidizing species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15

RESULT 2  
AAB59312  
ID AAB59312 standard; peptide; 15 AA.

XX AAB59312;

XX 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment A-3.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.  
XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB002128.

XX 02-JUN-1999; 99GB-00012852.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.

XX Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15

RESULT 3  
AAB72252  
ID AAB72252 standard; peptide; 15 AA.

XX AAB72252;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 7.

XX Colostrinin; immune response; cytokine; blood cell proliferation;  
XX central nervous system disorder; neurological disorder; mental disorder;  
XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
XX neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022818.

XX 17-AUG-1999; 99US-0149311P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.  
XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrin as an immunological  
PT regulator.  
XX  
XX Claim 1; Page 34; 50pp; English.  
XX  
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
CC have immune response modulatory activity, and are capable of inducing  
CC cytokines. Colostrin and its derived peptides are useful for inducing  
CC cytokine production, for modulating an immunological response and for  
CC inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15  
  
RESULT 4  
AAB72538  
ID AAB72538 standard; peptide; 15 AA.  
XX  
XX AAB72538;  
XX  
XX 09-MAY-2001 (first entry)  
XX  
XX Colostrin peptide #7.  
XX  
XX Neuroprotective; neural cell differentiation regulator; colostrin;  
XX colostrum.  
XX  
XX OS Unidentified.  
XX  
XX WO200112651-A2.  
XX  
XX PD 22-FEB-2001.  
XX  
XX PF 17-AUG-2000; 2000WO-US022774.  
XX  
XX PR 17-AUG-1999; 99US-0149633P.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX P1 Boldogh I;  
XX  
XX WPI; 2001-226545/23.  
XX  
XX Use of colostrin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating damaged  
PT neural cells in a patient.  
XX  
XX Claim 6; Page 21; 35pp; English.  
XX  
XX The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrin and  
CC colostrin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrin is a polypeptide complex found in colostrum  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15  
  
RESULT 5  
AA014583  
ID AA014583 standard; peptide; 15 AA.  
XX  
XX AA014583;  
XX  
XX 27-MAY-2002 (first entry)  
XX  
XX DE Neural cell regulatory colostrin peptide 7.  
XX  
XX KM Neural cell differentiation; neural cell regulator; colostrin peptide;  
XX KM neural cell formation; proline-rich polypeptide aggregate; colostrum;  
XX KM neural cell treatment.  
XX  
XX OS Unidentified.  
XX  
XX FH Key Location/Qualifiers  
FT Modified-site 15 /note="Optional C-terminal amide"  
XX  
XX PN WO200213851-A1.  
XX  
XX PD 21-FEB-2002.  
XX  
XX PF 17-AUG-2000; 2000WO-US022777.  
XX  
XX PR 17-AUG-2000; 2000WO-US022777.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX P1 Boldogh I, Stanton JG, Hughes TK;  
XX  
XX DR WPI; 2002-269152/31.  
XX  
XX PT Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrin, its constituent peptide and/or  
PT analog.  
XX  
XX PS Claim 7; Page 21; 37pp; English.  
XX  
XX CC The invention comprises a method for promoting cell differentiation (e.g.  
CC CC neural cell differentiation). The method involves contacting cells with a  
CC CC neural cell regulator (i.e. a colostrin peptide) in order to change the  
CC CC cells in morphology to form neural cells. Colostrin is a proline-rich  
CC CC polypeptide aggregate that is present in colostrum. The method of the  
CC CC invention is useful for promoting the differentiation of cells and for  
CC CC treating damaged neural cells in a patient. The present amino acid  
CC CC sequence represents a specifically claimed colostrin peptide used in  
CC CC the method of the invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15  
  
RESULT 6  
AAM51042

ID AAM51042 standard; peptide; 15 AA.  
XX  
XX AAM51042;  
XX  
XX 30-MAY-2002 (first entry)  
XX  
XX Colostrinin constituent peptide.  
XX  
XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
XX blood cell regulator; cytokine inducer; human.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 15 /note="optional C-terminal amidation"  
XX  
XX WO200213849-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022775.  
XX  
XX 17-AUG-2000; 2000WO-US022775.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX (REGE-) REGEN THERAPEUTICS PLC.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2002-269150/31.  
XX  
XX Modulation of blood cell proliferation in a patient involves use of blood  
XX cell regulator selected from colostrinin, its constituent peptide and/or  
XX analog.  
XX  
XX Claim 1; Page 34; 54pp; English.  
XX  
XX The present sequence is that of a colostrinin constituent peptide that is  
XX preferred for use as an immunological regulator and as a blood cell  
XX regulator in claimed methods of the invention. Methods are claimed for:  
XX inducing a cytokine in a cell by contact with an immunological regulator,  
XX where the cell is present in a cell culture, a tissue, an organ or an  
XX organism, and the cell is mammalian, including human; modulating an  
XX immune response in a cell by contact with the immunological regulator  
XX under conditions effective to induce a cytokine; modulating an immune  
XX response in a patient by administering an immunological regulator under  
XX conditions effective to induce a cytokine, where the immunological  
XX regulator is administered topically or as part of a dietary supplement,  
XX and where the immune response is specific or non specific, an interferon  
XX response or an antibody response; modulating blood cell proliferation by  
XX contacting blood cells with a blood cell regulator, where the blood cells  
XX are present in a cell culture or an organism, are mammalian or human, and  
XX where the blood cells are increased in number or differentiated; and a  
XX method for modulating blood cell proliferation in a patient. A claimed  
XX cytokine-inducing composition comprises a pharmaceutical carrier and an  
XX active agent such as the present peptide. Cytokines induced by this  
XX peptide in human leucocyte cultures include interferon-gamma, tumour  
XX necrosis factor-alpha, interleukin-4, interleukin-6 and interleukin-10  
XX  
XX Sequence 15 AA;  
SQ

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15  
| | | | | | | | | | | | | | |  
DB 1 VLEMKFPPPPQETVT 15

RESULT 7  
AAE20234

ID AAE20234 standard; peptide; 15 AA.  
XX  
XX AAE20234;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Colostrinin constituent peptide #7.  
XX  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX transplantation; implantation; dermatological; vulnerrary.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 15 /note="Optionally C-terminal amide"  
XX  
XX WO200213850-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022776.  
XX  
XX 17-AUG-2000; 2000WO-US022776.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a  
XX patient comprises a blood cell regulator selected from colostrinin, its  
XX constituent peptide and/or analog.  
XX  
XX Claim 6; Page 25; 51pp; English.  
XX  
XX The invention relates to a composition which comprises a blood cell  
XX regulator selected from colostrinin, its constituent peptide and/or  
XX analogue. The invention is used for modulating the oxidative stress level  
XX in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
XX organ, or organism; or for treating oxidative damage to the skin of a  
XX patient e.g. animal or human; to modulate oxidative stress during/ after  
XX a premature birth or normal birth, preventing/delaying aging in a  
XX patient, enhancing wound healing, and the reduction of side effects of  
XX cosmetic procedures. The method changes the level of an oxidising species  
XX in the cell, such as decreases or prevents increase in the level of  
XX damage to a biomolecule of the patient selected from DNA, protein and/or  
XX lipid, compared to the same conditions when the oxidative stress  
XX regulator is not present. The modulation of oxidative stress results in  
XX enhanced repair, regeneration, and replacement of cells, tissues and  
XX organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
XX external organs), as well as enhanced preservation of such organs for  
XX transplantation, implantation, or scientific research. The present  
XX sequence is a colostrinin constituent peptide  
XX  
XX Sequence 15 AA;  
SQ

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15  
| | | | | | | | | | | | | | |  
DB 1 VLEMKFPPPPQETVT 15

RESULT 8  
ADN60301  
ID ADN60301 standard; peptide; 15 AA.  
XX

AC ADN60301;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Constituent peptide of colostrinin SEQ ID NO:7.  
 XX  
 KW modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;  
 KW DNA damage; beta-amyloid; retinoic acid; cyclostatic; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal kinase inhibition.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037851-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033423.  
 XX  
 PR 22-OCT-2002; 2002US-0420369P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (BOLD/) BOLDG I.  
 PA (STAN/) STANTON J G.  
 PA (GEOR/) GEORGIADIS J A.  
 PA (HUGH/) HUGHES T K.  
 PA (KRUIZ/) KRUIZEL M.  
 XX  
 PI Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
 XX  
 DR WPI; 2004-365494/34.  
 XX  
 PT Use of colostrinin for e.g. modulating an intracellular signaling  
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 PT a cell.  
 XX  
 PS Claim 6; SEQ ID NO 7; 46pp; English.  
 XX  
 CC The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cyclostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 XX  
 SQ Sequence 15 AA;  
 QY  
 Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 VLEMKFPPPPPTVT 15  
 1 VLEMKFPPPPPTVT 15  
 RESULT 9  
 ADS74388 standard; peptide; 15 AA.  
 XX

AC ADS74388;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Ovine colostrinin peptide.  
 XX  
 KW Colostrum; colostrinin; sheep; peptide purification.  
 KW Ovis aries.  
 XX  
 PN WO2004081038-A1.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 10-MAR-2004; 2004WO-GB001014.  
 XX  
 PR 11-MAR-2003; 2003GB-00005552.  
 PR 08-MAR-2004; 2004GB-00005190.  
 XX  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
 XX  
 DR WPI; 2004-677519/66.  
 XX  
 PT Recovering peptides such as colostrinin from mammalian colostrum, by  
 PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 PT and precipitate, separating alcohol phase from precipitate, and  
 PT recovering alcohol phase.  
 XX  
 PS Example; SEQ ID NO 3; 41pp; English.  
 XX  
 CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrum using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids. In an example from the invention, the antigenic profile of  
 CC peptides recovered from sheep colostrum using the alcohol precipitation  
 CC methods was determined by ELISA using antibodies prepared against 9  
 CC synthetic peptides, including a peptide having the present sequence  
 CC (denoted antigen class A-3).  
 XX  
 SQ Sequence 15 AA;  
 QY  
 Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 VLEMKFPPPPPTVT 15  
 1 VLEMKFPPPPPTVT 15  
 RESULT 10  
 AAB59343  
 ID AAB59343 standard; peptide; 16 AA.  
 XX  
 AC AAB59343;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX

DE Ewe colostrinin peptide fragment derived sequence #3.  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX WO200075173-A2.  
 XX  
 XX 14-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-GB002128.  
 XX  
 XX 02-JUN-1999; 99GB-00012852.  
 XX  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Georgiades JA;  
 XX  
 XX WPI; 2001-071058/08.  
 XX  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 XX PS Claim 8; Page 27; 63pp; English.  
 XX  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX  
 XX SQ Sequence 16 AA;  
 XX  
 XX Query Match 100.0%; Score 81; DB 4; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 0.0001;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEMKRPPPPQETVT 15  
 DB 2 VLEMKRPPPPQETVT 16

RESULT 11  
 AAR06249  
 ID AAR06249 standard; protein; 14 AA.  
 XX  
 XX AAR06249;  
 XX  
 XX 09-JAN-2003 (revised)  
 DT 07-DEC-1990 (first entry)  
 XX  
 XX Antigenic peptide fragment selected from the 12 N-terminal AAs of  
 DE heptadecagastrin (G17).  
 DE  
 XX Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.  
 KW  
 XX Unidentified.  
 OS  
 XX EP380230-A.  
 PN  
 XX 01-AUG-1990.  
 PD  
 XX 17-JAN-1990; 90EP-00300456.  
 PF  
 XX 24-JAN-1988; 89US-00301353.  
 PR 12-MAY-1989; 89US-00351193.  
 XX

PA (APHT-) APHTON CORP.  
 XX  
 XX Gevas PC, Grimes S, Karr SL, Littenberg RL;  
 PI  
 XX WPI; 1990-233029/31.  
 XX  
 XX Immunogens against gastrin peptide(s) - used to induce antibodies that  
 PT specifically neutralise single form of gastrin, G17 or G34.  
 PT  
 XX Claim 8; Page 19; 32pp; English.  
 XX  
 XX Antigenic fragments may be attached to an immunogenic carrier and used to  
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide  
 CC fragments capable of binding to these Abs are useful in neutralising anti  
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)  
 CC  
 XX SQ Sequence 14 AA;  
 XX  
 XX Query Match 46.9%; Score 38; DB 2; Length 14;  
 XX Best Local Similarity 70.0%; Pred. No. 1e+02;  
 XX Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 LEMKRPBPQ 11  
 DB 5 LEMKRPBPQ 14

RESULT 12  
 ADJ38585  
 ID ADJ38585 standard; peptide; 15 AA.  
 XX  
 XX ADJ38585;  
 AC  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX HSV-4 latent membrane protein 2A late domain motif mutant peptide #4.  
 DB  
 XX Virucide; HSV infection; antiviral; late domain motif; mutant.  
 KW  
 XX Human herpesvirus 4.  
 OS  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 9 /note= "Wild-type residue replaced with Gln"  
 FT  
 XX WO2004009027-A2.  
 XX  
 XX 29-JAN-2004.  
 PD  
 XX 21-JUL-2003; 2003WO-US022828.  
 PF  
 XX 19-JUL-2002; 2002US-0397265P.  
 PR 19-JUL-2002; 2002US-0397477P.  
 PR 19-JUL-2002; 2002US-0397479P.  
 PR 03-MAR-2003; 2003US-0451903P.  
 XX  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA  
 XX Morham S, Zavitz K, Hobden A;  
 PI  
 XX WPI; 2004-123282/12.  
 DR  
 XX Use of cells displaying herpes simplex virus (HSV) altered budding  
 PT phenotype for the manufacture of a medicament for treating HSV infection.  
 PT  
 XX Example 12; Page 63; 74pp; English.  
 PS  
 XX The present invention relates to cells displaying herpes simplex virus  
 CC (HSV) altered budding phenotype which are useful for the manufacture of a  
 CC medicament for treating HSV infection. The medicament further comprises  
 CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL  
 CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and



CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid  
 CC encoding the polypeptide sufficient for virus-like particle assembly but  
 CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
 CC The genome is devoid of late domain motifs capable of effecting viral  
 CC budding. The composition also comprises a compound capable of interfering  
 CC with the protein-protein interaction between a host cell protein capable  
 CC of binding a late domain motif and a HSV protein containing a late domain  
 CC motif. The composition further comprises another HSV protein or its  
 CC immunogenic fragment, and/or a nucleic acid encoding the other HSV  
 CC protein or the immunogenic fragment. The present sequence is a mutant HSV  
 CC peptide, derived from the wild-type peptide ADJ3858L, used to illustrate  
 CC the invention.

SQ Sequence 15 AA;

Query Match 46.9%; Score 38; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPQG 12  
 |||||  
 Db 5 PPPQG 10

RESULT 13  
 AAM47567  
 ID AAM47567 standard; peptide; 18 AA.

AC AAM47567;  
 XX  
 DT 03-JUL-1998 (first entry)  
 XX

DE Exendin agonist (18).

KM Exendin agonist; gastric motility; gastric emptying; treatment; spasm;  
 KM postprandial dumping syndrome; postprandial hyperglycaemia;  
 KM type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
 KM Gila monster venom.

OS Synthetic.

FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "amidated"

PN WO9805351-A1.

PD 12-FEB-1998.

PF 08-AUG-1997; 97WO-US014199.

PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX WPI; 1998-145351/13.

DR  
 XX  
 PT Regulating gastrointestinal motility using exendins or their agonists -  
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
 PT glucose tolerance etc., also in diagnostic investigations.

PS Example 21, Fig 8, 70pp; English.

XX The present sequence is an exendin agonist, which reduces gastric  
 CC motility and delays gastric emptying. It can be used to treat spasm  
 CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to

CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Exendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of  
 CC hyperglycaemia

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLEMKPPPP 10  
 :||:|||||  
 Db 8 LFLFVPPPP 17

RESULT 14  
 AAM47571  
 ID AAM47571 standard; peptide; 18 AA.

AC AAM47571;  
 XX  
 DT 03-JUL-1998 (first entry)  
 XX

DE Exendin agonist (22).

KM Exendin agonist; gastric motility; gastric emptying; treatment; spasm;  
 KM postprandial dumping syndrome; postprandial hyperglycaemia;  
 KM type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
 KM Gila monster venom.

OS Synthetic.

FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "amidated"

PN WO9805351-A1.

PD 12-FEB-1998.

PF 08-AUG-1997; 97WO-US014199.

PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX WPI; 1998-145351/13.

DR  
 XX  
 PT Regulating gastrointestinal motility using exendins or their agonists -  
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
 PT glucose tolerance etc., also in diagnostic investigations.

PS Example 25, Fig 8, 70pp; English.

XX The present sequence is an exendin agonist, which reduces gastric  
 CC motility and delays gastric emptying. It can be used to treat spasm  
 CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to  
 CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Exendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of  
 CC hyperglycaemia

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XX SQ Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10
   :|::|
   8 LFLFPPPP 17

DB

RESULT 15
AAM47577
ID AAM47577 standard; peptide; 18 AA.
AC AAM47577;
DT 03-JUL-1998 (first entry)
DE Extendin agonist (28).
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
KW postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
KW Gila monster venom.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 14
FT /label= Hyp
FT Modified-site 15
FT /label= Hyp
FT Modified-site 16
FT /label= Hyp
FT Modified-site 17
FT /label= Hyp
FT Modified-site 18
FT /note= "amidated"
XX WO9805351-A1.
XX 12-FEB-1998.
XX 08-AUG-1997; 97WO-US014199.
XX 08-AUG-1996; 96US-00694954.
XX (AMYL-) AMYLIN PHARM INC.
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
XX for treating spasm, diabetic postprandial hyperglycaemia, impaired
XX glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 31; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Extendins,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been

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CC suggested (US5424286) for treatment of diabetes and prevention of
XX hyperglycaemia
XX SQ Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10
   :|::|
   8 LFLFPPPP 17

DB

RESULT 16
AAM47550
ID AAM47550 standard; peptide; 18 AA.
AC AAM47550;
DT 03-JUL-1998 (first entry)
DE Extendin agonist (1).
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
KW postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
KW Gila monster venom.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "amidated"
XX WO9805351-A1.
XX 12-FEB-1998.
XX 08-AUG-1997; 97WO-US014199.
XX 08-AUG-1996; 96US-00694954.
XX (AMYL-) AMYLIN PHARM INC.
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
XX for treating spasm, diabetic postprandial hyperglycaemia, impaired
XX glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 4; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the biliary
XX tract or sphincter of Oddi), postprandial dumping syndrome and
XX hyperglycaemia (particularly associated with type 2 diabetes), type 1
XX diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
XX is administered to prevent stomach contents passing into the intestines,
XX then the stomach pumped) and obesity. It can also be administered to
XX subjects undergoing gastrointestinal diagnostic investigation,
XX particularly radiological or by magnetic resonance imaging. Extendins,
XX components of Gila monster venom, have some sequence similarity to
XX glucagon-like peptides (GLP). They are GLP agonists and have been
XX suggested (US5424286) for treatment of diabetes and prevention of
XX hyperglycaemia
XX Sequence 18 AA;
Query Match 46.9%; Score 38; DB 2; Length 18;

```

Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10  
:|::|  
Db 8 LLFIEPPPP 17

## RESULT 17

AAV03738  
ID AAV03738 standard; peptide; 18 AA.

AC AAY03738;

DT 08-JUN-1999 (first entry)

DE Extendin agonist compound 18.

KW Extendin; agonist; diabetes; disorder; plasma glucose; gastric;  
diagnostic; gastro-intestinal; radiological.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 18  
/note= "C-terminal amide"

PN WO9907404-A1.

PD 18-FEB-1999.

PF 06-AUG-1998; 98WO-US016387.

PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.

PI Beley NRA, Prickett KS;

DR WPI; 1999-180403/15.

PT New extendin agonists - useful in the treatment of Type I and II diabetes.

PS Claim 17; Fig 1D-E; 70pp; English.

XX The invention relates to extendin agonists which slow gastric emptying and  
XX lower plasma glucose levels. The extendin agonists are used to treat Type  
XX I and II diabetes, disorders which would be benefited by agents which  
XX lower plasma glucose levels, and disorders which would be benefited by  
XX agents useful in delaying and/or slowing gastric emptying. Delayed  
XX gastric emptying is a useful diagnostic aid in gastro-intestinal  
XX radiological examinations. Sequences AAV03721-51 represent specifically  
XX claimed examples of the extendin agonist compounds of the invention. (Also  
XX see AAV03720 for extendin generic peptide formula and description)

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10  
:|::|  
Db 8 LLFIEPPPP 17

## RESULT 18

AAV03721  
ID AAV03721 standard; peptide; 18 AA.

AC AAY03721;

DT 08-JUN-1999 (first entry)

XX Extendin agonist compound 1.

DE Extendin; agonist; diabetes; disorder; plasma glucose; gastric;  
diagnostic; gastro-intestinal; radiological.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 18  
/note= "C-terminal amide"

PN WO9907404-A1.

PD 18-FEB-1999.

PF 06-AUG-1998; 98WO-US016387.

PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.

PI Beley NRA, Prickett KS;

DR WPI; 1999-180403/15.

PT New extendin agonists - useful in the treatment of Type I and II diabetes.

PS Claim 17; Fig 1A-B; 70pp; English.

XX The invention relates to extendin agonists which slow gastric emptying and  
XX lower plasma glucose levels. The extendin agonists are used to treat Type  
XX I and II diabetes, disorders which would be benefited by agents which  
XX lower plasma glucose levels, and disorders which would be benefited by  
XX agents useful in delaying and/or slowing gastric emptying. Delayed  
XX gastric emptying is a useful diagnostic aid in gastro-intestinal  
XX radiological examinations. Sequences AAV03721-51 represent specifically  
XX claimed examples of the extendin agonist compounds of the invention. (Also  
XX see AAV03720 for extendin generic peptide formula and description)

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKPPPP 10  
:|::|  
Db 8 LLFIEPPPP 17

## RESULT 19

AAV03720

ID AAV03720 standard; peptide; 18 AA.

AC AAB52880;

DT 28-FEB-2001 (first entry)

DE Extendin agonist compound #8.

KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
insulin-resistance syndrome; food intake.

OS Heloderma sp.

PN WO20006629-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US011814.

PR 30-APR-1999; 99US-0132018P.

XX (AMYL-) AMYLIN PHARM INC.  
PA Young A, Prickett K;  
PI WPI, 2000-672834/65.  
XX  
XX Modified extendin or an extendin agonist linked to one or more polyethylene  
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
PT treating disorders such as diabetes and obesity.  
XX  
XX Disclosure; Fig 3; 119pp; English.  
XX  
XX The present invention relates to extendins and their agonists which have  
CC been modified with molecular weight increasing agents such as  
CC polyethylene glycol (PEG). These can be used in the treatment of  
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
XX  
SQ Sequence 18 AA;  
Query Match 46.9%; Score 38; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VLEMKFPPPP 10  
:|::|  
Db 8 LLFVFPPPP 17  
RESULT 20  
AAB52886  
ID AAB52886 standard; peptide; 18 AA.  
XX  
XX AAB52886;  
XX  
XX 28-FEB-2001 (first entry)  
XX  
XX Extendin agonist compound #14.  
XX  
XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
XX insulin-resistance syndrome; food intake.  
XX  
XX Heloderma sp.  
XX  
XX WO200066629-A1.  
XX  
XX 09-NOV-2000.  
XX  
XX 28-APR-2000; 2000WO-US011814.  
XX  
XX 30-APR-1999; 99US-0132018P.  
XX  
XX (AMYL-) AMYLIN PHARM INC.  
XX  
XX Young A, Prickett K;  
XX  
XX WPI; 2000-672834/65.  
XX  
XX Modified extendin or an extendin agonist linked to one or more polyethylene  
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
PT treating disorders such as diabetes and obesity.  
XX  
XX Disclosure; Fig 3; 119pp; English.  
XX  
XX The present invention relates to extendins and their agonists which have  
CC been modified with molecular weight increasing agents such as  
CC polyethylene glycol (PEG). These can be used in the treatment of  
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
XX

SQ Sequence 18 AA;  
Query Match 46.9%; Score 38; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VLEMKFPPPP 10  
:|::|  
Db 8 LLFVFPPPP 17  
RESULT 21  
AAB52876  
ID AAB52876 standard; peptide; 18 AA.  
XX  
XX AAB52876;  
XX  
XX 28-FEB-2001 (first entry)  
XX  
XX Extendin agonist compound #4.  
XX  
XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
XX insulin-resistance syndrome; food intake.  
XX  
XX Heloderma sp.  
XX  
XX WO200066629-A1.  
XX  
XX 09-NOV-2000.  
XX  
XX 28-APR-2000; 2000WO-US011814.  
XX  
XX 30-APR-1999; 99US-0132018P.  
XX  
XX (AMYL-) AMYLIN PHARM INC.  
XX  
XX Young A, Prickett K;  
XX  
XX WPI; 2000-672834/65.  
XX  
XX Modified extendin or an extendin agonist linked to one or more polyethylene  
PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
PT treating disorders such as diabetes and obesity.  
XX  
XX Disclosure; Fig 3; 119pp; English.  
XX  
XX The present invention relates to extendins and their agonists which have  
CC been modified with molecular weight increasing agents such as  
CC polyethylene glycol (PEG). These can be used in the treatment of  
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
XX  
SQ Sequence 18 AA;  
Query Match 46.9%; Score 38; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VLEMKFPPPP 10  
:|::|  
Db 8 LLFVFPPPP 17  
RESULT 22  
AAB52885  
ID AAB52885 standard; peptide; 18 AA.  
XX  
XX AAB52885;  
XX  
XX 28-FEB-2001 (first entry)  
XX  
XX Extendin agonist compound #13.  
XX

XX Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
 KW insulin-resistance syndrome; food intake.  
 XX  
 OS Heloderma sp.  
 XX  
 PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified extendin or an extendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 11pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;  
 XX  
 Query Match 46.9%; Score 38; DB 3; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VLEMKFPPT 10  
 : : : : :  
 Db 8 LRFIFPPPP 17

RESULT 23  
 ABG72860  
 ID ABG72860 standard; peptide; 15 AA.  
 XX  
 AC ABG72860;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Human ribosomal protein 17.05 N-terminal.  
 XX  
 KW Human; ribosomal protein 17.05; malignant tumour; haemopathy;  
 KW human immunodeficiency virus; HIV; immunological disease; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1352106-A.  
 XX  
 PD 05-JUN-2002.  
 XX  
 PF 06-NOV-2000; 2000CN-00127235.  
 XX  
 PR 06-NOV-2000; 2000CN-00127235.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-683308/74.  
 XX

PT New human ribosomal protein 17.05 polypeptide for treating malignant  
 PT tumors, hemopathy, human immunodeficiency virus infection, immunological  
 PT diseases and various inflammations.  
 XX  
 PS Example 5; Page 18 (Disclosure); 33pp; Chinese.  
 XX  
 CC The present invention discloses a new kind of polypeptide, human  
 CC ribosomal protein 17.05, polynucleotides encoding the polypeptide and a  
 CC DNA recombination process to produce the polypeptide. The present  
 CC invention also describes applying the polypeptide in treating various  
 CC diseases, such as malignant tumours, haemopathy, human immunodeficiency  
 CC virus (HIV) infection, immunological diseases and various inflammations.  
 CC Also discloses is the antagonist resisting the polypeptide and its  
 CC treatment effect, and the application of the polynucleotides encoding  
 CC human ribosomal protein 17.05. This is the amino acid sequence of the  
 CC novel human ribosomal protein 17.05 N-terminal  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 45.7%; Score 37; DB 5; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 MKPPPPQETV 14  
 : : : : :  
 Db 3 VSFPPPPKQGV 13

RESULT 24  
 AAM05469  
 ID AAM05469 standard; peptide; 18 AA.  
 XX  
 AC AAM05469;  
 XX  
 DT 24-FEB-1998 (first entry)  
 XX  
 DE SH3-binding peptide bSH3020.  
 XX  
 KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
 KW cellular signalling element; cellular structural element; malignancy;  
 KW protein identification; functional domain; protein screening;  
 KW cellular signal transduction process; binding peptide.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9631625-A1.  
 XX  
 PD 10-OCT-1996.  
 XX  
 PF 04-APR-1996; 96WO-US004454.  
 XX  
 PR 07-APR-1995; 95US-00417872.  
 XX  
 PR 03-APR-1996; 96US-00630915.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 XX  
 PI (UNNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;  
 XX  
 DR WPI; 1996-465045/46.  
 XX  
 PT Identifying polypeptide(s) having specific functional domain (esp. SH3  
 PT domain) - comprises detecting selective binding to recognition unit,  
 PT regardless of sequence homology.  
 XX  
 PS Example; Fig 12B; 174pp; English.  
 XX  
 CC AAM05445-W05492 represent Src-homology region 3 (SH2) domain binding  
 CC peptides. These sequences were used as pairs of multivalent recognition  
 CC unit complexes used in the method of the invention. The method of the  
 CC invention is for identifying polypeptides containing functional domains  
 CC of interest (especially SH3 domains). It comprises contacting a  
 CC multivalent recognition unit (RU) complex with a number of peptides and

CC identifying polypeptides having a selective binding affinity for the RU  
 CC complex. The method is based on functional similarities and does not rely  
 CC on sequence similarities. Prior methods only gave limited success for  
 CC identifying proteins containing an SH3 domain due to the minimal sequence  
 CC homology among known SH3 proteins. Multivalent RU complexes are  
 CC particularly suited to screening for polypeptides containing functional  
 CC domains that are similar to, but not identical in sequence to, the  
 CC original target functional domain. The new method enables proteins having  
 CC a common function to be identified. Identification of novel SH3 proteins  
 CC will be useful for a better understanding of cell growth, malignancy,  
 CC signal transduction processes, etc. New candidate drugs can be  
 CC identified, and their specificities (e.g. pharmacological activities) can  
 CC be assessed using the method of the invention

XX SQ Sequence 18 AA:

QY Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 3 EMKPPPPPOE 12  
 7 EPDPFPPPPD 16

RESULT 25  
 AAW37677  
 ID AAW37677 standard; peptide; 18 AA.  
 AC AAW37677;  
 DT 23-APR-1998 (first entry)  
 DE PPPY motif containing peptide bSH3020 used to bind WW domains.  
 XX Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KM cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction; YAP protein; dystrophin.  
 XX  
 OS Synthetic.  
 XX WO9737223-A1.  
 PN 09-OCT-1997.  
 PD 03-APR-1997; 97WO-US005547.  
 PF 03-APR-1997; 97WO-US005547.  
 PR 03-APR-1996; 96US-00630916.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UNNC-) UNIV NORTH CAROLINA.  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 DR WPI; 1997-503234/46.  
 XX  
 PT Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are useful  
 PT in targeted drug selection.  
 XX  
 PS Example 6.3; Fig 7; 220pp; English.  
 CC Peptides AAW37653-77 contain PPPY-like motifs. The PPPY motif is found  
 CC in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
 CC containing this residue have been shown to bind the YAP WW domain, but  
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
 CC AAW37653-77 were biotinylated and complexed with alkaline streptavidin,  
 CC and used in a cross affinity mapping experiment. They were tested for  
 CC their ability to bind to the 12 individual novel WW domains of WWP1  
 CC (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which  
 CC were expressed as glutathione-S-transferase expression proteins. The  
 CC present peptide, derived from a vinculin protein, does not bind to WW  
 CC domains of the novel proteins. The WW domain is a small functional

CC domain. Its name is derived from the observation that two tryptophan  
 CC residues, one in the amino terminal portion of the WW domain and one in  
 CC the carboxyl terminal portion, are conserved. Most proteins containing WW  
 CC domains have a function involving cell signalling and growth regulation  
 CC or the organisation of the cytoskeleton. Polypeptides containing a WW  
 CC domain are identified by treating a multivalent recognition unit complex  
 CC that has selective binding affinity for a WW domain, with many  
 CC polypeptides and identifying those with selective affinity for the  
 CC complex. Proteins containing WW domains are used for targeted drug  
 CC screening, i.e. to identify potential modulators of specific WW domain  
 CC interactions

XX SQ Sequence 18 AA:

QY Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 3 EMKPPPPPOE 12  
 7 EPDPFPPPPD 16

RESULT 26  
 AAW38909  
 ID AAW38909 standard; peptide; 18 AA.  
 AC AAW38909;  
 DT 27-MAR-1998 (first entry)  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.  
 XX  
 DE Peptide resembling an SH3 domain binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;  
 KW PLCgamma; p53bp2; Ctk; Yes; Grb2.  
 XX  
 OS Synthetic.  
 XX WO9730074-A1.  
 PN 21-AUG-1997.  
 PD 14-FEB-1997; 97WO-US002298.  
 PF 14-FEB-1997; 97WO-US002298.  
 PR 16-FEB-1996; 96US-00602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UNNC-) UNIV NORTH CAROLINA.  
 PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;  
 PI Rider JB;  
 DR WPI; 1997-424972/39.  
 XX  
 PT Src homology region 3 binding peptide - used to activate Src tyrosine  
 PT kinase(s) and to stimulate immune response by increasing production of  
 PT certain lymphokine(s), e.g. interleukin-1.  
 XX  
 PS Claim 22; Page 90; 131pp; English.  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
 CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Ctk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
 CC can be used in the method to identify inhibitors of their binding to  
 CC their respective SH3 domains, which could be used to modulate the  
 CC pharmacological activity of proteins or polypeptide containing the SH3

CC domain. The peptides can also be used to activate Src or Src-related  
 CC protein tyrosine kinases, to stimulate the immune response by increasing  
 CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
 CC and interleukin-1, or to deliver a conjugated molecule to certain  
 CC cellular compartments containing Src or Src related proteins  
 CC  
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PPPPEQETV 14  
 ||||| : :  
 Db 7 PPPPEYQPI 15

RESULT 27  
 AAM47562  
 ID AAM47562 standard; peptide; 18 AA.  
 XX

AC AAM47562;

DT 03-JUN-1998 (first entry)

XX Extendin agonist (13).

DE Extendin agonist; gastric motility; gastric emptying; treatment; spasm;  
 KW postprandial dumping syndrome; postprandial hyperglycaemia;  
 KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
 KW Gila monster venom.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 8 /note= "pentylglycine"

FT Modified-site 18 /note= "amidated"

FT WO9805351-A1.

PD 12-FEB-1998.

PR 08-AUG-1997; 97MO-US014199.

PR 08-AUG-1996; 96US-00694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

DR WPI; 1998-145351/13.

XX Regulating gastrointestinal motility using extendins or their agonists -  
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
 PT glucose tolerance etc., also in diagnostic investigations.

XX Example 16; Fig 8; 70pp; English.

XX The present sequence is an extendin agonist, which reduces gastric  
 CC motility and delays gastric emptying. It can be used to treat spasm  
 CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to  
 CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Extendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of

CC hyperglycaemia  
 XX  
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKEPPPP 10  
 | : |||||  
 Db 9 LFIEPPPP 17

RESULT 28  
 AAY03733  
 ID AAY03733 standard; peptide; 18 AA.  
 XX

AC AAY03733;

DT 08-JUN-1999 (first entry)

XX Extendin agonist compound 13.

DE Extendin agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 8 /note= "pentylglycine"

FT Modified-site 18 /note= "C-terminal amide"

FT WO9907404-A1.

PD 18-FEB-1999.

PR 06-AUG-1998; 98MO-US016387.

PR 08-AUG-1997; 97US-0055404P.

PA (AMYL-) AMYLIN PHARM INC.

PI Beeley NRA, Prickett KS;

DR WPI; 1999-180403/15.

XX New extendin agonists - useful in the treatment of Type I and II diabetes.  
 PT Claim 17; Fig 1A-B; 70pp; English.

XX The invention relates to extendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The extendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the extendin agonist compounds of the invention. (Also  
 CC see AAY03720 for extendin generic peptide formula and description)

XX Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKEPPPP 10  
 | : |||||  
 Db 9 LFIEPPPP 17

```

RESULT 29
ADB49303
ID ADB49303 standard; peptide; 18 AA.
XX
XX ADB49303;
AC
XX 04-DEC-2003 (first entry)
DT
XX
XX Novel WW domain binding peptide #25.
DE
XX
XX MW domain; drug candidate screening; drug discovery; drug modification;
KM drug refinement; immunogen; WW binding protein; WW domain.
XX
XX Unidentified.
OS
XX
XX US200307577-A1.
PN
XX
XX 24-APR-2003.
PD
XX
XX 28-JUN-2002; 2002US-00185050.
PF
XX
XX 03-APR-1996; 96US-00630916.
PR
XX 03-APR-1997; 97US-00826516.
XX
XX (PIRO/) PIROZZI G.
PA (KAYB/) KAY B K.
PA (FOWL/) FOWLKES D M.
XX
XX Pirozzi G, Kay BK, Fowlkes DM;
PI
XX
XX WPI; 2003-635075/60.
DR
XX
XX Novel purified polypeptide comprising WW domain, useful for drug
PT discovery, modification and refinement, for discovering polypeptides
PT involved in pharmacological activities, or as an immunogen to generate
XX antibodies.
XX
XX Example; Fig 7; 133pp; English.
XX
XX The invention describes a purified polypeptide (I) comprising a WW domain
CC which has a sequence (S1) selected from 11 sequences fully defined in the
CC specification, a sequence (S2) selected from 48 sequences fully defined
CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725
CC amino acids fully defined in the specification. (I) is useful for
CC screening a potential drug candidate, by allowing (I) to come into
CC contact with at least one recognition unit having a selective affinity
CC for the WW domain in (I), in the presence of an amount of a potential
CC drug candidate, such that (I) and the recognition unit are capable of
CC interacting when brought into contact with one another in the absence of
CC the drug candidate, and determining the effect, if any, of the presence
CC of the amount of the drug candidate on the interaction of (I) with the
CC recognition unit. (I) is useful for drug discovery, modification and
CC refinement, for discovering polypeptides involved in pharmacological
CC activities, or as an immunogen to generate antibodies. This is the amino
CC acid sequence of a peptide that binds the novel WW domains of the
CC invention
XX
XX
XX Sequence 18 AA:
SQ
XX
XX Query Match 45.7%; Score 37; DB 7; Length 18;
XX Best Local Similarity 60.0%; Pred. No. 1.8e+02;
XX Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 EMKPPPPPOE 12
DB 7 EPPPPPPPPD 16

```

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XX
XX 31-JAN-1991 (first entry)
DT
XX
XX Smooth muscle myosin-2 immunogen for antibody prodn.
XX
XX DE
XX Smooth muscle myosin isoform 2; monoclonal antibody; immunogen;
XX diagnosis; arteriosclerosis.
XX
XX KM
XX Homo sapiens.
XX
XX OS
XX
XX WO9011520-A.
PN
XX
XX 04-OCT-1990.
PD
XX
XX 28-MAR-1989; 89JP-00075884.
PF
XX
XX 28-MAR-1989; 89JP-00075884.
PR
XX 28-MAR-1989; 89JP-00075884.
XX
XX (YAMS ) YAMASA SHOYU KK.
PA
XX
XX Nagai R, Kuroo M, Kato H;
PI
XX
XX WPI; 1990-320366/42.
DR
XX
XX Antibody against heavy chain of smooth muscle myosin - as reagent for
PT histological staining of smooth muscle or diagnosis of blood vessel
PT disorders.
XX
XX Claim 7; Page 42; 61pp; Japanese.
XX
XX The oligopeptide is used as immunogen for the prodn. of monoclonal
CC antibodies recognising isoform SM-2 of the heavy chain of smooth muscle
CC myosin, pref. from heart or skeletal muscle, esp. human. The peptide
CC contains the part which differs between isoforms SM1-3. The antibodies
CC may be obtained by immunisation with the immunogen, followed by cell
CC fusion to produce a hybridoma, cloning and culturing the chosen hybridoma
CC clone. The Ab is a reagent for the histological staining of smooth
CC muscle, and is useful in the diagnosis of arteriosclerosis, blood vessel
CC disorders etc. See also AAR07283-5
XX
XX
XX Sequence 10 AA:
SQ
XX
XX Query Match 44.4%; Score 36; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 PPOEET 13
DB 3 PPOEET 8

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RESULT 30
AAR07284
ID AAR07284 standard; protein; 10 AA.
XX
XX AAR07284;
AC

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RESULT 31
AAG79174
ID AAG79174 standard; peptide; 14 AA.
XX
XX AAG79174;
AC
XX
XX 03-JAN-2002 (first entry)
DT
XX
XX Peptide derived from ActA, and containing EVH1-binding site.
XX
XX ActA; Fyb/SlAP protein; EVH1 domain; cytoskeletal rearrangement;
XX enabled/vasodilator-stimulated phosphoprotein protein; T cell;
XX T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
XX infectious disease; cancer; autoimmune disease; inflammation;
XX platelet aggregation; wound healing; clotting.
XX
XX Listeria monocytogenes.
XX
XX OS
XX
XX WO200174858-A2.
PN
XX
XX 11-OCT-2001.
PD
XX

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PF 03-APR-2001; 2001WO-US010753.
XX
XX 03-APR-2000; 2000US-0194215P.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
XX Krause M, Sechi AS, Gertler FB, Wehland J;
XX WPI; 2001-616686/71.
XX
XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX activation for treating cancer, autoimmune disease, and infectious
XX disease, comprises contacting with a Fyb/SLAP complex modulator.
XX
XX Example 5; Page 43; 79pp; English.
XX
XX The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
XX ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated
XX phosphoprotein (VASP) proteins. The specification describes a method for
XX modulating cytoskeletal rearrangement in a cell, or T cell response to T
XX cell receptor stimulation. The method comprises contacting the cell or T
XX cell with a Fyb/SLAP complex modulator sufficient to modulate the
XX formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The
XX method is useful for modulating cytoskeletal rearrangement in a cell such
XX as a lymphocyte, preferably a T cell, a macrophage or a cell fragment
XX such as a platelet and for modulating T cell response to a T cell
XX receptor stimulation. T cell response is increased in a subject having or
XX at risk of developing infectious disease or cancer and T cell response is
XX inhibited in a subject having or is at risk of developing an autoimmune
XX disease or a condition characterized by inflammation. A composition
XX comprising a Fyb/SLAP complex inhibitor is useful for increasing platelet
XX aggregation for promoting wound healing or clotting. The present sequence
XX represents a peptide derived from Acta, which is used in the course of
XX the invention
XX
XX Sequence 14 AA;
XX
XX Query Match 44.4%; Score 36; DB 4; Length 14;
XX Best Local Similarity 62.5%; Pred. No. 1.9e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 KPPPPQQR 12
XX :|||||:
XX 2 EPPPPPTD 9
XX
XX Db
XX
XX RESULT 32
XX AAG79166
XX ID AAG79166 standard; peptide; 15 AA.
XX AC AAG79166;
XX
XX DT 03-JAN-2002 (first entry)
XX
XX DE Synthetic antigenic peptide derived from Acta.
XX
XX KW Acta; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
XX enabled/vasodilator-stimulated phosphoprotein protein; T cell;
XX T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
XX infectious disease; cancer; autoimmune disease; inflammation;
XX platelet aggregation; wound healing; clotting.
XX
XX OS Synthetic.
XX OS Liberia monocytogenes.
XX
XX PN WO200174858-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 03-APR-2001; 2001WO-US010753.
XX
XX PR 03-APR-2000; 2000US-0194215P.
XX

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```

XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
XX Krause M, Sechi AS, Gertler FB, Wehland J;
XX WPI; 2001-616686/71.
XX
XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX activation for treating cancer, autoimmune disease, and infectious
XX disease, comprises contacting with a Fyb/SLAP complex modulator.
XX
XX Example 1; Page 36; 79pp; English.
XX
XX The present sequence represents an antigenic peptide derived from Acta.
XX polyclonal antibodies raised against this peptide were used to screen
XX mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP
XX proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-
XX stimulated phosphoprotein (VASP) proteins. The specification describes a
XX method for modulating cytoskeletal rearrangement in a cell, or T cell
XX response to T cell receptor stimulation. The method comprises contacting
XX the cell or T cell with a Fyb/SLAP complex modulator sufficient to
XX modulate the formation of a complex of an Ena/VASP protein and a Fyb/SLAP
XX protein. The method is useful for modulating cytoskeletal rearrangement
XX in a cell such as a lymphocyte, preferably a T cell, a macrophage or a
XX cell fragment such as a platelet and for modulating T cell response to a
XX T cell receptor stimulation. T cell response is increased in a subject
XX having or at risk of developing infectious disease or cancer and T cell
XX response is inhibited in a subject having or is at risk of developing an
XX autoimmune disease or a condition characterized by inflammation. A
XX composition comprising a Fyb/SLAP complex inhibitor is useful for
XX increasing platelet aggregation for promoting wound healing or clotting
XX
XX Sequence 15 AA;
XX
XX Query Match 44.4%; Score 36; DB 4; Length 15;
XX Best Local Similarity 62.5%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 KPPPPQQR 12
XX :|||||:
XX Db 3 EPPPPPTD 10
XX
XX RESULT 33
XX AAW47569
XX ID AAW47569 standard; peptide; 18 AA.
XX AC AAW47569;
XX
XX DT 03-JUL-1998 (first entry)
XX
XX DB Exendin agonist (20).
XX
XX KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT Modified-site 18 /note= "tert-butylglycine"
XX FT /note= "amidated"
XX
XX PN WO9805351-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 08-AUG-1997; 97WO-US014199.
XX
XX

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PR 08-AUG-1996; 96US-00694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
XX
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
PT glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 23; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
CC motility and delays gastric emptying. It can be used to treat spasm
CC (where associated with acute diverticulitis or disorders of the biliary
CC tract or sphincter of Oddi), postprandial dumping syndrome and
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1
CC diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
CC is administered to prevent stomach contents passing into the intestines,
CC then the stomach pumped) and obesity. It can also be administered to
CC subjects undergoing gastrointestinal diagnostic investigation,
CC particularly radiological or by magnetic resonance imaging. Extendins,
CC components of Gila monster venom, have some sequence similarity to
CC glucagon-like peptides (GLP). They are GLP agonists and have been
CC suggested (US5424286) for treatment of diabetes and prevention of
CC hyperglycaemia
XX
XX Sequence 18 AA;
SQ
Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLEMKRPPPP 10
: |||||
DB 8 LIFXEPPPP 17

RESULT 34
AAW47552
ID AAW47552 standard; peptide; 18 AA.
XX
XX AAW47552;
AC
XX
XX 03-JUL-1998 (first entry)
DT
XX
XX Extendin agonist (3).
DE
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 18 /note="amidated"
FT
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US014199.
XX
XX 08-AUG-1996; 96US-00694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
PI
XX

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DR WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired
PT glucose tolerance etc., also in diagnostic investigations.
XX
XX Example 6; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
CC motility and delays gastric emptying. It can be used to treat spasm
CC (where associated with acute diverticulitis or disorders of the biliary
CC tract or sphincter of Oddi), postprandial dumping syndrome and
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1
CC diabetes, impaired glucose tolerance, toxin ingestion (an extendin agonist
CC is administered to prevent stomach contents passing into the intestines,
CC then the stomach pumped) and obesity. It can also be administered to
CC subjects undergoing gastrointestinal diagnostic investigation,
CC particularly radiological or by magnetic resonance imaging. Extendins,
CC components of Gila monster venom, have some sequence similarity to
CC glucagon-like peptides (GLP). They are GLP agonists and have been
CC suggested (US5424286) for treatment of diabetes and prevention of
CC hyperglycaemia
XX
XX Sequence 18 AA;
SQ
Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKRPPPP 10
: |||||
DB 11 IEPPPP 17

RESULT 35
AAW47564
ID AAW47564 standard; peptide; 18 AA.
XX
XX AAW47564;
AC
XX
XX 03-JUL-1998 (first entry)
DT
XX
XX Extendin agonist (15).
DE
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment; spasm;
XX postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;
XX Gila monster venom.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 9 /note="pentylglycine"
FT Modified-site 18 /note="amidated"
FT
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US014199.
XX
XX 08-AUG-1996; 96US-00694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Young AA, Gedulin B, Beeley NRA, Prickett KS;
PI
XX
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their agonists -
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired

```



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RESULT 38
AA03742
ID AAY03742 standard; peptide; 18 AA.
XX
AC AAY03742;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extendin agonist compound 22.
XX
KM Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
XX diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 18
FT /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US016387.
XX
PR 08-AUG-1997; 97US-0055404P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extendin agonists - useful in the treatment of Type I and II diabetes.
XX
PS Claim 17; Fig 1D-E; 70pp; English.
XX
CC The invention relates to extendin agonists which slow gastric emptying and
CC lower plasma glucose levels. The extendin agonists are used to treat Type
CC I and II diabetes, disorders which would be benefited by agents which
CC lower plasma glucose levels, and disorders which would be benefited by
CC agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extendin agonist compounds of the invention. (Also
CC see AAY03720 for extendin generic peptide formula and description)
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKPPPP 10
DB 11 IFFPPPP 17

RESULT 39
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ID AAY03735 standard; peptide; 18 AA.
XX
AC AAY03735;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extendin agonist compound 15.
XX
KM Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
XX diagnostic; gastro-intestinal; radiological.
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OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "pentyglycine"
FT Modified-site 18
FT /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US016387.
XX
PR 08-AUG-1997; 97US-0055404P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extendin agonists - useful in the treatment of Type I and II diabetes.
XX
PS Claim 17; Fig 1D-E; 70pp; English.
XX
CC The invention relates to extendin agonists which slow gastric emptying and
CC lower plasma glucose levels. The extendin agonists are used to treat Type
CC I and II diabetes, disorders which would be benefited by agents which
CC lower plasma glucose levels, and disorders which would be benefited by
CC agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extendin agonist compounds of the invention. (Also
CC see AAY03720 for extendin generic peptide formula and description)
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKPPPP 10
DB 11 IFFPPPP 17

RESULT 40
AAB52878
ID AAB52878 standard; peptide; 18 AA.
XX
AC AAB52878;
XX
DT 28-FEB-2001 (first entry)
XX
DE Extendin agonist compound #6.
XX
KM Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;
XX insulin-resistance syndrome; food intake.
XX
OS Heloderma sp.
XX
PN WO20006629-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011814.
XX
PR 30-APR-1999; 99US-0132018P.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Young A, Prickett K;

```

XX WPI: 2000-672834/65.

DR Modified extendin or an extendin agonist linked to one or more polyethylene  
XX glycol (PEG) polymers, modulate plasma glucose levels, useful for  
PT treating disorders such as diabetes and obesity.  
PT  
XX

PS Disclosure; Fig 3; 119pp; English.  
XX

CC The present invention relates to extendins and their agonists which have  
CC been modified with molecular weight increasing agents such as  
CC polyethylene glycol (PEG). These can be used in the treatment of  
CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
XX

SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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: |||||  
Db 8 LLFKEFPPPP 17

Search completed: June 7, 2005, 23:10:56  
Job time : 83.7273 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 22:57:32 ; Search time 20.4545 Seconds  
(without alignments)  
54.743 Million cell updates/sec

Title: US-10-691-157-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 183464

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Listing first 100 summaries

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5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	37	45.7	18	3	US-08-602-999A-305
4	37	45.7	18	3	US-08-630-915A-165
5	37	45.7	18	4	US-09-500-124-305
6	37	45.7	18	4	US-09-879-957-165
7	35	43.2	10	2	US-08-968-676-19
8	35	43.2	10	2	US-09-823-240A-1
9	35	43.2	12	4	US-09-261-894A-19
10	35	43.2	12	4	US-08-968-676-161
11	35	43.2	12	4	US-09-261-894A-161
12	35	43.2	13	3	US-08-630-916A-7
13	35	43.2	15	3	US-08-602-999A-349
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15	35	43.2	15	4	US-09-500-124-349
16	35	43.2	15	4	US-09-500-124-423
17	35	43.2	15	4	US-09-413-564C-4
18	35	43.2	16	2	US-08-968-676-1
19	35	43.2	16	4	US-09-396-813-1
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21	34	42.0	5	4	US-09-823-240A-3
22	34	42.0	5	4	US-09-377-285B-47
23	34	42.0	6	4	US-09-823-240A-12
24	34	42.0	6	4	US-09-823-240A-14
25	34	42.0	9	2	US-08-968-676-160
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29	34	42.0	10	4	US-09-261-894A-18	Sequence 18, Appl
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32	34	42.0	15	3	US-08-630-916A-55	Sequence 55, Appl
33	34	42.0	15	3	US-08-602-999A-339	Sequence 339, App
34	34	42.0	15	3	US-08-602-999A-405	Sequence 405, App
35	34	42.0	15	4	US-09-500-124-339	Sequence 339, App
36	34	42.0	15	4	US-09-500-124-405	Sequence 405, App
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53	33	40.7	15	3	US-08-602-999A-367	Sequence 367, App
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56	33	40.7	15	4	US-09-500-124-367	Sequence 367, App
57	33	40.7	15	4	US-09-500-124-373	Sequence 373, App
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67	31	38.3	9	4	US-09-295-846B-32	Sequence 32, Appl
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71	31	38.3	10	2	US-08-968-676-162	Sequence 162, App
72	31	38.3	10	4	US-09-261-894A-162	Sequence 162, App
73	31	38.3	11	1	US-08-336-343A-26	Sequence 26, App
74	31	38.3	11	3	US-08-652-877-23	Sequence 23, Appl
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78	31	38.3	12	3	US-09-460-384-25	Sequence 25, Appl
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80	31	38.3	12	4	US-09-428-082B-312	Sequence 312, App
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82	31	38.3	13	3	US-09-460-384-26	Sequence 26, Appl
83	31	38.3	14	3	US-08-630-916A-56	Sequence 56, Appl
84	31	38.3	15	3	US-08-602-999A-298	Sequence 298, App
85	31	38.3	15	3	US-08-602-999A-352	Sequence 352, App
86	31	38.3	15	3	US-08-602-999A-354	Sequence 354, App
87	31	38.3	15	3	US-08-602-999A-377	Sequence 377, App
88	31	38.3	15	4	US-09-500-124-298	Sequence 298, App
89	31	38.3	15	4	US-09-500-124-352	Sequence 352, App
90	31	38.3	15	4	US-09-500-124-354	Sequence 354, App
91	31	38.3	15	4	US-09-500-124-377	Sequence 377, App
92	31	38.3	16	1	US-08-064-400B-1	Sequence 1, Appl
93	31	38.3	16	1	US-08-477-509B-17	Sequence 17, Appl
94	31	38.3	16	2	US-08-844-312-11	Sequence 11, Appl
95	31	38.3	16	2	US-08-844-312-11	Sequence 11, Appl
96	31	38.3	16	3	US-08-630-916A-107	Sequence 107, App
97	31	38.3	16	3	US-08-482-085B-17	Sequence 17, Appl
98	31	38.3	16	3	US-08-602-999A-344	Sequence 344, App
99	31	38.3	16	3	US-08-602-999A-422	Sequence 422, App
100	31	38.3	16	3	US-08-630-915A-163	Sequence 163, App

## ALIGNMENTS

RESULT 1  
US-09-641-803-7  
; Sequence 7, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDGOH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265,00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-7

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4,1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15  
Db 1 VLEMKPPPPQETVT 15

RESULT 2  
US-08-630-916A-109  
; Sequence 109, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-109

Query Match 45.7%; Score 37; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPPQOE 12  
Db 7 EPDPFPPPPD 16

RESULT 3  
US-08-602-999A-305  
; Sequence 305, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: RAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-305

Query Match 45.7%; Score 37; DB 3; Length 18;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FPPPPQETV 14  
Db 7 FPPPPQPI 15



RESULT 4  
US-08-630-915A-165  
; Sequence 165, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELE: 66141 PENNTE  
; INFORMATION FOR SEQ ID NO: 165:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-165

Query Match 45.7%; Score 37; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EKKPPPPQ 12  
| | | | | :  
Db 7 EPPPPPPPD 16

RESULT 5  
US-09-500-124-305  
; Sequence 305, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OULILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELE: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 305:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-305

Query Match 45.7%; Score 37; DB 4; Length 18;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PPPPQETV 14  
| | | | | :  
Db 7 PPPPPYQPI 15

RESULT 6  
US-09-879-957-165  
; Sequence 165, Application US/09879957  
; Patent No. 6709821  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6709821h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,957  
; FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 165:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 165:  
US-09-879-957-165

Query Match 45.7%; Score 37; DB 4; Length 18;  
Best Local Similarity 60.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPPPOE 12  
| | | | |  
DB 7 EPDPPPPPPD 16

RESULT 7  
US-08-968-676-19  
Sequence 19, Application US/08968676  
Patent No. 5919639  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-19

Query Match 43.2%; Score 35; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
| | | | |  
DB 1 LMKLPKPPK 10

RESULT 8  
US-09-823-240A-1  
Sequence 1, Application US/09823240A  
Patent No. 6716597  
GENERAL INFORMATION:  
APPLICANT: Frank B. Gertler  
APPLICANT: James E. Bear  
APPLICANT: Jürgen Weiland  
APPLICANT: Joseph Loureiro  
TITLE OF INVENTION: Methods and Products for Regulating Cell  
FILE REFERENCE: M00656.70064.US  
CURRENT APPLICATION NUMBER: US/09/823,240A  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 60/194,564  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 1  
LENGTH: 10  
TYPE: PRT  
ORGANISM: listeria monocytogenes  
FEATURE:  
NAME/KEY: Misc.feature  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa is Asp or Glu  
NAME/KEY: Misc.feature  
LOCATION: (7)...(7)  
OTHER INFORMATION: Xaa is any amino acid  
US-09-823-240A-1

Query Match 43.2%; Score 35; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPPPPPOE 12  
| | | | |  
DB 2 FPPPPPD 8

RESULT 9  
US-09-261-894A-19  
Sequence 19, Application US/09261894A  
Patent No. 6835382  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT E.  
APPLICANT: ADAMS, SHARLENE  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION  
FILE REFERENCE: REH-2006  
CURRENT APPLICATION NUMBER: US/09/261,894A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 167  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO: 19  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-261-894A-19

Query Match 43.2%; Score 35; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11  
| | | | |  
| | | | |  
Db 1 LMKLPPKPPK 10

RESULT 10  
US-08-968-676-161  
; Sequence 161, Application US/08968676  
; Patent No. 5919639

GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 161:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-161

Query Match 43.2%; Score 35; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11  
| | | | |  
| | | | |  
Db 1 LMKLPPKPPK 10

RESULT 11  
US-09-261-894A-161

; Sequence 161, Application US/09261894A

; Patent No. 6835382

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT E.

APPLICANT: ADAMS, SHARLENE

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION

FILE REFERENCE: REH-2006

CURRENT APPLICATION NUMBER: US/09/261,894A

CURRENT FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 167

SOFTWARE: Patent In Ver. 3.2

SEQ ID NO 161

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-09-261-894A-161

Query Match 43.2%; Score 35; DB 4; Length 12;  
Best Local Similarity 60.0%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPPO 11  
| | | | |  
| | | | |  
Db 1 LMKLPPKPPK 10

RESULT 12  
US-08-630-916A-7  
; Sequence 7, Application US/08630916A  
; Patent No. 6011137

GENERAL INFORMATION:

APPLICANT: Pirozzi, Gregorio

APPLICANT: Kay, Brian K.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,916A

FILING DATE: 03-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MISROCK, S. LESLIE

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-203

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 896-8864/9741

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-630-916A-7

Query Match 43.2%; Score 35; DB 3; Length 13;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PPPPPQ 12  
| | | | |  
| | | | |  
Db 5 YPPPP 11

RESULT 13  
US-09-602-999A-349

```
; Sequence 349, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-349

Query Match          43.2%  Score 35;  DB 3;  Length 15;
Best Local Similarity 54.5%  Pred. No. 35;
Matches 6;  Conservative 2;  Mismatches 3;  Indels 0;  Gaps 0;
```

```
Qy      2 LEMKPPPPQ 12
      | : ||||| :
Db      1 LPSREPPPOK 11
```

```
RESULT 14
US-08-602-999A-423
; Sequence 423, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-423
```

```
Query Match          43.2%  Score 35;  DB 3;  Length 15;
Best Local Similarity 83.3%  Pred. No. 35;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy      7 PPPPP 12
      ||||| :
Db      8 PPPPE 13
```

```
RESULT 15
US-09-500-124-349
; Sequence 349, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
```

REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 349:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-349

Query Match 43.2%; Score 35; DB 4; Length 15;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 12  
| : |||| :  
Db 1 LPSRPPEPPQK 11

RESULT 16  
US-09-500-124-423

Sequence 423, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: OUILIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/500,124

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: MISTOCK, S. Leslie

REGISTRATION NUMBER: 18, 872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 423:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-09-500-124-423

Query Match 43.2%; Score 35; DB 4; Length 15;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 12  
| : |||| :  
Db 8 PPPPE 13

RESULT 17  
US-09-413-564C-4

Sequence 4, Application US/09413564C

Patent No. 6716428

GENERAL INFORMATION:

APPLICANT: The Ohio State University Research Foundation

APPLICANT: Stevens, Vernon

TITLE OF INVENTION: Antigenic modification of polypeptides

FILE REFERENCE: URF 2-056 AVI

CURRENT APPLICATION NUMBER: US/09/413,564C

CURRENT FILING DATE: 2002-08-27

PRIOR APPLICATION NUMBER: 09/413,564

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patent in version 3.0

SEQ ID NO 4

LENGTH: 15

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(15)

US-09-413-564C-4

Query Match 43.2%; Score 35; DB 4; Length 15;  
Best Local Similarity 71.4%; Pred. No. 35;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 13  
| : |||| :  
Db 4 PPPSDT 10

RESULT 18  
US-08-968-676-1

Sequence 1, Application US/08968676

Patent No. 5919639

GENERAL INFORMATION:

APPLICANT: Humphreys, Robert E

APPLICANT: Adams, Sharlene

APPLICANT: Xu, Minzhen

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. Box 999

CITY: York Harbor

STATE: ME

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/968,676

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: REH-9601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-1

Query Match 43.2%; Score 35; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKEPPPPQ 11  
| | | | |  
Db 1 LRMKLKPKPK 10

RESULT 19  
US-09-396-813-1  
; Sequence 1, Application US/09396813  
; Patent No. 6432409  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE  
; FILE REFERENCE: REH2007  
; CURRENT APPLICATION NUMBER: US/09/396,813  
; CURRENT FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-396-813-1

Query Match 43.2%; Score 35; DB 4; Length 16;  
Best Local Similarity 60.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKEPPPPQ 11  
| | | | |  
Db 1 LRMKLKPKPK 10

RESULT 20  
US-09-261-894A-1  
; Sequence 1, Application US/09261894A  
; Patent No. 6835382  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT E.  
; APPLICANT: ADAMS, SHARLENE  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION  
; FILE REFERENCE: REH-2006  
; CURRENT APPLICATION NUMBER: US/09/261,894A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 167  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-261-894A-1

Query Match 43.2%; Score 35; DB 4; Length 16;

Best Local Similarity 60.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKEPPPPQ 11  
| | | | |  
Db 1 LRMKLKPKPK 10

RESULT 21  
US-09-823-240A-3  
; Sequence 3, Application US/09823240A  
; Patent No. 6716597  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Wehlend  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; FILE REFERENCE: M00656.70064.US  
; CURRENT APPLICATION NUMBER: US/09/823,240A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-823-240A-3

Query Match 42.0%; Score 34; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
| | | | |  
Db 1 PPPPP 5

RESULT 22  
US-09-377-285B-47  
; Sequence 47, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1B PROTEIN (AS AMENDED)  
; FILE REFERENCE: JH01580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: optimal ligand

US-09-377-285B-47

Query Match 42.0%; Score 34; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
| | | | |  
Db 1 PPPPP 5

RESULT 23

US-09-823-240A-12  
; Sequence 12, Application US/09823240A  
; Patent No. 6716597  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Weiland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; FILE REFERENCE: M00656.70064.US  
; CURRENT APPLICATION NUMBER: US/09/823,240A  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-823-240A-12

Query Match 42.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
| | | | |  
Db 2 PPPPP 6

RESULT 24

US-09-823-240A-14  
; Sequence 14, Application US/09823240A  
; Patent No. 6716597  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Weiland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; FILE REFERENCE: M00656.70064.US  
; CURRENT APPLICATION NUMBER: US/09/823,240A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR FILING DATE: 60/194,564  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
; FEATURES:  
; NAME/KEY: Misc feature  
; LOCATION: (1)\_(1)  
; OTHER INFORMATION: Xaa is Asp or Glu  
US-09-823-240A-14

Query Match 42.0%; Score 34; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
| | | | |  
Db 2 PPPPP 6

RESULT 25

US-08-968-676-160  
; Sequence 160, Application US/08968676  
; Patent No. 5919639  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,676  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 160:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-968-676-160

Query Match 42.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPP 10  
| | | | |  
Db 1 LRMKLPPKP 9

RESULT 26

US-09-823-240A-7  
; Sequence 7, Application US/09823240A  
; Patent No. 6716597  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Weiland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; FILE REFERENCE: M00656.70064.US  
; CURRENT APPLICATION NUMBER: US/09/823,240A  
; CURRENT FILING DATE: 2001-03-30

;; PRIOR APPLICATION NUMBER: 60/194,564  
;; PRIOR FILING DATE: 2000-04-03  
;; NUMBER OF SEQ ID NOS: 14  
;; SOFTWARE: FASTSEQ for Windows Version 3.0  
;; SEQ ID NO: 7  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: Misc feature  
;; LOCATION: (9)...(9)  
;; OTHER INFORMATION: Xaa is any amino acid  
US-09-823-240A-7

Query Match 42.0%; Score 34; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||  
Db 1 FPPPP 5

RESULT 27  
US-09-261-894A-160  
; Sequence 160, Application US/09261894A  
; Patent No. 6835382  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT E.  
; APPLICANT: ADAMS, SHARLENE  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION  
; FILE REFERENCE: REH-2006  
; CURRENT APPLICATION NUMBER: US/09/261,894A  
; NUMBER OF SEQ ID NOS: 167  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 160  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-261-894A-160

Query Match 42.0%; Score 34; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPP 10  
|||  
Db 1 LEMKLPKPP 9

RESULT 28  
US-08-968-676-18  
; Sequence 18, Application US/08968676  
; Patent No. 5919639  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT E.  
; APPLICANT: ADAMS, SHARLENE  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/968,676  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Farrell, Kevin M  
;; REGISTRATION NUMBER: 35,505  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (207) 363-0558  
;; TELEFAX: (207) 363-0528  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-968-676-18

Query Match 42.0%; Score 34; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPP 10  
|||  
Db 1 LEMKLPKPP 9

RESULT 29  
US-09-261-894A-18  
; Sequence 18, Application US/09261894A  
; Patent No. 6835382  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT E.  
; APPLICANT: ADAMS, SHARLENE  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION  
; FILE REFERENCE: REH-2006  
; CURRENT APPLICATION NUMBER: US/09/261,894A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 167  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-261-894A-18

Query Match 42.0%; Score 34; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPP 10  
|||  
Db 1 LEMKLPKPP 9

RESULT 30  
5252466-18  
; Patent No. 5252466  
; APPLICANT: CRONAN, JOHN E.  
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN  
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND  
; PURIFYING THEM  
; NUMBER OF SEQUENCES: 24



;;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/525,568  
; FILING DATE: 18-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 354,266  
; FILING DATE: 19-MAY-1989  
; SEQ ID NO:18:  
; LENGTH: 10  
5252466-18  
Query Match 42.0%; Score 34; DB 6; Length 10;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 PPPQETV 14  
DB 3 PPPPQTV 10  
RESULT 31  
5252466-18  
; Patent No. 5252466  
; APPLICANT: CROMAN, JOHN E.  
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN  
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND  
; PURIFYING THEM  
; NUMBER OF SEQUENCES: 24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/525,568  
; FILING DATE: 18-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 354,266  
; FILING DATE: 19-MAY-1989  
; SEQ ID NO:18:  
; LENGTH: 10  
5252466-18  
Query Match 42.0%; Score 34; DB 6; Length 10;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 PPPQETV 14  
DB 3 PPPPQTV 10  
RESULT 32  
US-08-630-916A-55  
; Sequence 55, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435

;;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8664/9741  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-55  
Query Match 42.0%; Score 34; DB 3; Length 15;  
Best Local Similarity 75.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 PPPQETV 14  
DB 4 PPPPYTV 11  
RESULT 33  
US-08-602-999A-339  
; Sequence 339, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILTAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 339:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-339  
Query Match 42.0%; Score 34; DB 3; Length 15;

Best Local Similarity 83.3%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPOE 12  
|||||:  
Db 6 PPPPOK 11

RESULT 34  
US-08-602-999A-405

; Sequence 405, Application US/08602999A  
; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie

; REGISTRATION NUMBER: 18, 872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 405:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-602-999A-405

Query Match 42.0%; Score 34; DB 3; Length 15;

Best Local Similarity 85.7%; Pred. No. 49;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPPPQ 11  
|||||:  
Db 4 KPPPPQ 10

RESULT 35  
US-09-500-124-339

; Sequence 339, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie

; REGISTRATION NUMBER: 18, 872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 339:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-09-500-124-339

Query Match 42.0%; Score 34; DB 4; Length 15;

Best Local Similarity 83.3%; Pred. No. 49;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPOE 12  
|||||:  
Db 6 PPPPOK 11

RESULT 36  
US-09-500-124-405

; Sequence 405, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-405

Query Match 42.0%; Score 34; DB 4; Length 15;  
Best Local Similarity 85.7%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPEPPQ 11  
Db 4 KPPEPPQ 10

RESULT 37  
US-08-188-223-7  
Sequence 7, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Sciablenki, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: YES  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..6  
OTHER INFORMATION: /note= "spacer"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 7..16  
OTHER INFORMATION: /note= "immunomimic"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16  
OTHER INFORMATION: /label= GlyNH2  
OTHER INFORMATION: /note= "glycinamide"  
US-08-188-223-7

Query Match 42.0%; Score 34; DB 1; Length 16;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 12  
Db 2 PPPPQ 7

RESULT 38  
US-08-844-312-8  
Sequence 8, Application US/08844312  
Patent No. 5948639  
GENERAL INFORMATION:  
APPLICANT: Carlos J. Gimeno and Dean A. Falb  
TITLE OF INVENTION: No. 5948639el TGF-(SYMBOL 98 \f "Symbol") Pathway Genes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,312  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silveri, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-844-312-8

Query Match 42.0%; Score 34; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMKPPPP 10  
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Db 4 ELESPPPP 11

## RESULT 39

US-08-844-312-10  
; Sequence 10, Application US/08844312  
; Patent No. 5948639  
; GENERAL INFORMATION:  
; APPLICANT: Carlos J. Gimeno and Dean A. Falt  
; TITLE OF INVENTION: No. 5948639e1 TGF-[SYMBOL 98 \f "Symbol"] Pathway Genes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/844,312  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silveri, Jean M.  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MN1-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-844-312-10

Query Match 42.0%; Score 34; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMKPPPP 10  
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Db 4 ELESPPPP 11

RESULT 40  
US-08-968-466-7  
; Sequence 7, Application US/08968466  
; Patent No. 6132720  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: Immunogens Against Gonadotropin  
; TITLE OF INVENTION: Releasing Hormone  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA

ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,466  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-819-8286  
; TELEFAX: 212-354-8113  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..6  
; OTHER INFORMATION: /note= "spacer"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 7..16  
; OTHER INFORMATION: /note= "immunogenic"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 16  
; OTHER INFORMATION: /label= GlyNH2  
; OTHER INFORMATION: /note= "glycinamide"  
US-08-968-466-7

Query Match 42.0%; Score 34; DB 3; Length 16;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPP 12  
|||:  
Db 2 PPPPP 7

Search completed: June 7, 2005, 23:23:18  
Job time : 21.4545 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds  
(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-7

Perfect score: 81  
Sequence: 1 VLEMKFPPEPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 309695

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	81	100.0	15	US-10-691-157-7	Sequence 7, Appli
3	81	100.0	15	US-10-691-330-7	Sequence 7, Appli
4	38	46.9	9	US-09-825-144-10	Sequence 10, Appli
5	38	46.9	14	US-10-762-226-2	Sequence 2, Appli
6	38	46.9	17	US-10-981-434-4	Sequence 4, Appli
7	37	45.7	18	US-09-879-957-165	Sequence 165, App
8	37	45.7	18	US-10-185-050-109	Sequence 109, App
9	37	45.7	18	US-10-161-791-305	Sequence 305, App
10	37	45.7	18	US-10-807-856-165	Sequence 165, App
11	36	44.4	14	US-09-825-144-12	Sequence 12, Appli

12	36	44.4	15	US-09-825-144-1	Sequence 1, Appli
13	35	43.2	10	US-09-823-240-1	Sequence 1, Appli
14	35	43.2	10	US-09-261-894-19	Sequence 19, Appli
15	35	43.2	12	US-09-261-894-161	Sequence 161, App
16	35	43.2	13	US-10-185-050-7	Sequence 7, Appli
17	35	43.2	15	US-10-161-791-349	Sequence 349, App
18	35	43.2	15	US-10-161-791-423	Sequence 423, App
19	35	43.2	16	US-09-261-894-1	Sequence 1, Appli
20	35	43.2	16	US-10-197-000-1	Sequence 1, Appli
21	35	43.2	16	US-10-245-871-1	Sequence 1, Appli
22	35	43.2	16	US-10-253-886-1	Sequence 1, Appli
23	35	43.2	17	US-10-225-5678A-2084	Sequence 2084, Ap
24	34	42.0	5	US-09-825-144-15	Sequence 15, Appli
25	34	42.0	5	US-09-823-240-3	Sequence 3, Appli
26	34	42.0	5	US-09-989-188-1	Sequence 1, Appli
27	34	42.0	5	US-10-192-381-47	Sequence 47, Appli
28	34	42.0	6	US-09-943-944B-69	Sequence 69, Appli
29	34	42.0	9	US-09-823-240-7	Sequence 7, Appli
30	34	42.0	9	US-09-261-894-160	Sequence 160, App
31	34	42.0	10	US-09-261-894-18	Sequence 18, Appli
32	34	42.0	14	US-10-307-956-20	Sequence 20, Appli
33	34	42.0	15	US-10-185-050-55	Sequence 55, Appli
34	34	42.0	15	US-10-161-791-339	Sequence 339, App
35	34	42.0	15	US-10-161-791-405	Sequence 405, App
36	34	42.0	16	US-10-776-224-261	Sequence 261, App
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38	33	40.7	7	US-10-281-652-14	Sequence 14, Appli
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40	33	40.7	7	US-10-691-330-14	Sequence 14, Appli
41	33	40.7	10	US-10-415-014-495	Sequence 495, App
42	33	40.7	10	US-10-415-014-554	Sequence 554, App
43	33	40.7	10	US-10-415-014-681	Sequence 681, App
44	33	40.7	11	US-10-437-708-135	Sequence 135, App
45	33	40.7	11	US-10-437-708-139	Sequence 139, App
46	33	40.7	11	US-10-257-199-135	Sequence 135, App
47	33	40.7	11	US-10-257-199-135	Sequence 135, App
48	33	40.7	11	US-10-257-199-135	Sequence 135, App
49	33	40.7	11	US-10-418-032-139	Sequence 139, App
50	33	40.7	12	US-09-879-957-144	Sequence 144, App
51	33	40.7	12	US-10-185-050-52	Sequence 52, Appli
52	33	40.7	12	US-10-185-050-88	Sequence 88, Appli
53	33	40.7	12	US-10-807-856-144	Sequence 144, App
54	33	40.7	15	US-10-161-791-367	Sequence 367, App
55	33	40.7	15	US-10-161-791-373	Sequence 373, App
56	33	40.7	15	US-10-161-791-439	Sequence 439, App
57	33	40.7	16	US-10-185-050-11	Sequence 11, Appli
58	33	40.7	16	US-10-185-050-228	Sequence 228, App
59	33	40.7	17	US-10-161-791-336	Sequence 336, App
60	32	39.5	8	US-10-226-007-738	Sequence 738, App
61	32	39.5	8	US-10-226-007-751	Sequence 751, App
62	32	39.5	8	US-10-226-007-764	Sequence 764, App
63	32	39.5	8	US-10-226-007-1492	Sequence 1492, App
64	32	39.5	8	US-10-226-007-1493	Sequence 1493, App
65	32	39.5	8	US-10-022-066-378	Sequence 378, App
66	32	39.5	9	US-10-226-007-739	Sequence 739, App
67	32	39.5	9	US-10-226-007-752	Sequence 752, App
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69	32	39.5	9	US-10-226-007-778	Sequence 778, App
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71	32	39.5	9	US-10-226-007-1494	Sequence 1494, App
72	32	39.5	9	US-10-226-007-1496	Sequence 1496, App
73	32	39.5	10	US-10-226-007-740	Sequence 740, App
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78	32	39.5	10	US-10-226-007-1026	Sequence 1026, App
79	32	39.5	10	US-10-226-007-1039	Sequence 1039, App
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81	32	39.5	10	US-10-226-007-1499	Sequence 1499, App
82	32	39.5	11	US-10-226-007-741	Sequence 741, App
83	32	39.5	11	US-10-226-007-754	Sequence 754, App
84	32	39.5	11	US-10-226-007-767	Sequence 767, App

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86 32 39.5 11 14 US-10-226-007-792 Sequence 792, App  
87 32 39.5 11 14 US-10-226-007-803 Sequence 803, App  
88 32 39.5 11 14 US-10-226-007-1027 Sequence 1027, App  
89 32 39.5 11 14 US-10-226-007-1040 Sequence 1040, App  
90 32 39.5 11 14 US-10-226-007-1053 Sequence 1053, App  
91 32 39.5 11 14 US-10-226-007-1500 Sequence 1500, App  
92 32 39.5 11 14 US-10-226-007-1502 Sequence 1502, App  
93 32 39.5 12 10 US-09-990-832C-96 Sequence 96, App1  
94 32 39.5 12 14 US-10-226-007-742 Sequence 742, App  
95 32 39.5 12 14 US-10-226-007-755 Sequence 755, App  
96 32 39.5 12 14 US-10-226-007-768 Sequence 768, App  
97 32 39.5 12 14 US-10-226-007-781 Sequence 781, App  
98 32 39.5 12 14 US-10-226-007-793 Sequence 793, App  
99 32 39.5 12 14 US-10-226-007-804 Sequence 804, App  
100 32 39.5 12 14 US-10-226-007-814 Sequence 814, App

## ALIGNMENTS

## RESULT 1

US-10-281-652-7  
; Sequence 7, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDGCH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265,00220101  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-7

Query Match 100.0%; Score 81; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKRPPPPQETVT 15  
Db 1 VLEMKRPPPPQETVT 15

RESULT 2  
US-10-691-157-7  
; Sequence 7, Application US/10691157  
; Publication No. US20040266681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDGCH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUZEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265,00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-7

Query Match 100.0%; Score 81; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKRPPPPQETVT 15  
Db 1 VLEMKRPPPPQETVT 15

## RESULT 3

US-10-691-330-7  
; Sequence 7, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Krusel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265,00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-7

Query Match 100.0%; Score 81; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKRPPPPQETVT 15  
Db 1 VLEMKRPPPPQETVT 15

RESULT 4  
US-09-825-144-10  
; Sequence 10, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Weiland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation

US-09-825-144-10  
; Sequence 10, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Weiland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation

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; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-825-144-10

Query Match
Best Local Similarity 46.9%; Score 38; DB 9; Length 9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQETV 14
Db 1 FPPPPDDDI 9

RESULT 5
; US-10-762-226-2
; Sequence 2, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Pyroglutamic acid residue
; US-10-762-226-2

Query Match
Best Local Similarity 46.9%; Score 38; DB 17; Length 14;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11
Db 5 LEMKPPPPK 14

RESULT 6
; US-10-981-434-4
; Sequence 4, Application US/10981434
; Publication No. US20050112742A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Vicki S.
; APPLICANT: Apel, William A.
; APPLICANT: Schaller, Kasli D.
; TITLE OF INVENTION: HIGH TEMPERATURE AND ALKALINE STABLE CATALASE
; FILE REFERENCE: B-372
; CURRENT APPLICATION NUMBER: US/10/981,434
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Thermus brockianus
; US-10-981-434-4

Query Match
Best Local Similarity 46.9%; Score 38; DB 17; Length 17;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11
Db 8 LQIRLPPPE 17

RESULT 7
; US-09-879-957-165
; Sequence 165, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. US20020034755A1
; APPLICANT: KAY, Brian K.
; APPLICANT: FOMIKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mastrok, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
; US-09-879-957-165

Query Match
Best Local Similarity 45.7%; Score 37; DB 9; Length 18;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKPPPPQ 12
Db 1 EMKPPPPQ 12
```

Db 7 EPDPPEPPPD 16

RESULT 8  
US-10-185-050-109  
; Sequence 109, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8664/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
US-10-185-050-109

Query Match 45.7%; Score 37; DB 14; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKPEPPPE 12  
| | | | | :  
Db 7 EPDPPEPPPD 16

RESULT 9  
US-10-161-791-305  
; Sequence 305, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-305

Query Match 45.7%; Score 37; DB 14; Length 18;  
Best Local Similarity 55.6%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PPPPEQETV 14  
| | | | | :  
Db 7 PPPPEYQPI 15

RESULT 10  
US-10-807-856-165  
; Sequence 165, Application US/10807856  
; Publication No. US20040157216A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; HOFFMAN, Noah  
; KAY, Brian K.  
; FOWLKES, Dana M.  
; MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:



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; APPLICATION NUMBER: US/10/807,856
; FILING DATE: 23-Mar-2004
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-3090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-10-807-856-165

Query Match          45.7%; Score 37; DB 16; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPPQOE 12
   | | | | |
Db 7 BPDPPPPPD 16

RESULT 11
US-09-825-144-12
; Sequence 12, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehlard
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-825-144-12

Query Match          44.4%; Score 36; DB 9; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPPPQOE 12
   : | | | | :
Db 2 EPPPPPD 9

RESULT 12
US-09-825-144-1
; Sequence 1, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
```

```
; APPLICANT: Jorgen Wehlard
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-825-144-1

Query Match          44.4%; Score 36; DB 9; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPPPQOE 12
   : | | | | :
Db 3 EPPPPPD 10

RESULT 13
US-09-823-240-1
; Sequence 1, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James B. Bear
; APPLICANT: Jorgen Wehlard
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa is Asp or Glu
; NAME/KEY: UNSURE
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-1

Query Match          43.2%; Score 35; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PPPPPXD 12
   | | | | |
Db 2 PPPPPXD 8

RESULT 14
US-09-261-894-19
; Sequence 19, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
```

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,894  
FILING DATE: March 3, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-261-894-19

Query Match 43.2%; Score 35; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11  
Db 1 LMKLKPXPK 10

RESULT 15  
US-09-261-894-161  
Sequence 161, Application US/09261894  
Publication No. US20030207324A1  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,894  
FILING DATE: March 3, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 161:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-261-894-161

Query Match 43.2%; Score 35; DB 10; Length 12;  
Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPQ 11  
Db 1 LMKLKPXPK 10

RESULT 16  
US-10-185-050-7  
Sequence 7, Application US/10185050  
Publication No. US2003007577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-185-050-7

Query Match 43.2%; Score 35; DB 14; Length 13;  
Best Local Similarity 71.4%; Pred. No. 3.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PPPPQE 12

Db 5 YPPPEP 11

## RESULT 17

US-10-161-791-349  
; Sequence 349, Application US/10161791  
; Publication No. US2003018683A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OULLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Lealie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 349:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-349

Query Match 43.2%; Score 35; DB 14; Length 15;  
Best Local Similarity 54.5%; Pred. No. 3.8e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPPPPOE 12  
Db 1 LPSREPPPPPOK 11

## RESULT 18

US-10-161-791-423  
; Sequence 423, Application US/10161791  
; Publication No. US2003018683A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: OULLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Lealie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 423:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-423

Query Match 43.2%; Score 35; DB 14; Length 15;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPEP 12  
Db 8 PPPPEP 13

## RESULT 19

US-09-261-894-1  
; Sequence 1, Application US/09261894  
; Publication No. US2003020732A1  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert B  
; APPLICANT: Adams, Sparlene  
; APPLICANT: XU, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/261,894

FILING DATE: March 3, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fairrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-261-894-1

Query Match 43.2%; Score 35; DB 10; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
| | | | |  
Db 1 LRMKLPKPPK 10

RESULT 20  
US-10-197-000-1  
Sequence 1, Application US/10197000  
Publication No. US20030091582A1  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E.  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE  
FILE REFERENCE: REH2007  
CURRENT APPLICATION NUMBER: US/10/197,000  
CURRENT FILING DATE: 2002-07-17  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Mouse  
US-10-197-000-1

Query Match 43.2%; Score 35; DB 14; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
| | | | |  
Db 1 LRMKLPKPPK 10

RESULT 21  
US-10-245-871-1  
Sequence 1, Application US/10245871  
Publication No. US20030235594A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2013  
CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key  
US-10-245-871-1

Query Match 43.2%; Score 35; DB 15; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
| | | | |  
Db 1 LRMKLPKPPK 10

RESULT 22  
US-10-253-286-1  
Sequence 1, Application US/10253286  
Publication No. US20040058881A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2015  
CURRENT APPLICATION NUMBER: US/10/253,286  
CURRENT FILING DATE: 2003-01-13  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key  
US-10-253-286-1

Query Match 43.2%; Score 35; DB 15; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
| | | | |  
Db 1 LRMKLPKPPK 10

RESULT 23  
US-10-225-567A-2084  
Sequence 2084, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burnet, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2084  
LENGTH: 17  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-225-5567A-2084

Query Match 43.2%; Score 35; DB 14; Length 17;  
Best Local Similarity 70.0%; Pred. No. 4.3e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKPPPPQ 11  
DB 2 LEAKAPPPQ 11

RESULT 24  
US-09-825-144-15  
Sequence 15, Application US/09825144  
Patent No. US20020037286A1

GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Secchi  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgen Wehlend  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7065  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-825-144-15

Query Match 42.0%; Score 34; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10  
DB 1 PPPPP 5

RESULT 25  
US-09-823-240-3  
Sequence 3, Application US/09823240  
Patent No. US2002004813A1  
GENERAL INFORMATION:  
APPLICANT: Frank B. Gertler  
APPLICANT: James E. Bear  
APPLICANT: Jorgen Wehlend  
APPLICANT: Joseph Loureiro  
TITLE OF INVENTION: Methods and Products for Regulating Cell  
FILE REFERENCE: M0656/7064 (HCL)  
CURRENT APPLICATION NUMBER: US/09/823,240  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 60/194,564  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
US-09-823-240-3

Query Match 42.0%; Score 34; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10

DB 1 PPPPP 5

RESULT 26  
US-09-989-188-1  
Sequence 1, Application US/09989188  
Publication No. US20020136717A1  
GENERAL INFORMATION:  
APPLICANT: JORDAN, BIRGIT  
APPLICANT: DRUCKES, PETER  
APPLICANT: JARCHAU, THOMAS  
APPLICANT: WALTER, ULRICH  
TITLE OF INVENTION: PROCESS FOR SCREENING CHEMICAL COMPOUNDS FOR MODULATING  
TITLE OF INVENTION: THE INTERACTION OF AN EVH1 DOMAIN OR A PROTEIN HAVING  
TITLE OF INVENTION: AN EVH1 DOMAIN WITH AN EVH1 BINDING DOMAIN, AND A PROCESS FOR DETECTING  
FILE REFERENCE: 02481.1761-00000  
CURRENT APPLICATION NUMBER: US/09/989,188  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: DE 10058596.5  
PRIOR FILING DATE: 2000-11-25  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-989-188-1

Query Match 42.0%; Score 34; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPPP 10  
DB 1 PPPPP 5

RESULT 27  
US-10-192-381-47  
Sequence 47, Application US/10192381  
Publication No. US20030170807A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: MORLEY, Paul  
APPLICANT: TU, Jian  
APPLICANT: XIAO, Bo  
APPLICANT: LEAHY, Daniel  
APPLICANT: BENENEN, Jutta  
APPLICANT: LANAHAN, Anthony  
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS  
FILE REFERENCE: JHU1580-4  
CURRENT APPLICATION NUMBER: US/10/192,381  
CURRENT FILING DATE: 2002-07-09  
PRIOR APPLICATION NUMBER: US/09/377,285  
PRIOR FILING DATE: 1999-08-18  
PRIOR APPLICATION NUMBER: US 60/138,426  
PRIOR FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: US 60/138,493  
PRIOR FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: US 60/138,494  
PRIOR FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: US 60/097,334  
PRIOR FILING DATE: 1998-08-18  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 47

LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: optimal ligand  
US-10-192-381-47

Query Match 42.0%; Score 34; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPP 10  
|||  
Db 1 PPPP 5

RESULT 28  
US-09-943-944E-69  
Sequence 69, Application US/09943944E  
Publication No. US20040014036A1  
GENERAL INFORMATION:  
APPLICANT: Peasbne, et al.,  
TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses  
FILE REFERENCE: 0342941-0065  
CURRENT APPLICATION NUMBER: US/09/943,944E  
CURRENT FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Random peptide  
US-09-943-944E-69

Query Match 42.0%; Score 34; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPP 10  
|||  
Db 1 PPPP 5

RESULT 29  
US-09-823-240-7  
Sequence 7, Application US/09823240  
Patent No. US20020048813A1  
GENERAL INFORMATION:  
APPLICANT: Frank B. Gertler  
APPLICANT: James E. Bear  
APPLICANT: Jurgen Weiland  
APPLICANT: Joseph Lourelo  
TITLE OF INVENTION: Methods and Products for Regulating Cell  
FILE REFERENCE: M0566/7064 (HCL)  
CURRENT APPLICATION NUMBER: US/09/823,240  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 60/194,564  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (9)...(9)  
OTHER INFORMATION: Xaa is any amino acid

US-09-823-240-7

Query Match 42.0%; Score 34; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPPP 10  
|||  
Db 1 PPPP 5

RESULT 30  
US-09-261-894-160  
Sequence 160, Application US/09261894  
Publication No. US20030207324A1  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Shariene  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,894  
FILING DATE: March 3, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0528  
TELEFAX: (207) 363-0558  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-09-261-894-160

Query Match 42.0%; Score 34; DB 10; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMKPPPP 10  
|||  
Db 1 LMKLPKPP 9

RESULT 31  
US-09-261-894-18  
Sequence 18, Application US/09261894  
Publication No. US20030207324A1  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Shariene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,894  
FILING DATE: March 3, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-261-894-18

Query Match 42.0%; Score 34; DB 10; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKEPPP 10  
| | | | |  
DB 1 LMKLPKPP 9

RESULT 32  
US-10-307-956-20  
; Sequence 20, Application US/10307956  
; Publication No. US20030119072A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoekefira, Meryl F.  
; APPLICANT: Xie, Weilin  
; APPLICANT: Murray, Brian  
; APPLICANT: Mercutio, Frank  
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS  
; FILE REFERENCE: 860098.433  
; CURRENT APPLICATION NUMBER: US/10/307,956  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US/09/385,918  
; PRIOR FILING DATE: 1998-08-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FaSTSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-307-956-20

Query Match 42.0%; Score 34; DB 14; Length 14;  
Best Local Similarity 62.5%; Pred. No. 4.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMKEPPP 10  
| : : | | |  
DB 1 ELESPPP 8

RESULT 33  
US-10-185-050-55  
; Sequence 55, Application US/10185050  
; Publication No. US2003007577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowler, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-10-185-050-55

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 75.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPPQETV 14  
| | | | |  
DB 4 PPPPYTV 11

RESULT 34  
US-10-161-791-339  
; Sequence 339, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 339:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-339

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPOE 12  
| | | | |  
Db 6 PPPPOK 11

RESULT 35  
US-10-161-791-405  
Sequence 405, Application US/10161791  
Publication No. US2003018663A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: OULLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-405

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 85.7%; Pred. No. 5.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPPPQ 11  
| | | | |  
Db 4 KPPPPQ 10

RESULT 36  
US-10-776-224-261  
Sequence 261, Application US/10776224  
Publication No. US20050074849A1  
GENERAL INFORMATION:  
APPLICANT: Erickson, Jon Amund  
APPLICANT: Moller, Mona  
APPLICANT: Gjertsen, Marianne Klemp  
APPLICANT: Saeterdal, Ingvald  
TITLE OF INVENTION: Peptides  
FILE REFERENCE: 01702.401510  
CURRENT APPLICATION NUMBER: US/10/776,224  
CURRENT FILING DATE: 2004-02-12  
PRIOR APPLICATION NUMBER: US 09/674,973  
PRIOR FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 459  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 261  
LENGTH: 16  
TYPE: PPT  
ORGANISM: Homo sapiens  
US-10-776-224-261

Query Match 42.0%; Score 34; DB 17; Length 16;  
Best Local Similarity 66.7%; Pred. No. 5.5e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPQETVT 15  
| | | | |  
Db 5 PPPPAHGT 13

RESULT 37  
US-10-331-907-403  
Sequence 403, Application US/10331907  
Publication No. US20030181660A1  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hees, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly



```

; Hey, Patricia
; Kawaguchi, Yoshiniko
; Merriam, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixxon and Vanderhye
; STREET: 1100 No. US20030181660A1e1 Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-Apr-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-Apr-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-331-907-403

Query Match      42.0%; Score 34; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PPPP 10
        |||||
Db      6 PPPP 10

RESULT 38
US-10-281-652-14
; Sequence 14, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-14

Query Match      40.7%; Score 33; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 11
        |||||
Db      2 PPPP 6

RESULT 39
US-10-691-157-14
; Sequence 14, Application US/10691157
; Publication No. US20040266681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-14

Query Match      40.7%; Score 33; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 11
        |||||
Db      2 PPPP 6

RESULT 40
US-10-691-330-14
; Sequence 14, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy A.
; APPLICANT: HUGHES, Thomas K., Jr.
; APPLICANT: KRUEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265, 00390101
```

```
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patenclin version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-14

Query Match          40.7%; Score 33; DB 17; length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPPQ 11
        |||||
Db      2 PPPPQ 6
```

Search completed: June 7, 2005, 23:31:39  
Job time : 68.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:56:36 ; Search time 13.9091 Seconds  
(without alignments)  
103.763 Million cell updates/sec

Title: US-10-691-157-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	38.3	17	2	SS7991
2	29	35.8	15	2	PT0037
3	28	34.6	7	2	S71299
4	28	34.6	10	2	A36454
5	28	34.6	17	2	SS9481
6	27	33.3	12	2	B39690
7	27	33.3	13	2	S21152
8	27	33.3	16	2	JH0517
9	26	32.1	12	2	E45691
10	26	32.1	13	2	D39690
11	26	32.1	14	2	H64008
12	26	32.1	14	2	S12904
13	26	32.1	16	2	E58503
14	25	30.9	9	2	S26508
15	25	30.9	12	2	PN0663
16	24	29.6	11	2	D45900
17	24	29.6	11	2	C37196
18	24	29.6	11	2	D37196
19	24	29.6	13	2	A35245
20	24	29.6	13	2	B35245
21	24	29.6	17	2	C33098
22	24	29.6	17	2	A42920
23	23	28.4	9	2	S66607
24	23	28.4	10	2	H28027
25	23	28.4	13	2	A05174
26	23	28.4	15	2	F28587
27	23	28.4	15	2	I53284
28	23	28.4	15	2	A28965
29	23	28.4	17	2	D53284

30	23	28.4	18	2	A35704	cytochrome P450 o1
31	22.5	27.8	15	2	A54397	ubiquitin-carrier
32	22	27.2	8	2	S16324	hypothetical prote
33	22	27.2	13	2	PN0046	unidentified OM002
34	22	27.2	14	2	PA0104	protein QP20070 -
35	22	27.2	15	2	B39109	hypothetical 1.5K
36	22	27.2	15	2	PA0057	adenylate isopente
37	21	25.9	10	2	C35389	urase (EC 3.5.1.5
38	21	25.9	11	2	I52980	glucocorticoidase
39	21	25.9	12	2	C39109	hypothetical 1.2K
40	21	25.9	12	2	PH1567	hypothetical 1.2K
41	21	25.9	13	2	S09716	cerebrin 28 - huma
42	21	25.9	13	2	A40207	2S albumin large c
43	21	25.9	14	2	S11129	cell surface glyco
44	21	25.9	15	2	B61457	phosphoprotein, bo
45	21	25.9	18	2	PC2280	alpha-glucosidase
46	21	25.9	18	2	A54195	poly(endorphin)as
47	20	24.7	8	2	S21288	Na+/K+-exchanging
48	20	24.7	10	2	B59272	lectin - potato (f
49	20	24.7	10	2	B59272	peptide-M4-(N-acet
50	20	24.7	11	1	XASNBA	bradykinin-potent
51	20	24.7	11	1	A60654	bradykinin-potent
52	20	24.7	11	1	SFHO	substance P - quin
53	20	24.7	11	1	S23306	substance P - hirs
54	20	24.7	12	2	PE0213	substance P - Acta
55	20	24.7	12	2	PA0098	28K protein 4412 -
56	20	24.7	12	2	S07436	ribosomal protein
57	20	24.7	12	2	G37266	lacthykinin - Afri
58	20	24.7	14	2	PH0135	Ig heavy chain C r
59	20	24.7	14	2	S65392	Ig heavy chain C r
60	20	24.7	14	2	S48685	I-cell receptor be
61	20	24.7	17	2	A39117	cytochrome-c oxida
62	20	24.7	17	2	A49237	extensin protein
63	20	24.7	17	2	B25348	Ig light chain - P
64	19	23.5	10	2	C30572	45/47K antigen - M
65	19	23.5	10	2	S18396	glycogen(tetarch) s
66	19	23.5	11	1	XAVIBH	I-cell receptor be
67	19	23.5	11	2	C60409	probable glucose-6
68	19	23.5	11	2	D60409	bradykinin-potent
69	19	23.5	11	2	D60409	substance P - chic
70	19	23.5	14	2	C59137	kaesinin-like pept
71	19	23.5	14	2	A42473	kaesinin-like pept
72	19	23.5	15	2	PA0002	ermk leader peptid
73	19	23.5	15	2	PA0014	photoystem II oxy
74	19	23.5	15	2	PN0173	seed storage prote
75	19	23.5	15	2	A41436	seed storage prote
76	19	23.5	15	2	PK0031	alpha-macroglobuli
77	19	23.5	15	2	B59137	mixed lymphocyte r
78	19	23.5	16	2	PH1302	protein pfl - gold
79	19	23.5	16	2	PH0759	Ig heavy chain DJ
80	19	23.5	16	2	PH0759	T-cell receptor be
81	19	23.5	16	2	A45454	T-cell receptor be
82	19	23.5	16	2	JH0609	ankyrin-binding gl
83	19	23.5	17	2	PT0235	leukocyte chemoat
84	19	23.5	17	2	PT0235	Ig heavy chain CRD
85	19	23.5	18	2	A42576	steroid receptor c
86	18	22.2	6	2	A61049	halo-toxin - Pseud
87	18	22.2	6	2	A19780	transferrin - bovi
88	18	22.2	8	2	S10783	enamelin F - bovin
89	18	22.2	8	2	A05169	neuropeptide M-I -
90	18	22.2	9	2	B30572	T-cell receptor be
91	18	22.2	10	1	XASNPC	angiotensin-conver
92	18	22.2	12	2	S11286	exo-alpha-sialidas
93	18	22.2	12	2	S67528	napin - rape (frag
94	18	22.2	12	2	U00356	cycloleucorinin -
95	18	22.2	13	2	A60856	inhibitin alpha chai
96	18	22.2	13	2	S36668	hypothetical prote
97	18	22.2	13	2	S33800	chaperone, TCP1-re
98	18	22.2	14	2	A60737	pollen allergen lo
99	18	22.2	14	2	S00150	onostatin - duck (
100	18	22.2	15	2	B61280	probable proteolys
	18	22.2	15	2	S29207	avenin gamma-4 - o

## ALIGNMENTS

## RESULT 1

S57991

hydroxyproline-rich protein - Seebania rostrata (fragment)

C:Species: Seebania rostrata

C&gt;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S57991

R:Gormachy, S.; Valerio-Lepintec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Seebania rostrata genes ent

A:Reference number: S57991

A:Status: preliminary

A:Accession: S57991

A:Molecule type: mRNA

A:Residues: 1-17 &lt;GOO&gt;

A:Cross-references: UNIPROT:Q41400; EMBL:Z48673; NID:G859484; PID:G859485

C:Superfamily: hydroxyproline-rich glycoprotein

## Query Match

Best Local Similarity 38.3%; Score 31; DB 2; Length 17;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KRPPP 10

DB 8 KSPPP 13

## RESULT 2

P70037

light harvesting complex chain III/D, photosystem I - rice (fragment)

C:Species: Oryza sativa (rice)

C&gt;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C:Accession: P70037; P80205

R:Uchiyama, Y.; Teugita, A.

submitted to JIPID, June 1991

A:Reference number: P80189

A:Accession: P70037

A:Molecule type: protein

A:Residues: 1-15 &lt;UCH&gt;

A:Cross-references: UNIPROT:Q7M1V1

## Query Match

Best Local Similarity 35.8%; Score 29; DB 2; Length 15;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKRP 10

DB 4 EAAAP 11

## RESULT 3

S71299

IC12 protein - Parametium tetraurelia (fragment)

C:Species: Parametium tetraurelia

C&gt;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C:Accession: S71299

R:Madaddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin genes in Parametium.

A:Reference number: S71299; MUID:96248429; PMID:8665928

A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 &lt;MAD&gt;

A:Experimental source: strain d4-2

C:Genetics:

A:Genetic code: SGCS

## Query Match

Best Local Similarity 34.6%; Score 28; DB 2; Length 7;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPP 12

DB 3 PPP 7

## RESULT 4

A61630

trypsin-modulating coelastatic factor - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C&gt;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004

C:Accession: A61630; A61630

R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

PMSEB J. 4, 3015-3020, 1990

A:Title: Mosquito coelastatic factor: a novel decapeptide modulating trypsin-like enzyme bi.

A:Reference number: A61630; MUID:90367888; PMID:2394318

A:Accession: A61630

A:Molecule type: protein

A:Residues: 1-10 &lt;BOR&gt;

A:Cross-references: UNIPROT:P19425

R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating coel

A:Reference number: A61630; MUID:93357794; PMID:8353526

A:Accession: A61630

A:Molecule type: protein

A:Residues: 1-10 &lt;BO2&gt;

A:Note: none of the amino acids is modified

C:Function:

A:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep

C:Keywords: hormone

## Query Match

Best Local Similarity 34.6%; Score 28; DB 2; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 10

DB 5 PPP 8

## RESULT 5

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C&gt;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004

C:Accession: S59481

R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to differen

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59481

A:Molecule type: protein

A:Residues: 1-17 &lt;WOJ&gt;

A:Cross-references: UNIPROT:Q7M1I3

C:Keywords: glycoprotein; hydroxyproline

F.6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

## Query Match

Best Local Similarity 34.6%; Score 28; DB 2; Length 17;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 10

DB 8 PPP 11

## RESULT 6

B39690

neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C:Accession: B39690

R:Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991  
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
 A:Reference number: A39690; MUID:91141516; PMID:1996115  
 A:Accession: B39690  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <REV>  
 A:Cross-references: GB:M63970  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 33.3%; Score 27; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPPE 12  
 |||:  
 DB 6 PPPPE 10

## RESULT 7

S21152  
 tryptophyllin-related peptide - two-colored leaf frog  
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Aug-2004  
 C:Accession: S21152  
 R:Minogana, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erpagner, G.; Kreil, G.  
 FEBS Lett. 302, 151-154, 1992  
 A>Title: Identification and characterization of two dermorphins from skin extracts of th  
 A:Reference number: S21152; MUID:92339502; PMID:1633846  
 A:Accession: S21152  
 A:Molecule type: protein  
 A:Residues: 1-13 <WIG>  
 A:Cross-references: UNIPROT:Q7LZ51  
 A:Experimental source: skin

Query Match 33.3%; Score 27; DB 2; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKPPPP 10  
 |||:  
 DB 2 EKPPPPPP 9

## RESULT 8

JH0517  
 insulin-like growth factor-binding protein 4 - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C:Accession: JH0517  
 R:Coleman, M.E.; Pan, Y.C.E.; Eberton, T.D.  
 Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991  
 A>Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth  
 A:Reference number: JH0515; MUID:92109718; PMID:1723398  
 A:Accession: JH0517  
 A:Molecule type: protein  
 A:Residues: 1-16 <COL>  
 A:Cross-references: UNIPROT:P24854  
 A:Experimental source: serum  
 C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h

Query Match 33.3%; Score 27; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPPE 12  
 |||:  
 DB 7 PPPPE 12

RESULT 9  
 E55691  
 probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact

C:Species: Lactobacillus delbrueckii subsp. Lactis phage LR-H  
 C>Date: 24-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C:Accession: B45691  
 R:Vaasala, A.; Dupont, L.; Baumann, M.; Ritzenhaller, P.; Alatosava, T.  
 J. Virol. 67, 3061-3068, 1993  
 A>Title: Molecular comparison of the structural proteins encoding gene clusters of two r

A:Reference number: A45691; MUID:93267750; PMID:8497043  
 A:Accession: B45691  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-12 <VAS>  
 A:Cross-references: UNIPROT:Q04769  
 A:Notes: sequence extracted from NCBI Backbone (NCBIN:132363, NCBIPI:132373)

Query Match 32.1%; Score 26; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 MKPPPPQETVT 15  
 |||:  
 DB 1 MKLPPIPYQMAVS 12

## RESULT 10

D39690  
 neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C:Accession: D39690  
 R:Reyes, A.A.; Small, S.J.; Akesson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR  
 A:Reference number: A39690; MUID:91141516; PMID:1996115  
 A:Accession: D39690  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <REV>  
 A:Cross-references: GB:M63970  
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 32.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11  
 |||:  
 DB 6 PPPQ 9

## RESULT 11

H64008  
 hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
 C:Accession: H64008  
 R:Flatschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkease, E.F.; Kerlavage, A  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J  
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fulthman, J.L.; Geoghegan, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: H64000; MUID:95350630; PMID:7542800  
 A:Accession: H64008  
 A:Molecule type: DNA  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-14 <TIGR>  
 A:Cross-references: GB:U27231; GB:142023; NID:g1573465; PID:g1573478; TIGR:HI0492

Query Match 32.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFPFPPQ 11  
| | | | |  
Db 7 KMPFPRK 13

## RESULT 12

S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C:Species: Pisaster ochraceus  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S12904  
R:Sanghera, J.S.; Abersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FBS Lett. 273, 223-226, 1990  
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by  
A:Reference number: S12904; MUID:91032186; PMID:1699809  
A:Accession: S12904  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SAN>  
A:Cross-references: UNIPROT:Q7M3M4  
C:Keywords: phosphotransferase

Query Match 32.1%; Score 26; DB 2; Length 14;  
Best Local Similarity 36.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQ 11  
: | | | | |  
Db 2 IVTPRTPPSQ 12

## RESULT 13

E58503  
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)  
N:Alternate names: 21.3X bladder and kidney stone protein  
C:Species: unidentified bacterium  
C>Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: E58503  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The protein of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: E58503  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <BIN>  
A:Cross-references: UNIPROT:Q7M137  
A:Experimental source: human bladder and kidney stones  
C:Function:  
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C:Keywords: metalloprotein; oxidoreductase

Query Match 32.1%; Score 26; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMKFPFPPQ 12  
: | | | | |  
Db 1 MEHTLPPLPYE 11

## RESULT 14

S26508  
collagen alpha 2(VI) chain - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S26508  
R:Jander, R.; Rautenberg, J.; Glanville, R.W.  
Eur. J. Biochem. 133, 39-46, 1983  
A:Title: Further characterization of the three polypeptide chains of bovine and human sh  
A:Reference number: S26506; MUID:83209648; PMID:6652033  
A:Accession: S26508  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-9 <JAN>  
A:Cross-references: UNIPROT:Q7M2M9  
C:Keywords: hydroxyproline  
F:7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.9%; Score 25; DB 2; Length 9;  
Best Local Similarity 55.6%; Pred. No. 2.8e+05;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKFPFPP 10  
| | | | |  
Db 1 LEIPFPP 9

## RESULT 15

P0663  
dytrophin-associated glycoprotein A3a-II - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C:Accession: P0663  
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993

A:Title: A dytrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A:Reference number: P0662; MUID:94156881; PMID:8113213  
A:Accession: P0663  
A:Molecule type: protein  
A:Residues: 1-12 <YOS>  
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C:Keywords: glycoprotein; skeletal muscle

Query Match 30.9%; Score 25; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFPFPPQ 12  
| | | | |  
Db 1 KAPLPPE 8

## RESULT 16

D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: D45900  
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.  
J. Immunol. 144, 3581-3591, 1990  
A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gen  
A:Reference number: A45900; MUID:90229754; PMID:2139460  
A:Accession: D45900  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-11 <KUR>

Query Match 29.6%; Score 24; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKFPFPP 10  
| | | | |  
Db 4 EISCDPP 11

## RESULT 17

C37196  
bradykinin-potentiating peptide 3 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C>Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: C37196  
R:Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptides f

A:Reference number: A37196; MUID:90351557; PMID:2386615

A:Accession: C37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <CIN>

A:Cross-references: UNIPROT:P30423

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11

Db 4 PPRPQ 8

#### RESULT 18

D37196

bradykinin-potentiating peptide 4 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004

C:Accession: D37196

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A37196; MUID:90351557; PMID:2386615

A:Accession: D37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <CIN>

A:Cross-references: UNIPROT:P30424

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11

Db 4 PPRPQ 8

#### RESULT 19

A35245

histone H1a - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997

C:Accession: A35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: A35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <Aji>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPOPTVT 15

Db 5 PPVSELTIT 12

#### RESULT 20

B35245

histone H1.c - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997

C:Accession: B35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: B35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <Aji>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPOPTVT 15

Db 5 PPVSELTIT 12

#### RESULT 21

C33098

23kS exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: C33098

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <NIC>

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPOE 12

Db 3 PPOE 6

#### RESULT 22

A42920

fatty acid ethyl ester synthase-II - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A42920

R:Bora, P.S.; Wu, X.; Spillburg, C.A.; Lange, L.G.

J. Biol. Chem. 267, 13217-13221, 1992

A:Title: Purification and characterization of fatty acid ethyl ester synthase-II from hu

A:Reference number: A42920; MUID:92317032; PMID:1618826

A:Accession: A42920

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-17 <BOR>

A:Cross-references: UNIPROT:Q9UND6

A:Experimental source: myocardium

A>Note: sequence extracted from NCBI backbone (NCBI:P107742)

#### Query Match

Best Local Similarity 29.6%; Score 24; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPOPT 13

Db 3 PPDPVTT 9

## RESULT 23

S66607  
guinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)  
C/Species: Comamonas testosteroni  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C/Accession: S66607  
R/Schach, S.; Tetsuaka, B.; Fetzner, S.; Lingens, F.  
Eur. J. Biochem. 232, 536-544, 1995  
A/Title: Guinoline 2-oxidoreductase and 2-oxo-1,2-dihydroguinoline 5,6-dioxygenase from  
A/Reference number: S66606; PMID:96035889; PMID:7556204  
A/Accession: S66607  
A/Molecule type: protein  
A/Residues: 1-9 <SCH>  
A/Experimental source: strain 63

Query Match 28.4%; Score 23; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFP 7  
| | | |  
Db 1 MKFP 4

## RESULT 24

H28027  
protein P11 - curled-leaved tobacco (fragment)  
C/Species: Nicotiana glauca (curled-leaved tobacco)  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993  
C/Accession: H28027  
R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-  
A/Reference number: A94167  
A/Accession: H28027  
A/Molecule type: protein  
A/Residues: 1-10 <BAU>  
A/Note: 4-Val was also found

Query Match 28.4%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MKFP 10  
: | | | |  
Db 2 IKFGP 8

## RESULT 25

A05174  
tryptophyl11n-13 - Rohde's leaf frog  
C/Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C/Accession: A05174  
R/Montecucchi, P.C.; Gozzini, L.; Erespaner, V.  
Int. J. Pept. Protein Res. 27, 175-182, 1986  
A/Reference number: A05174  
A/Accession: A05174  
A/Molecule type: protein  
A/Residues: 1-13 <MON>  
A/Cross-references: UNIPROT:P04096  
C/Superfamily: unassigned animal peptides  
C/Keywords: pyroglutamic acid, skin  
F11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.4%; Score 23; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKFP 10  
| : | | |  
Db 2 EKPYW 9

## RESULT 26

F28587  
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: F28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; PMID:86094276; PMID:3866244  
A/Accession: F28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: GB:M4159; NID:G33852; PIDN:AAA60681.1; PID:G553692  
C/Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMKFP 15  
| | | : | | |  
Db 3 EYFGPGTKLTVT 15

## RESULT 27

I53284  
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C/Accession: I53284  
R/Hartdianath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and J  
A/Reference number: A53284; PMID:91342695; PMID:1678859  
A/Accession: I53284  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-15 <HAR>  
A/Cross-references: GB:S60737; NID:G233916; PIDN:AAI9525.1; PID:G233925  
A/Note: sequence extracted from NCBI Backbone (NCBIN:60737, NCBIR:60747)  
C/Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMKFP 15  
| | | : | | |  
Db 3 EYFGPGTKLTVT 15

## RESULT 28

A28965  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)  
C/Species: Spinacia oleracea (spinach)  
C/Date: 22-Dec-1988 #sequence\_revision 22-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A28965  
R/Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988  
A/Title: Reaction-intermediate analogue binding by ribulose bisphosphate carboxylase/oxy  
cetylated proline.  
A/Reference number: A28965; PMID:8814446; PMID:3422748  
A/Accession: A28965  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <MUL>  
A/Cross-references: UNIPROT:P00875

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMKFP 15  
| | | : | | |  
Db 3 EYFGPGTKLTVT 15



Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 KEPPPPQETV 14  
| | | | |  
| | | | |

Db 6 KEFPAMDIV 15  
| | | | |  
| | | | |

## RESULT 29

D53284

T-cell receptor beta 2 chain J region, Jbeta2.1 - rabbit

C.Species: Oryctolagus cuniculus (domestic rabbit)

C.Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C.Accession: D53284

R.Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 29, 881-888, 1991

A>Title: Evolutionarily conserved organization and sequences of germ-line diversity and J

A.Reference number: A53284; MUID:91342695; PMID:1678859

A.Accession: D53284

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-17 <RAR>

A.Cross-references: GB:S60737; NID:G233916; PIDN:AA19520.1; PID:G233920

A.Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P.60742)

C.Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EMKPPPPQETV 14  
| | | | |  
| | | | |

Db 5 ELFFPGTDLTV 16  
| | | | |  
| | | | |

## RESULT 30

A35704

Cytochrome P450 olf2 - bovine (fragment)

M.Contains: oxidoreductase (EC 1.-.-.-)

C.Species: Bos primigenius taurus (cattle)

C.Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C.Accession: A35704

R.Lazarov, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.

Biochemistry 29, 7433-7440, 1990

A>Title: Identification and biochemical analysis of novel olfactory-specific cytochrome

A.Reference number: A35704; MUID:91027757; PMID:2121272

A.Accession: A35704

A.Molecule type: protein

A.Residues: 1-18 <LAZ>

A.Cross-references: UNIPROT:P22779

C.Genetics:

A.Gene: CYP2A

C.Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C.Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protei

Query Match 28.4%; Score 23; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.6e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKPPPPQETV 12  
| | | | |  
| | | | |

Db 1 MKYLPQPOQ 9  
| | | | |  
| | | | |

## RESULT 31

A54397

ubiquitin-carrier protein E2-F1 - rabbit (fragment)

C.Species: Oryctolagus cuniculus (domestic rabbit)

C.Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C.Accession: A54397

R.Blumentfeld, N.; Gonen, H.; Mayer, A.; Smith, C.E.; Siegel, N.R.; Schwartz, A.L.; Clech

J. Biol. Chem. 269, 9574-9581, 1994

A>Title: Purification and characterization of a novel species of ubiquitin-carrier prote

A.Reference number: A54397; MUID:94193635; PMID:8144544

A.Accession: A54397

A.Status: preliminary

A.Molecule type: protein

A.Residues: 1-15 <BLU>

A.Cross-references: UNIPROT:Q9T584

A.Experimental source: reticulocyte

A.Note: sequence extracted from NCBI backbone (NCBIP:146038)

C.Superfamily: human ubiquitin-protein ligase E2

Query Match 27.8%; Score 22.5; DB 2; Length 15;

Best Local Similarity 33.3%; Pred. No. 1.5e+03;

Matches 5; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

Qy 2 LEMKPP-----PPQ 11  
| | | | |  
| | | | |

Db 1 IRINFPAPYPPKPK 15  
| | | | |  
| | | | |

## RESULT 32

S16324

hypothetical protein 2 - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000

C.Accession: S16324

R.Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A>Title: A novel class of plant proteins containing a homeodomain with a closely linked

A.Reference number: S16323; MUID:9126907; PMID:1675603

A.Accession: S16324

A.Status: translation not shown

A.Molecule type: mRNA

A.Residues: 1-8 <RUB>

A.Cross-references: EMBL:X58821; NID:G16327; PIDN:CAA1624.1; PID:G579259

Query Match 27.2%; Score 22; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKPPP 9  
| | | | |  
| | | | |

Db 1 MEYKLLPP 8  
| | | | |  
| | | | |

## RESULT 33

P00048

unidentified QM0023 protein - mouse (fragment)

C.Species: Mus musculus (house mouse)

C.Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C.Accession: P00048

R.Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A>Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neur

A.Reference number: P00041

A.Accession: P00048

A.Molecule type: protein

A.Residues: 1-13 <KAT>

A.Experimental source: neuroblastoma cell

C.Comment: The molecular mass is 30,500 and the pI is 6.19.

C.Keywords: brain

Query Match 27.2%; Score 22; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 PQETVT 15  
| | | | |  
| | | | |

Db 8 PNDIVT 13  
| | | | |  
| | | | |

## RESULT 34

PA0104

protein QP200070 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: *Fusarium sporotrichioides*  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0104  
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*  
 A:Reference number: PA0051  
 A:Accession: PA0104  
 A:Molecule type: protein  
 A:Residues: 1-14 <CHO>

Query Match 27.2%; Score 22; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EMKFPPEQ 11  
 DB 3 EMKFAFXPRQ 11

RESULT 35  
 B39109  
 hypothetical 1.5K protein - hepatitis C virus  
 N:Alternate names: hypothetical protein 2  
 C:Species: hepatitis C virus  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C:Accession: B39109; J01585  
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
 A:Reference number: A39109; MUID:91156678; PMID:1705704  
 A:Accession: B39109  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <HAN>  
 A:Cross-References: GB:M58406  
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992  
 A:Title: Cloning and sequencing of the structural region and expression of putative core  
 A:Reference number: J01584; MUID:92300349; PMID:1318944  
 A:Accession: J01585  
 A:Molecule type: genomic RNA  
 A:Residues: 1-15 <KUM>  
 A:Experimental source: strain U.K.

Query Match 27.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 1.8e+03;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VLEMKFPPEQ 12  
 DB 3 VVQPPGPPLRGE 14

RESULT 36  
 PA0057  
 adenylate isopentenyltransferase (EC 2.5.1.27) - fungus (*Fusarium sporotrichioides*) (Fr  
 C:Species: *Fusarium sporotrichioides*  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0057  
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*  
 A:Reference number: PA0051  
 A:Accession: PA0057  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: transferase

Query Match 27.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQETV 14  
 DB 4 PQOTT 8

RESULT 37  
 C35389  
 urease (EC 3.5.1.5) 6K chain - *Morganella morganii* (fragment)  
 C:Species: *Morganella morganii*  
 C:Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004  
 C:Accession: C35389  
 R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
 J. Bacteriol. 172, 3073-3080, 1990  
 A:Title: *Morganella morganii* urease: purification, characterization, and isolation of ge  
 A:Reference number: A35389; MUID:90264298; PMID:2345135  
 A:Accession: C35389  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <HUA>  
 A:Cross-References: UNIPROT:P17339  
 C:Keywords: hydrolase

Query Match 25.9%; Score 21; DB 2; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 MKFPPEQ 12  
 DB 1 MOUTPEVE 9

RESULT 38  
 I52980  
 glucocerebrosidase - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I52980; I65971  
 R:Reiner, O.; Miggerson, M.; Horowitz, M.  
 DNA 7, 107-116, 1988  
 A:Title: Structural analysis of the human glucocerebrosidase genes.  
 A:Reference number: I52980; MUID:88195776; PMID:3355914  
 A:Accession: I52980  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-11 <RES>  
 A:Cross-References: GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:G183024  
 A:Accession: I65971  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-11 <RE2>

Query Match 25.9%; Score 21; DB 2; Length 11;  
 Best Local Similarity 44.4%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MKFPPEQ 12  
 DB 1 MEFSFVRB 9

RESULT 39  
 C39109  
 hypothetical 1.2K protein - hepatitis C virus  
 N:Alternate names: hypothetical protein 3  
 C:Species: hepatitis C virus  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C:Accession: C39109; J01586  
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
 A:Reference number: A39109; MUID:91156678; PMID:1705704  
 A:Accession: C39109

A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <HAN>  
 A:Cross-references: GB:MS8406  
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992  
 A:Title: Cloning and sequencing of the structural region and expression of putative core  
 A:Reference number: JQ1584; MUID:92300349; PMID:1318944  
 A:Accession: JQ1586  
 A:Molecule type: genomic RNA  
 A:Residues: 1-12 <KUM>  
 A:Experimental source: strain U.K.

Query Match 25.9%; Score 21; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred.No. 2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPOE 12  
 |||:  
 Db 8 PPOD 11

## RESULT 40

PH1567  
 cerebrin 28 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004  
 C:Accession: PH1567  
 R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
 J. Neurochem. 61, 533-540, 1993  
 A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance  
 A:Reference number: PH1566; MUID:93329419; PMID:8336140  
 A:Accession: PH1567  
 A:Molecule type: protein  
 A:Residues: 1-12 <LEO>  
 A:Cross-references: UNIPROT:P41222

Query Match 25.9%; Score 21; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred.No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PPOETV 14  
 |||:  
 Db 2 PPOQVS 8

Search completed: June 7, 2005, 23:20:42  
 Job time : 14.9091 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-7  
Perfect score: 81  
Sequence: 1 VLEMKPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	ID	Description
1	33	40.7	15 1 PRP MYCBO	P80149 mycobacteri
2	32	39.5	15 2 O9TR14	O9TR14 bos taurus
3	31	38.3	15 2 O6LBP7	O6LBP7 glycine max
4	31	38.3	17 2 O49225	O49225 glycine max
5	31	38.3	17 2 O41400	O41400 seebania ro
6	30	37.0	15 2 P82439	P82439 nicotiana t
7	29	35.8	15 2 O7M1V1	O7M1V1 oryza sativ
8	28	34.6	10 1 TMOR AEADAE	P19425 aedes aegy
9	28	34.6	17 2 O9TR22	O9TR22 bos taurus
10	28	34.6	17 2 O7M1I3	O7M1I3 phaseolus v
11	27	33.3	9 2 O6SP94	O6SP94 chlamydomon
12	27	33.3	13 2 O7LZ51	O7LZ51 phylomedon
13	27	33.3	16 1 IBP4 PIG	P24854 sus scrofa
14	26	32.1	12 2 O9BZ49	O9BZ49 homo sapien
15	26	32.1	14 2 O7M3M4	O7M3M4 plaaster oc
16	26	32.1	16 2 O7M137	O7M137 unidentified
17	25	30.9	9 2 O9UC19	O9UC19 homo sapien
18	25	30.9	9 2 O7M2M9	O7M2M9 bos taurus
19	25	30.9	17 2 O9PRU7	O9PRU7 gallus galli
20	25	30.9	18 2 O6A417	O6A417 archangiopt
21	24	29.6	10 2 O8TV66	O8TV66 polymomaviru
22	24	29.6	10 2 O8TV68	O8TV68 polymomaviru
23	24	29.6	10 2 O8TV70	O8TV70 polymomaviru
24	24	29.6	10 2 O8TV72	O8TV72 polymomaviru
25	24	29.6	10 2 O8TV74	O8TV74 polymomaviru
26	24	29.6	10 2 O8TV76	O8TV76 polymomaviru
27	24	29.6	10 2 O8TV80	O8TV80 polymomaviru
28	24	29.6	10 2 O8TV82	O8TV82 polymomaviru
29	24	29.6	10 2 O9Q0V7	O9Q0V7 polymomaviru
30	24	29.6	10 2 O9Q0V9	O9Q0V9 polymomaviru
31	24	29.6	10 2 O9Q0W1	O9Q0W1 polymomaviru

32	24	29.6	10 2 O9Q0W3	O9Q0W3 polymomaviru
33	24	29.6	10 2 O9Q0W5	O9Q0W5 polymomaviru
34	24	29.6	10 2 O9Q0W7	O9Q0W7 polymomaviru
35	24	29.6	10 2 O9Q0W9	O9Q0W9 polymomaviru
36	24	29.6	10 2 O9Q0X1	O9Q0X1 polymomaviru
37	24	29.6	10 2 O9Q0X3	O9Q0X3 polymomaviru
38	24	29.6	10 2 O9Q0X5	O9Q0X5 polymomaviru
39	24	29.6	10 2 O9Q0X9	O9Q0X9 polymomaviru
40	24	29.6	11 1 BPP3 BOTIN	P30423 boehrops in
41	24	29.6	11 1 BPP4 BOTIN	P30424 boehrops in
42	24	29.6	13 2 O9UDC6	O9UDC6 homo sapien
43	24	29.6	14 1 TY13_BOWVA	P84215 bombina var
44	24	29.6	15 2 O9BX4	O9BX4 homo sapien
45	24	29.6	15 2 O6LCH6	O6LCH6 mus musculu
46	24	29.6	17 2 O9UDD6	O9UDD6 homo sapien
47	24	29.6	17 2 O6PUY4	O6PUY4 hepatitis c
48	24	29.6	17 2 O6PUY5	O6PUY5 hepatitis c
49	24	29.6	17 2 O6PUY8	O6PUY8 hepatitis c
50	24	29.6	17 2 O6PUZ0	O6PUZ0 hepatitis c
51	24	29.6	17 2 O6PUZ1	O6PUZ1 hepatitis c
52	23	28.4	9 2 O99193	O99193 pseudomonas
53	23	28.4	10 1 Q2OB_COMTE	P80465 comamonas t
54	23	28.4	13 1 TY13_PHYRO	P04096 phylomedon
55	23	28.4	17 1 RAYE_RAMES	P83663 rana esculie
56	23	28.4	17 2 O9R4T1	O9R4T1 rhodobacter
57	23	28.4	17 2 O6PUY7	O6PUY7 hepatitis c
58	23	28.4	18 1 CPAX_BOVIN	P22779 bos taurus
59	23	28.4	18 2 O8NFB4	O8NFB4 homo sapien
60	23	28.4	18 2 O9H1I3	O9H1I3 homo sapien
61	23	27.2	12 1 PIFI_SARBU	P83349 sarcophaga
62	22	27.2	12 1 HS9A_RAT	P82995 rattus norv
63	22	27.2	13 2 O817B1	O817B1 hepatitis c
64	22	27.2	15 2 O9TRA6	O9TRA6 bos taurus
65	22	27.2	15 2 O9S8N8	O9S8N8 hordium vul
66	22	27.2	15 2 O9S929	O9S929 glycine max
67	22	27.2	16 1 IEC_DELRB	P83511 delonix reg
68	22	27.2	16 2 O6ZZ04	O6ZZ04 lychnis cha
69	22	27.2	16 2 O6ZZ06	O6ZZ06 atocion arm
70	22	27.2	16 2 O6ZZ07	O6ZZ07 agrostema
71	22	27.2	16 2 O6ZZ08	O6ZZ08 silene ajan
72	22	27.2	16 2 O6ZZ10	O6ZZ10 lychnis aby
73	22	27.2	16 2 O6ZZ11	O6ZZ11 silene frut
74	22	27.2	16 2 O6ZZ13	O6ZZ13 silene berg
75	22	27.2	16 2 O6ZZ15	O6ZZ15 silene scha
76	22	27.2	16 2 O6ZZ17	O6ZZ17 silene bac
77	22	27.2	16 2 O6ZZ19	O6ZZ19 silene acan
78	22	27.2	16 2 O6ZZ20	O6ZZ20 silene coel
79	22	27.2	16 2 O6ZZ22	O6ZZ22 lychnis flo
80	22	27.2	16 2 O9PRU6	O9PRU6 gallus galli
81	22	27.2	17 1 APID_BOMPA	P81464 bombus pasc
82	22	27.2	17 2 O6ZZ24	O6ZZ24 silene bac
83	22	27.2	17 2 O9ULAV	O9ULAV mus musculu
84	22	27.2	18 2 O9UB42	O9UB42 homo sapien
85	22	27.2	18 2 O9UB99	O9UB99 mus musculu
86	22	27.2	18 2 O84129	O84129 influenza a
87	22	27.2	18 2 O6WTX0	O6WTX0 eleutheroda
88	22	27.2	18 2 O6WTZ8	O6WTZ8 eleutheroda
89	22	27.2	18 2 O6WU54	O6WU54 eleutheroda
90	22	27.2	18 2 O6WU67	O6WU67 eleutheroda
91	21	25.9	10 1 URE3_MORWO	P17339 morganella
92	21	25.9	11 2 O6PK01	O6PK01 homo sapien
93	21	25.9	11 2 O9C057	O9C057 homo sapien
94	21	25.9	11 2 P82436	P82436 nicotiana t
95	21	25.9	12 1 OBO2_CONAC	P83708 c dihydroli
96	21	25.9	13 2 O7M3T0	O7M3T0 zea mays (m
97	21	25.9	13 2 O7M3T0	O7M3T0 dictyosteli
98	21	25.9	15 1 SODM_STRGR	P80733 streptomyce
99	21	25.9	15 2 O9TR45	O9TR45 bos taurus
100	21	25.9	15 2 O6WFA4	O6WFA4 sturnus vul

## ALIGNMENTS

RESULT 1  
PRP MYCBO STANDARD; PRT; 15 AA.  
AC P80149;  
DT 01-JUN-1993 (Rel. 26, Created)  
DT 01-JUN-1993 (Rel. 26, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Proline-rich protein (Fragment).  
OS Mycobacterium bovis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=BCG / Paris 1173 P2;  
RX MEDLINE=93281750; PubMed=8506381;  
RA Roman F., Augier J., Pescher P., Marchal G.A.;  
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-  
RT type hypersensitivity reactions only in guinea pigs immunized with  
RT living mycobacteria."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MISCELLANEOUS: Immunodominant for delayed-type hypersensitivity  
CC reactions in guinea pigs.  
KW Direct protein sequencing.  
FT NON TER  
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 40.7%; Score 33; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
DB 7 PPPPQ 11

RESULT 2  
Q9TR14 PRELIMINARY; PRT; 15 AA.  
AC Q9TR14;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Tropomyosin-T homolog/ptoteolysis CONDITIONING INDICATOR peptide  
DE (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96187584; PubMed=8611748;  
RA Nakai Y., Nishimura T., Shinizu M., Arai S.;  
RT "Effects of freezing on the proteolysis of beef during storage at 4  
RT degrees C."  
RU Biocci Biotechnol. Biochem. 59:2255-2258(1995).  
SQ SEQUENCE 15 AA; 1597 MW; C98A5B4A79E4777 CRC64;

Query Match 39.5%; Score 32; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPPQ 12  
DB 2 PPPPQ 7

RESULT 3  
Q6LBP7 PRELIMINARY; PRT; 15 AA.

AC Q6LBP7;  
DT 05-JUN-2004 (TrEMBLrel. 27, Created)  
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
DE Glycine B(1b) subunit (15 AA) (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eustosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90332420; PubMed=2377465;  
RA Kitamura Y., Arahira M., Itoh Y., Fukazawa C.;  
RT "The complete nucleotide sequence of soybean glycinin A2b1a gene  
RT spanning to another glycinin gene AlaB1d."  
RL Nucleic Acids Res. 18:4245-4245(1990).  
DR EMBL; X53404; CAA37479.1; -.  
FT NON TER  
SQ SEQUENCE 15 AA; 1698 MW; 68D29896D30C431C CRC64;

Query Match 38.3%; Score 31; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 6.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFPFPQ 13  
DB 1 KFLVPPQ 9

RESULT 4  
O49225 PRELIMINARY; PRT; 17 AA.  
AC O49225;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hydroxyproline-rich glycoprotein (Fragment).  
GN Name=hrgp;  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eustosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RX MEDLINE=94211912; PubMed=8159793; DOI=10.1104/pp.104.2.793;  
RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;  
RT "Isolation and characterization of three soybean extensin cDNAs."  
RL Plant Physiol. 104:793-796(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Roots;  
RA Mahalingam R., Knap H.T.;  
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047052; AAC03558.1; -.  
FT NON TER  
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 38.3%; Score 31; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 7.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFPFPQ 10  
DB 9 KSPFPQ 14

RESULT 5  
Q41400 PRELIMINARY; PRT; 17 AA.  
AC Q41400;  
AC Q41400;

```

DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Goommachitig S., Valerio-Lepliniec M., Szczylowski K., Van Montagu M.,
RA Holsters M. De Brulin F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Azorhizobium caulinodans infection.";
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL, 248673; CAA8592.1; -.
DR PIR, S57991; S57991.
FT NON TER
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match
Best Local Similarity 38.3%; Score 31; DB 2; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KPPPP 10
Db 8 KSPPP 13

RESULT 6
P82439 PRELIMINARY; PRT; 15 AA.
ID P82439;
AC P82439;
DT 01-JUN-2000 (TREMblrel. 14, Created)
DT 01-JUN-2000 (TREMblrel. 14, last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE 200 Kda cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO: GO:0005618; C:cell wall; IEA.
KM Cell wall; Hydroxylation.
FT MOD RES
FT NON TER
SQ SEQUENCE 15 AA; 1870 MW; 3E1B05A20A3C5681 CRC64;

Query Match
Best Local Similarity 37.0%; Score 30; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPE 12
Db 7 PPPPK 12

RESULT 7
Q7M1V1 PRELIMINARY; PRT; 15 AA.

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AC Q7M1V1;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE Light harvesting complex chain III/b, photosystem I (fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Uchiyama Y., Tsugita A.;
RL Submitted (JUN-1991) to the PIR data bank.
DR PIR, PT0037; PT0037.
DR Gramene; Q7M1V1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1441 MW; 3D9222273333672 CRC64;

Query Match
Best Local Similarity 35.8%; Score 29; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EKKPPPP 10
Db 4 EAAAPPP 11

RESULT 8
TMOF_AEDAE STANDARD; PRT; 10 AA.
ID TMOF_AEDAE
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
RT enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
CC and drops at 56 hrs.
DR PIR, A36454; A36454.
KM Direct protein sequencing; Hormone.
FT DOMAIN
FT VARIANT
FT VARIAT
SQ SEQUENCE 10 AA; 1047 MW; 236D0A77777776DC7 CRC64;

Query Match
Best Local Similarity 34.6%; Score 28; DB 1; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 PPP 10  
|||  
Db 5 PPP 8

## RESULT 9

Q9TR22 PRELIMINARY; PRT; 17 AA.  
ID O9TR22  
AC O9TR22  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE NONAMELOGENIN glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP MEDLINE=96126798; PubMed=8564801;  
RA Punzi J.S., DenBesten P.K.;  
RT "Purification of nonamelogenin proteins from bovine secretory enamel."  
RL Calif. Tissue Int. 57:379-384(1995).  
SQ SEQUENCE 17 AA; 2032 MW; 9D811C8228B615D CRC64;

Query Match 34.6%; Score 28; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 10  
|||  
Db 8 PPP 11

RESULT 10  
Q7MI13 PRELIMINARY; PRT; 17 AA.  
ID O7MI13  
AC O7MI13  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hydroxyproline-rich cell wall glycoprotein, 230K (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP MEDLINE=96011753; PubMed=7548825;  
RA Wojtaszek P., Trethowan J., Bolwell G.P.;  
RT "Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.)."  
RL Plant Mol. Biol. 28:1075-1087(1995).  
DR PIR: S59481; S59481.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 1929 MW; 7C0525B0179CE555 CRC64;

Query Match 34.6%; Score 28; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 10  
|||  
Db 8 PPP 11

## RESULT 11

Q6SP94 PRELIMINARY; PRT; 9 AA.  
ID Q6SP94  
AC Q6SP94  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE PF26 (Fragment).  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CC-2290;  
RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;  
RA Kathir P., Lavoie M., Brazelton W.J., Haas N.A., Lefebvre P.A., Silflow C.D.;  
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome."  
RL Eukaryotic Cell 2:362-379(2003).  
DR EMBL: AY454155; AAR20844.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;

Query Match 33.3%; Score 27; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPP 12  
|||  
Db 1 PAPPE 6

RESULT 12  
Q7LZ51 PRELIMINARY; PRT; 13 AA.  
ID Q7LZ51  
AC Q7LZ51  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Trypophyllin-related peptide.  
OS Phyllomedusa bicolor (Two-colored leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae.  
OX NCBI\_TaxID=8393;  
RN [1]  
RP MEDLINE=92339502; PubMed=1633846; DOI=10.1016/0014-5793(92)80427-I;  
RA Mignogna G., Severini C., Simmaco M., Negri L., Falconieri Erapamer G., Kreil G., Barra D.;  
RT "Identification and characterization of two dermorphins from skin extracts of the Amazonian frog Phyllomedusa bicolor."  
RL FEBS Lett. 307:151-154(1992).  
DR PIR: S21152; S21152.  
SQ SEQUENCE 13 AA; 1575 MW; 094C33A21BC5777B CRC64;

Query Match 33.3%; Score 27; DB 2; Length 13;  
Best Local Similarity 62.5%; Pred. No. 2e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EMKEPPPP 10  
|||  
Db 2 EKPFPFP 9

RESULT 13  
IBP4\_PIG STANDARD; PRT; 16 AA.  
ID IBP4\_PIG  
AC P24854;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4) (IGF-



DE binding protein 4) (Fragment).  
 GN Name=IGFBP4;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92109718; PubMed=1722398;  
 RA Coleman M.E., Pan Y.-C.E., Ehterton T.D.;  
 RT "Identification and NH<sub>2</sub>-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum."  
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
 CC -1- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Contains 1 IGFBP domain.  
 CC PIR: JH0517; JH0517.  
 DR InterPro: IPR000867; Insl\_gro\_fac\_pr.  
 DR InterPro: IPR000716; Thyroglobulin\_1.  
 DR PROSITE: PS00222; IGF\_BINDING; PARTIAL.  
 DR PROSITE: PS00484; THYROGLOBULIN\_1; PARTIAL.  
 KW Direct protein sequencing; Growth factor binding.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1799 MW; 409888400965582 CRC64;

Query Match 33.3%; Score 27; DB 1; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 7 PPPPQE 12  
 Db 7 PPPSEB 12

RESULT 14  
 O9BZ49 PRELIMINARY; PRT; 12 AA.  
 AC O9BZ49;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Glycophorin C (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Patel S.S., Mehloctra R.K., Kastens W., Ngone C.S., Kazura J.W., Zimmerman P.A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF342984; AAK01459.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;  
 Query Match 32.1%; Score 26; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PPPQ 11  
 Db 9 PPPQ 12

RESULT 15  
 O7M3M4 PRELIMINARY; PRT; 14 AA.  
 AC O7M3M4;  
 DT 07M3M4;

DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Protein kinase (EC 2.7.1.37).  
 OS Pisaster ochraceus (Sea star).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;  
 OC Asteroidea; Forcipulatacea; Forcipulataida; Asteriidae; Pleaster.  
 OX NCBI\_TaxID=7612;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91032186; PubMed=1699809; DOI=10.1016/0014-5793(90)81090-B;  
 RA Sanghera J.S., Abercrombie R., Morrison H.D., Bures E.J., Pelech S.L.;  
 RT "Identification of the sites in myelin basic protein that are phosphorylated by meiosis-activated protein kinase p44 (mpk).";  
 RL FEBS Lett. 273:223-226(1990).  
 DR PIR: S12904; S12904.  
 DR GO: GO:0004672; P:protein kinase activity; IEA.  
 DR GO: GO:0004672; P:protein kinase activity; IEA.  
 SQ SEQUENCE 14 AA; 1492 MW; 90E7368373068171 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 36.4%; Pred. No. 3e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 VLEMKPPPPQ 11  
 Db 2 IVTPRTPPPSQ 12

RESULT 16  
 O7M137 PRELIMINARY; PRT; 16 AA.  
 AC O7M137;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Superoxide dismutase (EC 1.15.1.1) (Fragment).  
 OS unidentified bacterium.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=2338;  
 RN [1]  
 RP SEQUENCE.  
 RA Binette J.P., Binette M.B.;  
 RL Submitted (OCT-1996) to the PIR data bank.  
 CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (by similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.  
 DR PIR: B58503; B58503.  
 DR GO: GO:0046872; F:metal ion binding; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0004784; F:superoxide dismutase activity; IEA.  
 DR GO: GO:0006801; P:superoxide metabolism; IEA.  
 DR InterPro: IPR001189; SODismutase.  
 DR Pfam: PF00081; Sod\_Fe\_N; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 16  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1828 MW; 12DE78949AC43609 CRC64;  
 Query Match 32.1%; Score 26; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 3.4e+03;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 LEMKPPPPQ 12  
 Db 1 MEHTLPPLPYE 11

RESULT 17  
 O9UCT9 PRELIMINARY; PRT; 18 AA.  
 AC O9UCT9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)  
 DE PRG-PROLINE-rich glycoprotein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373355; PubMed=1894623;  
 RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leflier H.,  
 RA Fisher S.U.;  
 RT "Structure and bacterial receptor activity of a human salivary  
 RT proline-rich glycoprotein."  
 RL J. Biol. Chem. 266:17358-17368(1991).  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.  
 DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 1780 MW; 961F6PB0A83D2E40 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPOQ 11  
 ||||  
 DB 14 PPOQ 17

RESULT 18  
 O7M2M9 PRELIMINARY; PRT; 9 AA.  
 AC O7M2M9;  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
 DE Collagen alpha 2(VI) chain (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83209648; PubMed=6852033;  
 RA Jander R., Rautenberg U., Gianvillie R.W.;  
 RT "Further characterization of the three polypeptide chains of bovine  
 RT and human short-chain collagen (intima collagen).";  
 RL Eur. J. Biochem. 133:39-46(1983).  
 DR PIR: S26508; S26508.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 876 MW; 681A67776867605B CRC64;

Query Match 30.9%; Score 25; DB 2; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LEMKEPPPP 10  
 ||: |||  
 DB 1 LEIPGPFGP 9

RESULT 19  
 O9PRU7 PRELIMINARY; PRT; 17 AA.  
 AC O9PRU7;  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO

DE (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95105151; PubMed=7806494;  
 RA Sakai R., Iwamoto A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
 RA Yazaki Y., Hirai H.;  
 RT "Characterization, partial purification, and peptide sequencing of  
 RT p130, the main phosphoprotein associated with v-Crk oncoprotein."  
 RL J. Biol. Chem. 269:32740-32746(1994).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 30.9%; Score 25; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PPOQ 11  
 ||||  
 DB 13 PPOQ 17

RESULT 20  
 O6A417 PRELIMINARY; PRT; 18 AA.  
 AC O6A417;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)  
 DE Ribulose biphosphate carboxylase large subunit (EC 4.1.1.39)  
 DE (Fragment).  
 GN Name=rdcl;  
 OS Archangiopteris somai.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Monilliformes; Filicophyta; Marattiopsida; Marattiales;  
 OC Marattiaceae; Archangiopteris.  
 OX NCBI\_TaxID=203826;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chiang T., Chiang Y., Chou C., Cheng Y., Chiou W.;  
 RT "Phylogeography and conservation of Archangiopteris somai and A. itoi  
 RT (Marattiaceae, Pteridophyta) based on nucleotide variation of cpDNA  
 RT atps-ribL intergenic spacer."  
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Chiang Y.C.;  
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ505216; CAD43797.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0016829; F:lyase activity; IEA.  
 DR GO; GO:0016984; F:ribulose-biphosphate carboxylase activity; IEA.  
 KW Chloroplast; lyase.  
 FT NON\_TER 18  
 FT NON\_TER 18  
 SQ SEQUENCE 18 AA; 1924 MW; AAEC25AA8268869 CRC64;

Query Match 30.9%; Score 25; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 5.4e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 8 PPOETVT 15  
 |||||  
 DB 2 PPOETVT 9

RESULT 21  
 O8UV66

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ID Q8JV66 PRELIMINARY; PRT; 10 AA.
AC Q8JV66;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
ON NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 22
Q8JV68 PRELIMINARY; PRT; 10 AA.
ID Q8JV68;
AC Q8JV68;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
ON NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 23
Q8JV70 PRELIMINARY; PRT; 10 AA.
ID Q8JV70;
AC Q8JV70;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.

```

```

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
ON NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 24
Q8JV72 PRELIMINARY; PRT; 10 AA.
ID Q8JV72;
AC Q8JV72;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
ON NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304386; AAM97802.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KPPP 9
DB 5 KTRPP 9

RESULT 25
Q8JV74 PRELIMINARY; PRT; 10 AA.
ID Q8JV74;
AC Q8JV74;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
ON NCBI_TaxId=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465052; PubMed=11581397;
DOI=10.1128/JVI.75.21.10290-10299.2001;
RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL, AF303948; AAM97800.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

## RESULT 26

O8JV76 PRELIMINARY; PRT; 10 AA.  
ID O8JV76  
AC O8JV76;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21465052; PubMed=11581397;  
RX DOI=10.1128/JVI.75.21.10290-10299.2001;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL, AF303947; AAM97798.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

## RESULT 27

O8JV80 PRELIMINARY; PRT; 10 AA.  
ID O8JV80  
AC O8JV80;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21465052; PubMed=11581397;  
RX DOI=10.1128/JVI.75.21.10290-10299.2001;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL, AF303945; AAM97794.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

## RESULT 28

O8JV82 PRELIMINARY; PRT; 10 AA.  
ID O8JV82  
AC O8JV82;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21465052; PubMed=11581397;  
RX DOI=10.1128/JVI.75.21.10290-10299.2001;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL, AF303944; AAM97792.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

## RESULT 29

O9QOV7 PRELIMINARY; PRT; 10 AA.  
ID O9QOV7  
AC O9QOV7;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20087544; PubMed=10618230;  
RX Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage."  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL, AF119356; AAF24118.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

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RESULT 30
O9Q0V9 PRELIMINARY; PRT; 10 AA.
ID O9Q0V9
AC O9Q0V9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; deDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA BoFill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 31
O9Q0W1 PRELIMINARY; PRT; 10 AA.
ID O9Q0W1
AC O9Q0W1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; deDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA BoFill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 32
O9Q0W3 PRELIMINARY; PRT; 10 AA.
ID O9Q0W3
AC O9Q0W3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; deDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

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OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA BoFill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 33
O9Q0W5 PRELIMINARY; PRT; 10 AA.
ID O9Q0W5
AC O9Q0W5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; deDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA BoFill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119352; AAF24110.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KPPP 9
Db 5 KPPP 9

RESULT 34
O9Q0W7 PRELIMINARY; PRT; 10 AA.
ID O9Q0W7
AC O9Q0W7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; deDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087544; PubMed=10618230;
RA BoFill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

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Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KRPP 9  
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|  
|  
|  
Db 5 KTRPP 9

RESULT 35  
Q9Q0W9 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20087544; PubMed=10618230;  
RA BoFill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119350; AAF24106.1; --.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KRPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

RESULT 36  
Q9Q0X1 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20087544; PubMed=10618230;  
RA BoFill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119349; AAF24104.1; --.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KRPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

RESULT 37

Q9Q0X3 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20087544; PubMed=10618230;  
RA BoFill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119348; AAF24102.1; --.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KRPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

RESULT 38  
Q9Q0X5 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X5;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20087544; PubMed=10618230;  
RA BoFill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119347; AAF24100.1; --.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A9771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KRPP 9  
|  
|  
|  
|  
Db 5 KTRPP 9

RESULT 39  
Q9Q0X9 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Boffill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RL populations by studying their presence in urban sewage."; Appl. Environ. Microbiol. 66:238-245(2000).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RA Boffill-Mas S., Pina S., Girones R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF119345; AAF24096.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 4e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KPPPP 9  
 | | | |  
 Db 5 KTRPP 9

RESULT 40  
 BPP3\_BOTIN  
 ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30423;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintrá A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."; J. Protein Chem. 9:221-227(1990).  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -I- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it. It acts  
 CC as an indirect hypotensive agent.  
 DR PIR: C37196; C37196.  
 KM Direct protein sequencing; Hypotensive agent;  
 KM Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1  
 FT MOD\_RES 1  
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C741777 CRC64;

Query Match 29.6%; Score 24; DB 1; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PPPPQ 11  
 | | | |  
 Db 4 PPRPQ 8

Search completed: June 7, 2005, 23:19:03  
 Job time : 67 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 22:52:07 ; Search time 80.7273 Seconds  
(without alignments)  
71.864 Million cell updates/sec

Title: US-10-691-157-8  
Perfect score: 82  
Sequence: 1 LKPFKLVKVEFPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 679757

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	15	4	AA72507 Colostrin
2	82	100.0	15	4	AA59313 Ewe colos
3	82	100.0	15	4	AA72253 Colostrin
4	82	100.0	15	4	AA72539 Colostrin
5	82	100.0	15	5	AA014584 Neural ce
6	82	100.0	15	5	AAW51043 Colostrin
7	82	100.0	15	5	AAE20235 Colostrin
8	82	100.0	15	8	ADN60302 Constitue
9	82	100.0	15	8	AD574389 Ewe col
10	82	100.0	16	4	AA59344 Ewe colos
11	38	46.3	14	7	ADP14848 T cell st
12	38	46.3	14	7	ADP14527 Eptlope o
13	38	46.3	14	7	ADP14511 Gluten-de
14	38	46.3	14	7	ADP14519 Eptlope o
15	38	46.3	14	7	ADP14535 Eptlope o
16	38	46.3	14	7	ADP14531 Eptlope o
17	37.5	45.7	14	8	ADH14824 Gliadin r
18	37.5	45.7	14	2	AAW48879 Cyclic pe
19	37	45.1	18	4	AAW48904 Cyclic pe
20	37	45.1	18	4	AAW48904 Cyclic pe
21	37	45.1	18	4	AAW48904 Cyclic pe
22	37	45.1	18	4	AAW48904 Cyclic pe
23	37	45.1	18	4	AAW48904 Cyclic pe
24	37	45.1	18	4	AAW48904 Cyclic pe
25	37	45.1	18	4	AAW48904 Cyclic pe

26	36	43.9	18	4	AA72520 Colostrin
27	36	43.9	18	4	AA59330 Ewe colos
28	36	43.9	18	4	AA72267 Colostrin
29	36	43.9	18	4	AA72552 Colostrin
30	36	43.9	18	5	AA014598 Neural ce
31	36	43.9	18	5	AAW51056 Colostrin
32	36	43.9	18	5	AAE20249 Colostrin
33	36	43.9	18	8	ADN60316 Constitue
34	36	43.9	18	8	AD574406 Ovine col
35	35	42.7	16	8	ADH14831 Gliadin r
36	35	42.7	18	8	ADH14841 Gliadin r
37	34.5	42.1	11	4	AAE07188 Colostrin
38	34.5	42.1	11	4	AAE07198 Colostrin
39	34.5	42.1	14	2	AAW48877 Cyclic pe
40	34.5	42.1	14	2	AAW48878 Cyclic pe
41	34	41.5	10	4	AAE07187 Colostrin
42	34	41.5	15	4	AAW72504 Colostrin
43	34	41.5	15	4	AAW59322 Ewe colos
44	34	41.5	15	4	AAW72250 Colostrin
45	34	41.5	15	4	AAW72536 Colostrin
46	34	41.5	15	5	AA014581 Neural ce
47	34	41.5	15	5	AAW51040 Colostrin
48	34	41.5	15	5	AAE20232 Colostrin
49	34	41.5	15	8	ADN60299 Constitue
50	34	41.5	15	8	AD574398 Ovine col
51	34	41.5	16	4	AAW59352 Ewe colos
52	34	41.5	17	8	ADH14827 Gliadin r
53	34	41.5	18	8	ADH14832 Gliadin r
54	33.5	40.9	14	2	AAW48905 Cyclic pe
55	33	40.2	14	2	AAW58339 Hypotensi
56	33	40.2	14	7	ADP14518 Eptlope o
57	33	40.2	14	7	ADP14510 Gluten-de
58	33	40.2	14	7	ADP14534 Eptlope o
59	33	40.2	14	7	ADP14847 Eptlope o
60	33	40.2	14	7	ADP14526 Eptlope o
61	33	40.2	14	8	ADG37024 Bovine ca
62	33	40.2	17	8	ADH14823 Gliadin r
63	33	40.2	18	8	ADH14821 Gliadin r
64	32.5	39.6	14	2	AAW48906 Cyclic pe
65	32	39.0	9	5	ABU01855 158P1D7 r
66	32	39.0	9	5	ABU01751 158P1D7 r
67	32	39.0	9	5	ABU01996 158P1D7 r
68	32	39.0	10	5	ABU01907 158P1D7 r
69	32	39.0	10	5	ABU01366 158P1D7 r
70	32	39.0	13	7	ADW75628 Potential
71	32	39.0	14	7	ADP14852 T cell st
72	32	39.0	14	7	ADP14531 Eptlope o
73	32	39.0	14	7	ADP14523 Eptlope o
74	32	39.0	14	7	ADP14539 Eptlope o
75	32	39.0	14	7	ADP14515 Gluten-de
76	32	39.0	16	2	AAW38528 S. pneumo
77	32	39.0	16	5	ABW77148 C1a5ical
78	32	39.0	16	6	ABP82437 G protein
79	32	39.0	17	6	AAE34141 T-cell st
80	31.5	38.4	12	2	AAW48876 Cyclic pe
81	31.5	38.4	14	2	AAW48876 Cyclic pe
82	31.5	38.4	14	5	ABW81248 GS14K4 an
83	31.5	38.4	17	4	AAU01835 Wheat Gli
84	31.5	38.4	17	8	ADH14595 Gliadin r
85	31.5	38.4	17	8	ADH16198 Gliadin r
86	31.5	38.4	17	8	ADH14663 Gliadin r
87	31	37.8	13	4	AAW74265 Exemplyar
88	31	37.8	13	4	AAW80871 Angiostac
89	31	37.8	13	5	ABG97548 Antiangio
90	31	37.8	14	7	ADP14522 Eptlope o
91	31	37.8	14	7	ADP14851 T cell st
92	31	37.8	14	7	ADP14538 Eptlope o
93	31	37.8	14	7	ADP14514 Gluten-de
94	31	37.8	14	7	ADP14530 Eptlope o
95	30.5	37.2	15	8	ADP91447 Immunogen
96	30.5	37.2	15	8	AAW93461 GST-P13K
97	30.5	37.2	17	4	AAU01804 Wheat A-g
98	30.5	37.2	17	4	AAU01816 Wheat Gli

99 30.5 37.2 17 4 AAU01798  
100 30.5 37.2 17 4 AAU01803

AAU01798 Wheat A-9  
AAU01803 Wheat A-9

## ALIGNMENTS

## RESULT 1

AA072507  
ID AAB72507 strand; peptide; 15 AA.

AC AAB72507;

DT 09-MAY-2001 (first entry)

DE Colostriin peptide #8.

KW Dermatological; oxidative stress regulator; colostriin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022665.

PR 17-AUG-1999; 99US-0149310P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR MPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostriin, its constituent peptide, analog or their combinations.

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostriin, or its constituent peptide (e.g. the present peptide), CC to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient

CC Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.2e-07; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKFPFKLKVPPFP 15  
1 LKFPFKLKVPPFP 15

Db 1 LKFPFKLKVPPFP 15

## RESULT 2

AA059313  
ID AAB59313 strand; peptide; 15 AA.

AC AAB59313;

DT 21-MAR-2001 (first entry)

DE Ewe colostriin peptide fragment A-4.

KW Sheep; colostriin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB002128.

PR 02-JUN-1999; 99GB-00012852.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR MPI; 2001-071058/08.

PT Peptides having an N-terminal amino acid sequence isolated from colostriin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.

PS Claim 7; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides found in ewe's colostriin. Colostriin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques

CC Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.2e-07; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKFPFKLKVPPFP 15  
1 LKFPFKLKVPPFP 15

Db 1 LKFPFKLKVPPFP 15

## RESULT 3

AA072253  
ID AAB72253 strand; peptide; 15 AA.

AC AAB72253;

DT 14-MAY-2001 (first entry)

DE Colostriin derived cytokine inducing peptide SEQ ID 8.

KW Colostriin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological disorder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.

OS Synthetic.

PN WO20011937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US022818.

PR 17-AUG-1999; 99US-0149311P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial, and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 PS  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 82; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKPPKLVKEVPPF 15  
 DB 1 LKPPKLVKEVPPF 15  
 RESULT 4  
 AAB72539  
 ID AAB72539 standard; peptide; 15 AA.  
 AC AAB72539;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #8.  
 XX  
 KW Neutroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 PT  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKPPKLVKEVPPF 15  
 DB 1 LKPPKLVKEVPPF 15  
 RESULT 5  
 AA014584  
 ID AA014584 standard; peptide; 15 AA.  
 AC AA014584;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX  
 DE Neural cell regulatory colostrinin peptide 8.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15 /note="Optional C-terminal amide"  
 FT  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022777.  
 XX  
 PR 17-AUG-2000; 2000WO-US022777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 82; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKPPKLVKEVPPF 15  
 DB 1 LKPPKLVKEVPPF 15  
 RESULT 6  
 AAM51043

ID	AA	AMS1043 standard; peptide; 15 AA.
XX	AC	AAMS1043;
XX	DT	30-MAY-2002 (first entry)
XX	DE	Colostrinin constituent peptide.
XX	KW	Colostrinin; colostrum; immunomodulator; cardiovascular;
XX	KW	blood cell regulator; cytokine inducer; human.
OS	XX	Homo sapiens.
XX	FH	Key Location/Qualifiers
FT	FT	Modified-site 15 /note= "optional C-terminal amidation"
XX	PN	WO200213849-A1.
XX	PD	21-FEB-2002.
XX	PP	17-AUG-2000; 2000WO-US022775.
XX	PR	17-AUG-2000; 2000WO-US022775.
XX	PA	(TEXA ) UNIV TEXAS SYSTEM.
XX	PA	(REGE-) REGEN THERAPEUTICS PLC.
PI	J	Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
DR	J	WPI; 2002-269150/31.
PT	PT	Modulation of blood cell proliferation in a patient involves use of blood
PT	PT	cell regulator selected from colostrinin, its constituent peptide and/or
PT	PT	analog.
XX	PS	Claim 1; Page 34; 5app; English.
XX	PS	The present sequence is that of a colostrinin constituent peptide that is
CC	CC	preferred for use as an immunological regulator and as a blood cell
CC	CC	regulator in claimed methods of the invention. Methods are claimed for:
CC	CC	inducing a cytokine in a cell by contact with an immunological regulator,
CC	CC	where the cell is present in a cell culture, a tissue, an organ or an
CC	CC	organism, and the cell is mammalian, including human; modulating an
CC	CC	immune response in a cell by contact with the immunological regulator
CC	CC	under conditions effective to induce a cytokine; modulating an immune
CC	CC	response in a patient by administering an immunological regulator under
CC	CC	conditions effective to induce a cytokine, where the immunological
CC	CC	regulator is administered topically or as part of a dietary supplement,
CC	CC	and where the immune response is specific or non specific, an interferon
CC	CC	response or an antibody response; modulating blood cell proliferation by
CC	CC	contacting blood cells with a blood cell regulator, where the blood cells
CC	CC	are present in a cell culture or an organism, are mammalian or human, and
CC	CC	where the blood cells are increased in number or differentiated; and a
CC	CC	method for modulating blood cell proliferation in a patent. A claimed
CC	CC	cytokine-inducing composition comprises a pharmaceutical carrier and an
CC	CC	active agent such as the present peptide. Cytokines induced by this
CC	CC	peptide in human leucocyte cultures include interferon-gamma, tumour
CC	CC	necrosis factor-alpha, interleukin-6 and interleukin-10
XX	XX	
SQ	XX	Sequence 15 AA;
QY	Query Match	100.0%; Score 82; DB 5; Length 15;
	Best Local Similarity	100.0%; Pred. No. 6.2e-07;
DB	Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0
	1 LKPFKLKVEVFPF 15	
	1 LKPFKLKVEVFPF 15	

RESULT 7  
AAE20235

ID		AAB20235 standard; peptide; 15 AA.
XX	AC	AAB20235;
XX	D7	18-JUN-2002 (first entry)
XX	DE	Colostrinin constituent peptide #8.
XX	KW	Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnereary.
OS	XX	Unidentified.
FH	Key	Location/Qualifiers
FT	Modified-site	15 /note= "Optionally C-terminal amide"
NN	M0200213850-A1.	
PD	21-FEB-2002.	
PX	17-AUG-2000; 2000WO-US022776.	
PR	17-AUG-2000; 2000WO-US022776.	
PA	(TEXA ) UNIV TEXAS SYSTEM.	
PI	Stanton GJ, Hughes TK, Boldogh I;	
DR	WPI; 2002-269151/31.	
PT	Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.	
PS	Claim 6; Page 25; Sipp; English.	
XX	The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, organ, or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/ after a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stres regulator is not present. The modulation of oxidative stress results in enhanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implanation, or scientific research. The present sequence is a colostrinin constituent peptide	
SQ	Sequence 15 AA;	
Query Match	100.0%; Score 82; DB 5; Length 15;	
Best Local Similarity	100.0%; Pred. No. 6.2e-07;	
Matches	15; Conservativity 0; Mismatches 0; Indels 0; Gaps 0,	
OY	1 LKPPPKLVKEVFPF 15	
DB	1 LKPPEKLVEVPFP 15	
ADN60302		
ADN60302		
ADN60302 standard; peptide; 15 AA.		

ID	ADN60302	standard; peptide; 15 AA.
XX		

AC ADN60302;  
XX  
XX 29-JUL-2004 (first entry)  
DE Constituent peptide of colostrinin SEQ ID NO:8.  
XX  
XX  
KW modulator; colostrinin; intracellular signaling molecule modulator;  
KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition;  
KW DNA damage; beta-amyloid; retinoic acid; cyclostatin; 4HNE inhibitor;  
KW 4HNE-protein adduct formation reduction;  
KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
KW c-Jun NH2-terminal kinase inhibition.  
XX  
XX Synthetic.  
XX  
XX WO2004037851-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033423.  
XX  
XX 22-OCT-2002; 2002US-0420369P.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX PA (BOLD/) BOLDG I.  
XX PA (STAN/) STANTON J G.  
XX PA (GEOR/) GEORGIADIS J A.  
XX PA (HUGH/) HUGHES T K.  
XX PA (KRUZ/) KRUZEL M.  
XX  
XX Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
XX WPI; 2004-365494/34.  
XX  
XX Use of colostrinin for e.g. modulating an intracellular signaling  
XX molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
XX cell, inhibiting apoptosis in a cell, or protecting against DNA damage in a  
XX cell.  
XX  
XX Claim 6; SEQ ID NO 8; 46pp; English.  
XX  
XX The present invention describes the use of a modulator selected from  
XX colostrinin, its constituent peptide, its active analogue, and a  
XX combination of these, for modulating an intracellular signaling molecule  
XX in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
XX inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
XX and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
XX The modulator has cyostatic activity, and can be used as a 4HNE  
XX inhibitor. The modulator is useful in the manufacture of a medicament for  
XX reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
XX glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
XX and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
XX Colostrinin, or its constituent peptide or active analogue is useful for  
XX inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
XX or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
XX The present sequence represents a synthetic constituent peptide of  
XX colostrinin, which can be used as a modulator in the present invention.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 100.0%; Score 82; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPFKLKVVEVPPF 15  
|||  
DB 1 LKPPFKLKVVEVPPF 15

RESULT 9  
ADS74389  
ID ADS74389 standard; peptide; 15 AA.  
XX

AC ADS74389;  
XX  
XX 16-DEC-2004 (first entry)  
XX  
XX Ovine colostrinin peptide.  
DE  
XX  
XX Colostrum; colostrinin; sheep; peptide purification.  
KW  
XX  
XX Ovis aries.  
XX  
XX WO2004081038-A1.  
XX  
XX 23-SEP-2004.  
XX  
XX 10-MAR-2004; 2004WO-GB001014.  
XX  
XX 11-MAR-2003; 2003GB-00005552.  
XX  
XX 08-MAR-2004; 2004GB-00005190.  
XX  
XX (REGB-) REGEN THERAPEUTICS PLC.  
XX  
XX Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
XX WPI; 2004-677519/66.  
XX  
XX Recovering peptides such as colostrinin from mammalian colostrum, by  
XX mixing colostrum with alcohol to form alcohol phase containing peptides  
XX and precipitate, separating alcohol phase from precipitate, and  
XX recovering alcohol phase.  
XX  
XX Disclosure; SEQ ID NO 4; 41pp; English.  
XX  
XX The present sequence is that of a peptide that can be recovered from  
XX ovine colostrum using the method of the invention. The invention  
XX provides a method for the recovery of peptides (especially colostrinin)  
XX from colostrum in substantially pure, biologically active form and in  
XX high yield. The method involves mixing the colostrum with an alcohol to  
XX form an alcohol phase containing the colostrinin and a precipitate  
XX containing higher molecular weight caseins and other proteins. Best  
XX results are obtained using methanol or ethanol of at least 80%, and  
XX preferably up to 100%, purity. The alcohol phase is then separated from  
XX the precipitate, and the colostrinin is separated from the alcohol,  
XX preferably by evaporation, to form a colostrinin-rich phase, which is  
XX recovered. A precipitation agent, such as ammonium sulfate, may be added  
XX either to the alcohol phase or, preferably, to the colostrinin-rich phase  
XX to induce precipitation of the colostrinin peptides. The method is  
XX generally applicable to the separation of peptides from fluids containing  
XX higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
XX acids.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 100.0%; Score 82; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPFKLKVVEVPPF 15  
|||  
DB 1 LKPPFKLKVVEVPPF 15

RESULT 10  
AAB59344  
ID AAB59344 standard; peptide; 16 AA.  
XX

XX AAB59344;  
XX

XX 21-MAR-2001 (first entry)  
XX

DE Ewe colostrinin peptide fragment derived sequence #4.  
XX  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX

XX Ovis sp.  
XX WO20075173-A2.  
XX 14-DEC-2000.  
XX 02-JUN-2000; 2000WO-GB002128.  
XX 02-JUN-1999; 99GB-00012852.  
XX (REG- ) REGEN THERAPEUTICS PLC.  
XX Georgiades JA;  
XX WPI; 2001-071058/08.  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
XX by amyloid plaques.  
XX Claim 8; Page 27; 63pp; English.  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
XX  
SQ Sequence 16 AA;  
Query Match 100.0%; Score 82; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKPPKLVKVEVPPF 15  
DB 2 LKPPKLVKVEVPPF 16  
RESULT 11  
ADFI4848  
ID ADFI4848 standard; peptide; 14 AA.  
XX ADFI4848;  
AC  
XX 12-FEB-2004 (first entry)  
DT  
XX  
DE T cell stimulatory pool-derived peptide 4.  
XX  
XX plant; deamidation; tissue transglutaminase; celiac disease; CD;  
KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
KW systemic lupus erythematosus; sjogren syndrome; diabetes;  
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
KW dermatological; antiinflammatory; T cell stimulatory pool.  
XX  
XX Unidentified.  
OS  
XX  
XX EPI332760-A1.  
PN  
XX  
XX 06-AUG-2003.  
PD  
XX  
XX 04-FEB-2002; 2002EP-00075456.  
PF  
XX  
XX 04-FEB-2002; 2002EP-00075456.  
PR  
XX  
XX (ZIER-) ACAD ZIEKENHUIS LEIDEN.  
PA  
XX  
XX WPI; 2003-647889/62.  
DR

XX New gluten peptides or epitopes prone to deamidation by tissue  
PT transglutaminase, useful for treating celiac disease or an autoimmune  
PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
PT erythematosus, or diabetes.  
XX  
XX Disclosure; Fig 2B; 143pp; English.  
XX  
XX The invention relates to a novel peptide or epitope which is prone to  
CC deamidation by tissue transglutaminase (tTG) and is a causative factor of  
CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as  
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
CC sjogren syndrome or diabetes. The peptide of the invention demonstrates  
CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,  
CC dermatological and antiinflammatory activities whilst pharmaceutical  
CC compositions comprising the peptides or epitopes may be useful for the  
CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
CC arthritis, multiple sclerosis, systemic lupus erythematosus, sjogren  
CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
CC preparation of therapeutic agents capable of eliminating a subset of  
CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
CC The current sequence is that of the T cell stimulatory pool-derived  
CC peptide of the invention.  
XX  
SQ Sequence 14 AA;  
Query Match 46.3%; Score 38; DB 7; Length 14;  
Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 3 PPKLVKLVKVEVPPF 15  
DB 1 PPKLVKLVKVEVPPF 13  
RESULT 12  
ADFI4527  
ID ADFI4527 standard; peptide; 14 AA.  
XX ADFI4527;  
AC  
XX  
XX 12-FEB-2004 (first entry)  
DT  
XX  
DE Epitope of gluten-derived tTG substrate peptide - SEQ ID 20.  
XX  
XX plant; deamidation; tissue transglutaminase; celiac disease; CD;  
KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
KW systemic lupus erythematosus; sjogren syndrome; diabetes;  
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
KW dermatological; antiinflammatory; substrate epitope.  
XX  
XX Unidentified.  
OS  
XX  
XX EPI332760-A1.  
PN  
XX  
XX 06-AUG-2003.  
PD  
XX  
XX 04-FEB-2002; 2002EP-00075456.  
PF  
XX  
XX 04-FEB-2002; 2002EP-00075456.  
PR  
XX  
XX (ZIER-) ACAD ZIEKENHUIS LEIDEN.  
PA  
XX  
XX WPI; 2003-647889/62.  
DR  
XX  
XX New gluten peptides or epitopes prone to deamidation by tissue  
PT transglutaminase, useful for treating celiac disease or an autoimmune  
PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
PT erythematosus, or diabetes.  
XX  
XX Claim 2; SEQ ID NO 20; 143pp; English.  
XX  
XX The invention relates to a novel peptide or epitope which is prone to  
CC

CC deamidation by tissue transglutaminase (tTG) and is a causative factor of  
CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as  
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates  
CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,  
CC dermatological and antiinflammatory activities whilst pharmaceutical  
CC compositions comprising the peptides or epitopes may be useful for the  
CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren  
CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
CC preparation of therapeutic agents capable of eliminating a subset of  
CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
CC The current sequence is that of the epitope of the gluten-derived tTG  
CC substrate peptide of the invention.

CC  
XX  
SQ Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;  
Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPKLKVVFPP 15  
|||:|:|  
DB 1 PPKLQVQPP 13

RESULT 13

ADFI4511  
ID ADFI4511 standard; peptide; 14 AA.

XX  
AC ADFI4511;

XX  
DT 12-FEB-2004 (first entry)

XX  
DE Gluten-derived tissue transglutaminase substrate peptide - SEQ ID 4.

XX  
XX plant; deamidation; tissue transglutaminase; tTG; celiac disease; CD;  
XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
XX systemic lupus erythematosus; Sjogren syndrome; diabetes;  
XX immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
XX dermatological; antiinflammatory; substrate.

XX  
OS Unidentified.

XX  
PN EPI332760-A1.

XX  
PD 06-AUG-2003.

XX  
PF 04-FEB-2002; 2002EP-00075456.

XX  
PR 04-FEB-2002; 2002EP-00075456.

XX  
PA (ZIER-) ACAD ZIEKENHUIS LEIDEN.

XX  
PS WPI; 2003-647889/62.

XX  
PT New gluten peptides or epitopes prone to deamidation by tissue  
PT transglutaminase, useful for treating celiac disease or an autoimmune  
PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
PT erythematosus, or diabetes.

XX  
PS Claim 1; SEQ ID NO 4; 143pp; English.

XX  
CC The invention relates to a novel peptide or epitope which is prone to  
CC deamidation by tissue transglutaminase (tTG) and is a causative factor of  
CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as  
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates  
CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,  
CC dermatological and antiinflammatory activities whilst pharmaceutical  
CC compositions comprising the peptides or epitopes may be useful for the  
CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren

CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
CC preparation of therapeutic agents capable of eliminating a subset of  
CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
CC The current sequence is that of the gluten-derived tissue  
CC transglutaminase substrate peptide of the invention.

CC  
XX  
SQ Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;  
Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPKLKVVFPP 15  
|||:|:|  
DB 1 PPKLQVQPP 13

RESULT 14

ADFI4519  
ID ADFI4519 standard; peptide; 14 AA.

XX  
AC ADFI4519;

XX  
DT 12-FEB-2004 (first entry)

XX  
DE Epitope of gluten-derived tTG substrate peptide - SEQ ID 12.

XX  
XX plant; deamidation; tissue transglutaminase; tTG; celiac disease; CD;  
XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
XX systemic lupus erythematosus; Sjogren syndrome; diabetes;  
XX immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
XX dermatological; antiinflammatory; substrate epitope.

XX  
OS Unidentified.

XX  
PN EPI332760-A1.

XX  
PD 06-AUG-2003.

XX  
PF 04-FEB-2002; 2002EP-00075456.

XX  
PR 04-FEB-2002; 2002EP-00075456.

XX  
PA (ZIER-) ACAD ZIEKENHUIS LEIDEN.

XX  
PS WPI; 2003-647889/62.

XX  
PT New gluten peptides or epitopes prone to deamidation by tissue  
PT transglutaminase, useful for treating celiac disease or an autoimmune  
PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
PT erythematosus, or diabetes.

XX  
PS Claim 2; SEQ ID NO 12; 143pp; English.

XX  
CC The invention relates to a novel peptide or epitope which is prone to  
CC deamidation by tissue transglutaminase (tTG) and is a causative factor of  
CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as  
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates  
CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,  
CC dermatological and antiinflammatory activities whilst pharmaceutical  
CC compositions comprising the peptides or epitopes may be useful for the  
CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren  
CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
CC preparation of therapeutic agents capable of eliminating a subset of  
CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
CC The current sequence is that of the epitope of the gluten-derived tTG  
CC substrate peptide of the invention.

XX  
SQ Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;

Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PEPKLVKEVPP 15  
| | | | |  
| | | | |  
Db 1 PEPQLQPPQPP 13

## RESULT 15

ADP14535  
ID ADP14535 standard; peptide; 14 AA.

AC ADP14535;

DT 12-FEB-2004 (first entry)

DE Epitope of gluten-derived cTG substrate peptide - SEQ ID 28.

XX plant; deamidation; tissue transglutaminase; cTG; celiac disease; CD;  
XX gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
XX systemic lupus erythematosus; Sjogren syndrome; diabetes;  
XX immunosuppressive; antirheumatic; anticholelithic; antidiabetic;  
XX dermatological; antiinflammatory; substrate epitope.

OS Unidentified.

PN EP132760-A1.

PD 06-AUG-2003.

PF 04-FEB-2002; 2002EP-00075456.

PR 04-FEB-2002; 2002EP-00075456.

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

DR WPI; 2003-647889/62.

XX New gluten peptides or epitopes prone to deamidation by tissue  
XX transglutaminase, useful for treating celiac disease or an autoimmune  
XX disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
XX erythematosus, or diabetes.

PS Claim 2; SEQ ID NO 28; 143pp; English.

XX The invention relates to a novel peptide or epitope which is prone to  
XX deamidation by tissue transglutaminase (tTG) and is a causative factor of  
XX celiac disease (CD, gluten intolerance) or an autoimmune disease such as  
XX rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
XX Sjogren syndrome or diabetes. The peptide of the invention demonstrates  
XX immunosuppressive, antirheumatic, anticholelithic, antidiabetic,  
XX dermatological and antiinflammatory activities whilst pharmaceutical  
XX compositions comprising the peptide or epitopes may be useful for the  
XX treatment of a celiac disease or an autoimmune disease such as rheumatoid  
XX arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren  
XX syndrome or diabetes. Gluten-derived peptides may be useful in the  
XX preparation of therapeutic agents capable of eliminating a subset of  
XX cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
XX The current sequence is that of the epitope of the gluten-derived cTG  
XX substrate peptide of the invention.

SQ Sequence 14 AA;

Query Match 46.3%; Score 38; DB 7; Length 14;

Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PEPKLVKEVPP 15  
| | | | |  
| | | | |  
Db 1 PEPQLQPPQPP 13

## RESULT 16

ADH14824  
ID ADH14824 standard; peptide; 17 AA.

AC ADH14824;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent  
XX which are wheat gliadin T cell epitope capable of being recognized by T  
XX cell receptor.

PS Example 13; Page 95; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating  
XX coeliac disease. M1 comprises administering an agent (A) comprising a  
XX gliadin T cell epitope, which is capable of being recognised by a T cell  
XX receptor, to an individual. Gliadin is a component of gluten. (A) has  
XX gastrointestinal activity, and can be used in vaccines. The agent (A) can  
XX be used in the preparation of a medicament for treating or preventing  
XX coeliac disease. (A) can also be used in the preparation of a diagnostic  
XX means for use in diagnosing coeliac disease, or susceptibility to coeliac  
XX disease, in an individual, which involves determining whether T cells of  
XX the individual recognise the agent, recognition by the T cells indicating  
XX that the individual has, or is susceptible to, coeliac disease. The  
XX present sequence represents a peptide which is used in the  
XX exemplification of the present invention.

SQ Sequence 17 AA;

Query Match 46.3%; Score 38; DB 8; Length 17;

Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKPPKLVKEVPP 15  
| | | | |  
| | | | |  
Db 2 LQPPQPPQPP 16

## RESULT 17

AAW48879  
ID AAW48879 standard; peptide; 14 AA.

AC AAW48879;

DT 23-SEP-1998 (first entry)

XX Cyclic peptide gramicidin S14 (GS14) analogue 3.

XX Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;  
XX hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;  
XX mycoplasma; food additive; antimicrobial activity; GS14.



OS Synthetic.  
 XX WO9816549-A1.  
 XX 23-APR-1998.  
 PD  
 XX 10-OCT-1997; 97WO-US018693.  
 XX 11-OCT-1996; 96US-0028315P.  
 XX  
 XX (PENCE-) PENCE INC.  
 XX (DEHL/) DEHLINGER P J.  
 XX  
 PI Kondelowski LH, Hodges RS, Wishart DS, Hancock RM, McElhaney R;  
 PI Premier EJ, Lewis RNAH;  
 XX WPI; 1998-251231/22.  
 DR  
 XX Cyclic peptide analogues of gramicidin S with broad spectrum  
 PT antimicrobial activity - and reduced haemolytic activity, have beta-  
 PT pleated sheet structure disrupted or eliminated by amino acid  
 PT substitutions.  
 PS  
 XX Claim 39; Page 65; 88pp; English.  
 CC  
 CC The invention provides for cyclic peptide analogues of gramicidin S14  
 CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14  
 CC analogues do not have the beta-pleated structure present in GS as, for  
 CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be  
 CC substituted with the respective D-form residue. These analogues are  
 CC claimed to have an advantage over GS as they have broad spectrum  
 CC antimicrobial activity and an increased therapeutic index because they  
 CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are  
 CC also claimed to be useful therapeutically in human or veterinary medicine  
 CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and  
 CC mycoplasma. They may also be used to control mycoplasma contamination of  
 CC cultured cells and as food additives  
 XX  
 SQ Sequence 14 AA;  
 QY  
 Query Match 45.7%; Score 37.5; DB 2; Length 14;  
 Best Local Similarity 69.2%; Pred. No. 19;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
 Db 1 LKPPKLVKVEVP 13  
 3 LKVFP-LKVGLFP 14  
 RESULT 18  
 ID AAM48904 standard; peptide; 14 AA.  
 XX  
 AC AAM48904;  
 XX  
 DT 23-SEP-1998 (first entry)  
 XX  
 DE Cyclic peptide gramicidin S14 analogue Y2/F2.  
 XX  
 KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index;  
 KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;  
 KW mycoplasma; food additive; antimicrobial activity.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1. 14  
 FT /note= "Residue 1 is in a peptide linkage with residue  
 FT 14"  
 FT Misc-difference 4  
 FT /note= "D-form residue"  
 FT 6  
 FT Misc-difference  
 FT /note= "D-form residue"

FT Misc-difference 13  
 FT /note= "D-form residue"  
 FT  
 XX WO9816549-A1.  
 XX 23-APR-1998.  
 PD  
 XX 10-OCT-1997; 97WO-US018693.  
 XX 11-OCT-1996; 96US-0028315P.  
 XX  
 XX (PENCE-) PENCE INC.  
 XX (DEHL/) DEHLINGER P J.  
 XX  
 PI Kondelowski LH, Hodges RS, Wishart DS, Hancock RM, McElhaney R;  
 PI Premier EJ, Lewis RNAH;  
 XX WPI; 1998-251231/22.  
 DR  
 XX Cyclic peptide analogues of gramicidin S with broad spectrum  
 PT antimicrobial activity - and reduced haemolytic activity, have beta-  
 PT pleated sheet structure disrupted or eliminated by amino acid  
 PT substitutions.  
 PS  
 XX Disclosure; Page 45; 88pp; English.  
 CC  
 CC The invention provides for cyclic peptide analogues of gramicidin S14  
 CC (GS14; AAM48876), such as the present one. These cyclic peptide GS14  
 CC analogues do not have the beta-pleated structure present in gramicidin S  
 CC (GS). These analogues are claimed to have an advantage over GS as they  
 CC have broad spectrum antimicrobial activity and an increased therapeutic  
 CC index because they lack the hemolytic effect of GS. The cyclic peptide  
 CC GS14 analogues are also claimed to be useful therapeutically in human or  
 CC veterinary medicine to kill or inhibit Gram-positive and -negative  
 CC bacteria, fungi and mycoplasma. They may also be used to control  
 CC mycoplasma contamination of cultured cells and as food additives  
 XX  
 SQ Sequence 14 AA;  
 QY  
 Query Match 45.7%; Score 37.5; DB 2; Length 14;  
 Best Local Similarity 69.2%; Pred. No. 19;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
 Db 1 LKPPKLVKVEVP 13  
 3 LKVFP-LKVGLFP 14  
 RESULT 19  
 ID ABB41738 standard; peptide; 18 AA.  
 XX  
 AC ABB41738;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX  
 DE Peptide #9244 encoded by human foetal liver single exon probe.  
 XX  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
 KW Homo sapiens.  
 OS  
 XX WO200157277-A2.  
 XX  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000669.  
 PF  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
PS Claim 27; SEQ ID NO 34373; 639bp + Sequence Listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 45.1%; Score 37; DB 4; Length 18;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 8 KVEVFPFP 15  
: || |||  
Db 3 RVEAFPPF 10  
XX  
RESULT 20  
AAM35535  
ID AAM35535 standard; protein; 18 AA.  
XX  
AC AAM35535;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #9572 encoded by probe for measuring placental gene expression.  
XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
XX genetic disorder.  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488897/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 27; SEQ ID NO 35804; 654bp; English.

XX  
CC The present invention relates to single exon nucleic acid probes (SENP;  
CC see A4131315-A4157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 45.1%; Score 37; DB 4; Length 18;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 8 KVEVFPFP 15  
: || |||  
Db 3 RVEAFPPF 10  
XX  
RESULT 21  
ABB25488  
ID ABB25488 standard; protein; 18 AA.  
XX  
AC ABB25488;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Protein #7487 encoded by probe for measuring heart cell gene expression.  
XX  
KW Human; gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000666.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488899/53.  
DR  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX  
PS Claim 15; SEQ ID NO 27258; 530bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting, the  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 18 AA:

Query Match 45.1%; Score 37; DB 4; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVFPFP 15  
 :|||  
 Db 3 RVEAFPPF 10

RESULT 22

AAM75423  
 ID AAM75423 standard; protein; 18 AA.

AC AAM75423;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35729.

KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

gene expression in human bone marrow.  
 Example 4; SEQ ID NO 35729; 658bp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 bone marrow. They can be used to measure gene expression in bone marrow  
 samples, which may enable the improved diagnosis and treatment of cancers  
 such as lymphoma, leukaemia and myeloma. The present sequence is a  
 protein encoded by one of the probes of the invention

SQ Sequence 18 AA:

Query Match 45.1%; Score 37; DB 4; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVFPFP 15  
 :|||  
 Db 3 RVEAFPPF 10

RESULT 23

AAM62611  
 ID AAM62611 standard; protein; 18 AA.

AC AAM62611;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34716.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
 Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human

brain.

Example 4; SEQ ID NO 34716; 650bp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 brain. They can be used to measure gene expression in brain cell samples,  
 which may enable the diagnosis and improved treatment of nervous system  
 diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 epilepsy and cancer. The present sequence is a protein encoded by one of  
 the probes of the invention

SQ Sequence 18 AA:

Query Match 45.1%; Score 37; DB 4; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVFPFP 15  
 :|||  
 Db 3 RVEAFPPF 10

RESULT 24

ABG57176  
 ID ABG57176 standard; peptide; 18 AA.

AC ABG57176;

DT 25-FEB-2003 (first entry)

DE Human liver peptide, SEQ ID NO 35824.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

PN WO200157273-A2.

PD 09-AUG-2001.

```

XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 35824; 658bp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/fragments). The probe hybridizes at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (1) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 18 AA;
XX
XX Query Match 45.1%; Score 37; DB 4; Length 18;
XX Best Local Similarity 75.0%; Pred. No. 31;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 KVEVPPFP 15
   :|||
   3 RVEARPPF 10
Db
RESULT 25
ABG45003
ID ABG45003 standard; peptide; 18 AA.
AC ABG45003;
DT 19-AUG-2002 (first entry)
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34668.
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Heremansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX PD 15-NOV-2001.

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XX PF 30-JAN-2001; 2001WO-US000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX PT measure gene expression in human lung samples.
XX PS Claim 27; SEQ ID NO 34668; 634bp; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12387 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of probes
XX CC ; the novel set of probes which hybridize at high stringency to a nucleic
XX CC acid expressed in the human lung; measuring gene expression in a sample
XX CC collected from human lung; comprising (a) contacting the array with a
XX CC collection of detectably labeled nucleic acids derived from human lung
XX CC mRNA, and (b) measuring the label detectably bound to each probe of the
XX CC array; identifying exons in a eukaryotic genome, comprising (a)
XX CC algorithmically predicting at least one exon from genomic sequences of
XX CC the eukaryote; and (b) detecting specific hybridization of detectably
XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX CC having a fragment identical to the predicted exon, the probe is included
XX CC in the above mentioned microarray; assigning exons to a single gene,
XX CC comprising (a) identifying exons from genomic sequence by the method
XX CC (above) and (b) measuring the expression of each of the exons in several
XX CC tissues and/or cell types using hybridization to a single exon
XX CC microarray having a probe with the exon, where a common pattern of
XX CC expression of the exons in the tissues and/or cell types indicates that
XX CC the exons should be assigned to a single gene; a peptide comprising one
XX CC of 12011 sequences, mentioned in the specification, or encoded by the
XX CC probes/open reading frames (ORF). The probes are used for gene expression
XX CC analysis, and for identifying exons in a gene, particularly using human
XX CC lung derived mRNA and for the study of lung diseases such as asthma, lung
XX CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Heremansky-
XX CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX CC present sequence is a peptide/protein encoded by a single exon probe of
XX CC the invention. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 18 AA;
XX
XX Query Match 45.1%; Score 37; DB 5; Length 18;
XX Best Local Similarity 75.0%; Pred. No. 31;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 KVEVPPFP 15
   :|||
   3 RVEARPPF 10
Db
RESULT 26

```

AAB72520  
ID AAB72520 standard; peptide; 18 AA.  
XX  
AC AAB72520;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostriin peptide #21.  
XX  
KW Dermatological; oxidative stress regulator; colostriin.  
XX  
OS Unidentified.  
XX  
PN WO200112650-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US022665.  
XX  
PR 17-AUG-1999; 99US-0149310P.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the cell  
PT with an oxidative stress regulator selected from colostriin, its  
PT constituent peptide, analog or their combinations.  
XX  
PS Claim 6; Page 26; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostriin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient  
CC  
SQ Sequence 18 AA;  
XX  
Query Match 43.9%; Score 36; DB 4; Length 18;  
Best Local Similarity 70.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 PPPKLKVEVF 12  
DB 5 PPPKYRVERPF 14  
XX  
RESULT 27  
AAB59330  
ID AAB59330 standard; peptide; 18 AA.  
XX  
AC AAB59330;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostriin peptide fragment C-5.  
XX  
KW Sheep; colostriin; proline rich polypeptide; colostriin; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX  
OS Ovis sp.  
XX  
PN WO200075173-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-GB002128.  
XX

PR 02-JUN-1999; 99GB-00012852.  
XX  
XX (REGG-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2001-071058/08.  
XX  
PT Peptide having an N-terminal amino acid sequence isolated from  
PT colostriin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.  
XX  
PS Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostriin. Colostriin is the proline-rich polypeptide  
CC fragment of colostriin. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
CC  
SQ Sequence 18 AA;  
XX  
Query Match 43.9%; Score 36; DB 4; Length 18;  
Best Local Similarity 70.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 PPPKLKVEVF 12  
DB 5 PPPKYRVERPF 14  
XX  
RESULT 28  
AAB72267  
ID AAB72267 standard; peptide; 18 AA.  
XX  
AC AAB72267;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostriin derived cytokine inducing peptide SEQ ID 22.  
XX  
KW Colostriin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
PN WO200111937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US022818.  
XX  
PR 17-AUG-1999; 99US-0149311P.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGG-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
DR WPI; 2001-202804/20.  
XX  
PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostriin as an immunological  
PT regulator.  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX

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XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYVPEPF 14

RESULT 29
AAB72552
ID AAB72552 standard; peptide; 18 AA.
XX
AC AAB72552;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #21.
XX
KW Neuropeptide; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
PI WPI; 2001-226545/23.
XX
DR
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYVPEPF 14

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RESULT 30
AA014598
ID AA014598 standard; peptide; 18 AA.
XX
AC AA014598;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 21.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FH Modified-site 18 /note="Optional C-terminal amide"
FT
FT
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
PI WPI; 2002-269152/31.
XX
DR
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 18 AA;

Query Match      43.9%; Score 36; DB 5; Length 18;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKVEVF 12
   |||||
DB 5 PPKKYVPEPF 14

RESULT 31
AAM51056
ID AAM51056 standard; peptide; 18 AA.
XX
AC AAM51056;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 121-138).
XX

```

KW Colostrotin; colostrotin; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; beta-casein; human.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 18  
FT /note= "optional C-terminal amidation"  
XX  
XX WO200213849-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022775.  
XX  
XX 17-AUG-2000; 2000WO-US022775.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX (REGS-) REGEN THERAPEUTICS PLC.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2002-269150/31.  
XX  
XX Modulation of blood cell proliferation in a patient involves use of blood  
PT cell regulator selected from colostrotin, its constituent peptide and/or  
PT analog.  
XX  
XX Claim 1; Page 34; 54pp; English.  
XX  
XX The present sequence is that of a colostrotin constituent peptide that is  
CC preferred for use as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. It is classified as having  
CC a beta-casein homologue precursor, and corresponds to casein amino acids  
CC 121-138. Methods are claimed for: inducing a cytokine in a cell by  
CC contact with an immunological regulator, where the cell is present in a  
CC cell culture, a tissue, an organ or an organism, and the cell is  
CC mammalian, including human; modulating an immune response in a cell by  
CC contact with the immunological regulator under conditions effective to  
CC induce a cytokine; modulating an immune response in a patient by  
CC administering an immunological regulator under conditions effective to  
CC induce a cytokine, where the immunological regulator is administered  
CC topically or as part of a dietary supplement, and where the immune  
CC response is specific or non specific, an interferon response or an  
CC antibody response; modulating blood cell proliferation by contacting  
CC blood cells with a blood cell regulator, where the blood cells are  
CC present in a cell culture or an organism, are mammalian or human, and  
CC where the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patient. A claimed  
CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
CC active agent such as the present peptide. Cytokines induced by this  
CC peptide in human leucocyte cultures include interferon-gamma, tumour  
CC necrosis factor-alpha and interleukin-10  
XX  
XX SQ Sequence 18 AA;  
XX  
XX Query Match 43.9%; Score 36; DB 5; Length 18;  
XX Best Local Similarity 70.0%; Pred. No. 46;  
XX Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX QY 3 PPKXKVEVF 12  
XX |||||  
XX 5 PPKXPVBP 14  
XX  
XX Db  
XX  
XX RESULT 32  
XX AAE20249  
XX ID AAE20249 standard; peptide; 18 AA.  
XX  
XX AC AAE20249;  
XX  
XX 18-JUN-2002 (first entry)  
XX

DE Colostrotin constituent peptide #21.  
XX  
XX Blood cell regulator; colostrotin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; veterinary.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 18  
FT /note= "Optionally C-terminal amide"  
XX  
XX WO200213850-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US022776.  
XX  
XX 17-AUG-2000; 2000WO-US022776.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrotin, its  
PT constituent peptide and/or analog.  
XX  
XX Claim 6; Page 26; 51pp; English.  
XX  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrotin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress level  
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
CC organ, or organism; or for treating oxidative damage to the skin of a  
CC patient e.g. animal or human; to modulate oxidative stress during/ after  
CC a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrotin constituent peptide  
XX  
XX SQ Sequence 18 AA;  
XX  
XX Query Match 43.9%; Score 36; DB 5; Length 18;  
XX Best Local Similarity 70.0%; Pred. No. 46;  
XX Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX QY 3 PPKXKVEVF 12  
XX |||||  
XX 5 PPKXPVBP 14  
XX  
XX Db  
XX  
XX RESULT 33  
XX ADN60316  
XX ID ADN60316 standard; peptide; 18 AA.  
XX  
XX AC ADN60316;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Constituent peptide of colostrotin SEQ ID NO:22.  
XX

KW modulator; colostrinin; intracellular signaling molecule modulator;  
 KW 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibitor;  
 KW DNA damage; beta-amyloid; retinoic acid; cytosolic; 4HNE inhibitor;  
 KW 4HNE-protein adduct formation reduction;  
 KW 4HNE-mediated glutathione depletion inhibition; p53 inhibition;  
 KW c-Jun NH2-terminal Kinase inhibition.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037651-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033423.  
 XX  
 PR 22-OCT-2002; 2002US-0420369P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (BOLD/) BOLDG I.  
 PA (STAN/) STANTON J G.  
 PA (GEOR/) GEORGIADIS J A.  
 PA (HUGH/) HUGHES T K.  
 PA (KRUIZ/) KRUIZEL M.  
 XX  
 PI Boldogh I, Stanton JG, Georgiades JA, Hughes TK, Kruzel M;  
 XX  
 DR WPI; 2004-365494/34.  
 XX  
 PT Use of colostrinin for e.g. modulating an intracellular signaling  
 PT molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a  
 PT cell, inhibiting apoptosis in a cell, or protecting against DNA damage in  
 PT a cell.  
 XX  
 PS Claim 6, SEQ ID NO 22; 46pp; English.  
 XX  
 CC The present invention describes the use of a modulator selected from  
 CC colostrinin, its constituent peptide, its active analogue, and a  
 CC combination of these, for modulating an intracellular signaling molecule  
 CC in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell,  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC and reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The modulator has cytostatic activity, and can be used as a 4HNE  
 CC inhibitor. The modulator is useful in the manufacture of a medicament for  
 CC reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated  
 CC glutathione depletion, inhibiting 4HNE-induced activation of p53 protein,  
 CC and/or inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases.  
 CC Colostrinin, or its constituent peptide or active analogue is useful for  
 CC inhibiting apoptosis in a cell, protecting against DNA damage in a cell,  
 CC or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.  
 CC The present sequence represents a synthetic constituent peptide of  
 CC colostrinin, which can be used as a modulator in the present invention.  
 CC  
 XX  
 SQ Sequence 18 AA.  
 Query Match 43.9%; Score 36; DB 8; Length 18;  
 Best Local Similarity 70.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 PPKKLKVEVF 12  
 Db 5 PPKKYVPEPF 14  
 RESULT 34  
 ADS74406  
 ID ADS74406 standard; peptide; 18 AA.  
 AC ADS74406;  
 XX  
 XX 16-DEC-2004 (first entry)  
 DT  
 XX  
 DE Ovine colostrinin peptide.  
 XX

KW Colostrum; colostrinin; sheep; peptide purification.  
 XX  
 OS Ovis aries.  
 XX  
 PN WO2004081038-A1.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 10-MAR-2004; 2004WO-GB001014.  
 XX  
 PR 11-MAR-2003; 2003GB-00005552.  
 PR 08-MAR-2004; 2004GB-00005190.  
 XX  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA, Polanowski A, Wilusz T, Kruzel ML;  
 XX  
 DR WPI; 2004-677519/66.  
 XX  
 PT Recovering peptides such as colostrinin from mammalian colostrum, by  
 PT mixing colostrum with alcohol to form alcohol phase containing peptides  
 PT and precipitate, separating alcohol phase from precipitate, and  
 PT recovering alcohol phase.  
 XX  
 PS Disclosure; SEQ ID NO 23; 41pp; English.  
 XX  
 CC The present sequence is that of a peptide that can be recovered from  
 CC ovine colostrum using the method of the invention. The invention  
 CC provides a method for the recovery of peptides (especially colostrinin)  
 CC from colostrum in substantially pure, biologically active form and in  
 CC high yield. The method involves mixing the colostrum with an alcohol to  
 CC form an alcohol phase containing the colostrinin and a precipitate  
 CC containing higher molecular weight caseins and other proteins. Best  
 CC results are obtained using methanol or ethanol of at least 80%, and  
 CC preferably up to 100%, purity. The alcohol phase is then separated from  
 CC the precipitate, and the colostrinin is separated from the alcohol,  
 CC preferably by evaporation, to form a colostrinin-rich phase, which is  
 CC recovered. A precipitation agent, such as ammonium sulfate, may be added  
 CC either to the alcohol phase or, preferably, to the colostrinin-rich phase  
 CC to induce precipitation of the colostrinin peptides. The method is  
 CC generally applicable to the separation of peptides from fluids containing  
 CC higher molecular weight proteins, lipids, carbohydrates and/or nucleic  
 CC acids.  
 CC  
 XX  
 SQ Sequence 18 AA;  
 Query Match 43.9%; Score 36; DB 8; Length 18;  
 Best Local Similarity 70.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 PPKKLKVEVF 12  
 Db 5 PPKKYVPEPF 14  
 RESULT 35  
 ADH14831  
 ID ADH14831 standard; peptide; 16 AA.  
 AC ADH14831;  
 XX  
 XX 11-MAR-2004 (first entry)  
 DT  
 XX  
 DE Gliadin related epitope peptide.  
 KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 KW vaccine.  
 XX  
 OS Synthetic.  
 OS  
 PN WO2003104273-A2.  
 XX  
 PD 18-DEC-2003.



XX 05-JUN-2003; 2003WO-GB002450.  
 XX  
 XX 05-JUN-2002; 2002GB-00012885.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Anderson RP, Hill AVS, Jewell DP;  
 XX  
 XX WPI; 2004-043640/04.  
 XX  
 XX Preventing or treating coeliac disease comprises administering agent  
 XX PT which are wheat gliadin T cell epitope capable of being recognized by T  
 XX cell receptor.  
 XX  
 XX Example 13; Page 96; 177pp; English.  
 XX  
 XX The present invention describes a method (M1) for preventing or treating  
 XX CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 XX CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 XX CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 XX CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 XX CC be used in the preparation of a medicament for treating or preventing  
 XX CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 XX CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 XX CC disease, in an individual, which involves determining whether T cells of  
 XX CC the individual recognise the agent, recognition by the T cells indicating  
 XX CC that the individual has, or is susceptible to, coeliac disease. The  
 XX CC present sequence represents a peptide which is used in the  
 XX CC exemplification of the present invention.  
 XX  
 XX Sequence 16 AA:  
 XX  
 XX Query Match 42.7%; Score 35; DB 8; Length 16;  
 XX Best Local Similarity 42.9%; Pred. No. 59;  
 XX Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 KPFPKLVFPFP 15  
 :|||:|  
 Db 2 QPFPQPPQPP 15

RESULT 36  
 ADH14841  
 ID ADH14841 standard; peptide; 18 AA.  
 XX  
 XX ADH14841;  
 XX  
 XX 11-MAR-2004 (first entry)  
 XX  
 XX Gliadin related epitope peptide.  
 XX  
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;  
 XX KW vaccine.  
 XX  
 XX Synthetic.  
 XX  
 XX WO2003104273-A2.  
 XX  
 XX 18-DEC-2003.  
 XX  
 XX 05-JUN-2003; 2003WO-GB002450.  
 XX  
 XX 05-JUN-2002; 2002GB-00012885.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Anderson RP, Hill AVS, Jewell DP;  
 XX  
 XX WPI; 2004-043640/04.  
 XX  
 XX Preventing or treating coeliac disease comprises administering agent  
 XX PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.  
 XX  
 XX Example 13; Page 96; 177pp; English.  
 XX  
 XX The present invention describes a method (M1) for preventing or treating  
 XX CC coeliac disease. M1 comprises administering an agent (A) comprising a  
 XX CC gliadin T cell epitope, which is capable of being recognised by a T cell  
 XX CC receptor, to an individual. Gliadin is a component of gluten. (A) has  
 XX CC gastrointestinal activity, and can be used in vaccines. The agent (A) can  
 XX CC be used in the preparation of a medicament for treating or preventing  
 XX CC coeliac disease. (A) can also be used in the preparation of a diagnostic  
 XX CC means for use in diagnosing coeliac disease, or susceptibility to coeliac  
 XX CC disease, in an individual, which involves determining whether T cells of  
 XX CC the individual recognise the agent, recognition by the T cells indicating  
 XX CC that the individual has, or is susceptible to, coeliac disease. The  
 XX CC present sequence represents a peptide which is used in the  
 XX CC exemplification of the present invention.  
 XX  
 XX Sequence 18 AA:  
 XX  
 XX Query Match 42.7%; Score 35; DB 8; Length 18;  
 XX Best Local Similarity 42.9%; Pred. No. 67;  
 XX Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 KPFPKLVFPFP 15  
 :|||:|  
 Db 4 QPFPQPPQPP 17

RESULT 37  
 AAE07188  
 ID AAE07188 standard; peptide; 10 AA.  
 XX  
 XX AAE07188;  
 XX  
 XX 06-NOV-2001 (first entry)  
 XX  
 XX Colostriin peptide 4.  
 XX  
 XX Colostriin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 XX KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 XX KW acquired immunological deficiency; neurological disorder; dementia;  
 XX KW antiviral.  
 XX  
 XX Unidentified.  
 XX  
 XX WO200155199-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 26-JAN-2001; 2001WO-GB000329.  
 XX  
 XX 26-JAN-2000; 2000GB-00001825.  
 XX  
 XX (REG- ) REGEN THERAPEUTICS PLC.  
 XX  
 XX Georgiades JA;  
 XX  
 XX WPI; 2001-488775/53.  
 XX  
 XX Peptide useful as an interalia in the treatment of e.g. disorders of the  
 XX PT immune system and the central nervous system comprises ten amino-terminal  
 XX PT amino acid sequence derived from peptides present in colostriin.  
 XX  
 XX Claim 1; Page 15; 40pp; English.  
 XX  
 XX The invention relates to colostriin peptide fragments which are useful,  
 XX CC inter alia, in the treatment of chronic disorders of the immune system  
 XX CC and the central nervous system. Colostriin peptides are used as a  
 XX CC medicament in the treatment of neurological disorders e.g., dementia,  
 XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostriin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostriin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostriin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is colostriin peptide 4 related to the invention

CC Sequence 10 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 10;  
 Best Local Similarity 81.8%; Pred. No. 43;  
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PRLKXVEVPFP 15  
 |||||  
 Db 1 PRLKXVEV-PEP 10

# RESULT 38

AAE07198 standard; peptide; 11 AA.

AAE07198;  
 06-NOV-2001 (first entry)

Modified colostriin cyclic peptide #4.

Colostriin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 central nervous system disorder; neurodegenerative disorder; weight loss;  
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 acquired immunological deficiency; neurological disorder; dementia;  
 antiviral; cyclic.

Synthetic.

Key Location/Qualifiers  
 Modified-site 1 /note="N-terminal acetyl; this residue forms a cyclic  
 linkage with Pro found at the C-terminal end"

WO200155199-A1.

02-AUG-2001.

26-JAN-2001; 2001WO-GB000329.

26-JAN-2000; 2000GB-00001825.

(REGG-) REGEN THERAPEUTICS PLC.

Georgiades JA;

WPI; 2001-488775/53.

Peptide useful as an interalia in the treatment of e.g. disorders of the  
 immune system and the central nervous system comprises ten amino-terminal  
 amino acid sequence derived from peptides present in colostriin.

Example 2; Page 8; 40pp; English.

The invention relates to colostriin peptide fragments which are useful,  
 inter alia, in the treatment of chronic disorders of the immune system  
 and the central nervous system. Colostriin peptides are used as a

CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostriin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostriin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostriin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is modified colostriin cyclic peptide #4 related to the  
 CC invention

CC Sequence 11 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 11;  
 Best Local Similarity 81.8%; Pred. No. 48;  
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PRLKXVEVPFP 15  
 |||||  
 Db 2 PRLKXVEV-PEP 11

# RESULT 39

AAW48877 standard; peptide; 14 AA.

AAW48877;

23-SEP-1998 (first entry)

Cyclic peptide gramicidin S14 (GS14) analogue 1.

Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;  
 hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;  
 mycoplasma; food additive; antimicrobial activity; GS14.

Synthetic.

Key Location/Qualifiers  
 Misc-difference 1, 14 /note="Residue 1 is in a peptide linkage with residue  
 14"

Misc-difference 2 /note="Optionally D-form residue"

Misc-difference 4 /note="Optionally D-form residue"

Misc-difference 5 /note="Optionally D-form residue"

Misc-difference 6 /note="Optionally D-form residue"

Misc-difference 8 /note="D-form residue"

Misc-difference 9 /note="Optionally D-form residue"

Misc-difference 10 /note="Optionally D-form residue"

Misc-difference 11 /note="Optionally D-form residue"

Misc-difference 13 /note="Optionally D-form residue"

WO9816549-A1.

23-APR-1998.

10-OCT-1997; 97WO-US018693.

```

XX 11-OCT-1996; 96US-0028315P.
PR (PENC-) PENCE INC.
XX (DEHL/) DEHLINGER P J.
PA Kondejowski LH, Hodges RS, Wishart DS, Hancock REM, McElhaney R;
XX Premier EJ, Lewis RNAM;
XX WPI; 1998-251231/22.
DR
XX Cyclic peptide analogues of gramicidin S with broad spectrum
PT antimicrobial activity - and reduced haemolytic activity, have beta-
PT pleated sheet structure disrupted or eliminated by amino acid
PT substitutions.
XX
XX Claim 39; Page 65; 88pp; English.
PS
XX The invention provides for cyclic peptide analogues of gramicidin S14
CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14
CC analogues do not have the beta-pleated structure present in GS as, for
CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
CC substituted with the respective D-form residue. These analogues are
CC claimed to have an advantage over GS as they have broad spectrum
CC antimicrobial activity and an increased therapeutic index because they
CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
CC also claimed to be useful therapeutically in human or veterinary medicine
CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
CC mycoplasma. They may also be used to control mycoplasma contamination of
CC cultured cells and as food additives
XX
XX Sequence 14 AA:
SQ
Query Match 42.1%; Score 34.5; DB 2; Length 14;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 LKPPKLYEVFP 13
Db 3 LKVP-LKVKLP 14
RESULT 40
AAM48878
ID AAM48878 standard; peptide; 14 AA.
XX
XX AAM48878;
AC
XX
XX 23-SEP-1998 (first entry)
DT
XX
XX Cyclic peptide gramicidin S14 (GS14) analogue 2.
DE
XX Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;
KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
KW mycoplasma; food additive; antimicrobial activity; GS14.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1. 14
FT /note= "Residue 1 is in a peptide linkage with residue
FT 14"
FT Misc-difference 2
FT /note= "Optionally D-form residue"
FT Misc-difference 4
FT /note= "Optionally D-form residue"
FT Misc-difference 5
FT /note= "Optionally D-form residue"
FT Misc-difference 6
FT /note= "D-form residue"
FT Misc-difference 8
FT /note= "Optionally D-form residue"
FT Misc-difference 9

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FT /note= "Optionally D-form residue"
FT Misc-difference 10
FT /note= "Optionally D-form residue"
FT Misc-difference 11
FT /note= "Optionally D-form residue"
FT Misc-difference 13
FT /note= "D-form residue"
XX
XX WO9816549-A1.
XX
XX 23-APR-1998.
PD
XX
XX 10-OCT-1997; 97WO-US018693.
XX
XX 11-OCT-1996; 96US-0028315P.
XX
XX (PENC-) PENCE INC.
PA (DEHL/) DEHLINGER P J.
XX
XX Kondejowski LH, Hodges RS, Wishart DS, Hancock REM, McElhaney R;
PI Premier EJ, Lewis RNAM;
XX WPI; 1998-251231/22.
DR
XX Cyclic peptide analogues of gramicidin S with broad spectrum
PT antimicrobial activity - and reduced haemolytic activity, have beta-
PT pleated sheet structure disrupted or eliminated by amino acid
PT substitutions.
XX
XX Claim 39; Page 65; 88pp; English.
PS
XX
XX The invention provides for cyclic peptide analogues of gramicidin S14
CC (GS14; AAM48876) such as the present one. These cyclic peptide GS14
CC analogues do not have the beta-pleated structure present in GS as, for
CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
CC substituted with the respective D-form residue. These analogues are
CC claimed to have an advantage over GS as they have broad spectrum
CC antimicrobial activity and an increased therapeutic index because they
CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
CC also claimed to be useful therapeutically in human or veterinary medicine
CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
CC mycoplasma. They may also be used to control mycoplasma contamination of
CC cultured cells and as food additives
XX
XX Sequence 14 AA:
SQ
Query Match 42.1%; Score 34.5; DB 2; Length 14;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 LKPPKLYEVFP 13
Db 3 LKVP-LKVKLP 14

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Pred. No. is the number of results predicted by chance to have a  
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## SUMMARIES

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2	36	43.9	18	4	US-09-641-803-22
3	34	41.5	15	4	US-09-641-803-5
4	31	37.8	13	3	US-09-385-442-39
5	31	37.8	16	1	US-07-906-871-3
6	29	35.4	18	3	US-08-477-928A-26
7	28	34.1	14	3	US-09-369-364A-29
8	27.5	33.5	14	3	US-08-949-059A-7
9	27.5	33.5	14	3	US-08-949-059A-14
10	27	32.9	11	1	US-08-347-198A-1
11	27	32.9	11	3	US-08-335-844A-25
12	27	32.9	11	4	US-09-129-366-25
13	27	32.9	12	4	US-09-095-639A-3
14	27	32.9	12	4	US-09-095-639A-4
15	27	32.9	14	3	US-09-092-000-1
16	27	32.9	15	4	US-09-514-245-80
17	27	32.9	15	4	US-09-514-245-81
18	27	32.9	15	4	US-09-774-633-257
19	27	32.9	16	1	US-08-347-198A-16
20	27	32.9	16	3	US-08-335-844A-0
21	27	32.9	16	4	US-09-129-366-40
22	26.5	32.3	13	3	US-08-915-314-22
23	26.5	32.3	13	3	US-08-702-054B-28
24	26.5	32.3	13	4	US-08-702-054B-29
25	26.5	32.3	13	4	US-09-030-619-93
26	26.5	32.3	13	4	US-09-030-619-100
27	26.5	32.3	13	4	US-09-667-486-22

28	26.5	32.3	13	4	US-10-225-087-8	Sequence 8, Appl
29	26	31.7	8	3	US-08-477-928A-46	Sequence 46, Appl
30	26	31.7	8	6	5459077-5	Parent No. 5459077
31	26	31.7	8	6	5459077-5	Parent No. 5459077
32	26	31.7	12	1	US-08-347-198A-7	Sequence 7, Appl
33	26	31.7	12	3	US-08-335-844A-31	Sequence 31, Appl
34	26	31.7	12	4	US-09-129-366-31	Sequence 31, Appl
35	26	31.7	13	1	US-08-325-509-24	Sequence 34, Appl
36	26	31.7	15	1	US-08-347-198A-19	Sequence 19, Appl
37	26	31.7	17	4	US-09-552-802B-40	Sequence 40, Appl
38	25	30.5	11	3	US-08-366-385-4	Sequence 4, Appl
39	25	30.5	11	3	US-09-287-221-4	Sequence 4, Appl
40	25	30.5	12	2	US-08-811-492-144	Sequence 144, Appl
41	25	30.5	12	3	US-08-602-999A-281	Sequence 281, Appl
42	25	30.5	12	3	US-08-949-059A-30	Sequence 30, Appl
43	25	30.5	12	4	US-09-500-124-281	Sequence 281, Appl
44	25	30.5	12	4	US-09-446-787B-95	Sequence 95, Appl
45	25	30.5	14	1	US-07-824-247-39	Sequence 39, Appl
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47	25	30.5	15	1	US-08-383-753-43	Sequence 43, Appl
48	25	30.5	15	2	US-08-586-772-43	Sequence 43, Appl
49	25	30.5	15	2	US-08-959-512-43	Sequence 43, Appl
50	25	30.5	15	3	US-09-512-983-43	Sequence 43, Appl
51	25	30.5	15	4	US-09-807-278-5	Sequence 5, Appl
52	25	30.5	16	3	US-08-602-999A-181	Sequence 181, Appl
53	25	30.5	16	3	US-08-602-999A-239	Sequence 239, Appl
54	25	30.5	16	3	US-09-029-785-6	Sequence 6, Appl
55	25	30.5	16	4	US-09-500-124-181	Sequence 181, Appl
56	25	30.5	16	4	US-09-500-124-239	Sequence 239, Appl
57	25	30.5	16	4	US-09-489-847-252	Sequence 252, Appl
58	25	30.5	18	3	US-08-974-549A-163	Sequence 163, Appl
59	25	30.5	18	3	US-09-056-226-7	Sequence 7, Appl
60	25	30.5	18	4	US-09-402-181B-163	Sequence 163, Appl
61	25	30.5	18	4	US-09-721-466-163	Sequence 163, Appl
62	24.5	29.9	14	3	US-08-949-059A-25	Sequence 25, Appl
63	24.5	29.9	15	4	US-09-069-827A-100	Sequence 100, Appl
64	24.5	29.9	15	4	US-09-069-827A-108	Sequence 108, Appl
65	24	29.3	8	3	US-08-828-712-12	Sequence 12, Appl
66	24	29.3	8	3	US-08-993-165-25	Sequence 25, Appl
67	24	29.3	8	3	US-08-993-165-28	Sequence 28, Appl
68	24	29.3	8	3	US-08-993-165-30	Sequence 30, Appl
69	24	29.3	8	3	US-09-063-276-12	Sequence 12, Appl
70	24	29.3	8	4	US-09-540-448-25	Sequence 25, Appl
71	24	29.3	8	4	US-09-540-448-28	Sequence 28, Appl
72	24	29.3	8	4	US-09-496-761-1	Sequence 1, Appl
73	24	29.3	8	4	US-09-496-761-4	Sequence 4, Appl
74	24	29.3	8	4	US-09-496-761-6	Sequence 6, Appl
75	24	29.3	8	4	US-09-324-782-12	Sequence 12, Appl
76	24	29.3	8	4	US-09-668-143-12	Sequence 12, Appl
77	24	29.3	8	4	US-08-913-612A-46	Sequence 46, Appl
78	24	29.3	8	4	US-08-928-847-26	Sequence 26, Appl
79	24	29.3	8	4	US-08-928-847-29	Sequence 29, Appl
80	24	29.3	8	4	US-09-813-484-26	Sequence 26, Appl
81	24	29.3	8	4	US-09-813-484-29	Sequence 29, Appl
82	24	29.3	8	4	US-10-046-801-25	Sequence 25, Appl
83	24	29.3	8	4	US-10-046-801-28	Sequence 28, Appl
84	24	29.3	8	4	US-10-265-463A-46	Sequence 46, Appl
85	24	29.3	9	1	US-08-447-702-2	Sequence 2, Appl
86	24	29.3	9	1	US-08-465-615-2	Sequence 2, Appl
87	24	29.3	9	2	US-08-934-222-128	Sequence 128, Appl
88	24	29.3	9	2	US-08-934-222-128	Sequence 128, Appl
89	24	29.3	9	2	US-09-207-651-128	Sequence 128, Appl
90	24	29.3	9	2	US-08-993-581B-22	Sequence 22, Appl
91	24	29.3	9	2	US-08-533-818-128	Sequence 128, Appl
92	24	29.3	9	3	US-08-828-712-13	Sequence 13, Appl
93	24	29.3	9	3	US-08-828-712-14	Sequence 14, Appl
94	24	29.3	9	3	US-09-231-797-128	Sequence 128, Appl
95	24	29.3	9	3	US-08-934-224-128	Sequence 128, Appl
96	24	29.3	9	3	US-08-933-843-128	Sequence 128, Appl
97	24	29.3	9	3	US-09-063-276-13	Sequence 13, Appl
98	24	29.3	9	3	US-09-063-276-14	Sequence 14, Appl
99	24	29.3	9	3	US-08-934-223-128	Sequence 128, Appl
100	24	29.3	9	3	US-09-413-492-128	Sequence 128, Appl

## ALIGNMENTS

```
RESULT 1
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-8
```

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Query Match          100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LKPPKLVKVEVPF 15
         |||||
DB       1 LKPPKLVKVEVPF 15
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RESULT 2
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-22
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Query Match          43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      3 PPKKLVKVEVPF 12
         |||||
DB       5 PPKKLVKVEVPF 14
```

```
RESULT 3
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-5
```

```
Query Match          41.5%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      5 PVLKLVKVEVPF 14
         |||||
DB       5 PVLKLVKVEVPF 14
```

```
RESULT 4
US-09-385-442-39
; Sequence 39, Application US/09385442
; Patent No. 6200954
; GENERAL INFORMATION:
; APPLICANT: Ge, Ruowen
; APPLICANT: Kni, R. Manjunatha
; TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
; FILE REFERENCE: 1781-170P
; CURRENT APPLICATION NUMBER: US/09/385,442
; PRIOR FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 60/099,313
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: sHLPT2
US-09-385-442-39
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```
Query Match          37.8%; Score 31; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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```
QY      1 LKPPKLVKVEVP 12
         |||||
DB       1 LVLPKRVKSTP 12
```

```
RESULT 5
US-07-906-871-3
; Sequence 3, Application US/07906871
; Patent No. 5340739
```

GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
TITLE OF INVENTION: HEMATOPOIETIC CELL SPECIFIC  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Avenue, N.W., Suite 300  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/906,871  
FILING DATE: 19920103  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/816,289  
FILING DATE: 03 JAN 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/635,544  
FILING DATE: 18-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US89/03051  
FILING DATE: 13-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/224,035  
FILING DATE: 13-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0627.2830004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)833-8716  
FAX: (202)833-7533  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-906-871-3

Query Match 37.8%; Score 31; DB 1; Length 16;  
Best Local Similarity 44.4%; Pred. No. 1e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKLXKVEVP 13  
|:|:|:|:|:  
Db 5 PRLRTDLP 13

RESULT 6  
US-08-477-928A-26  
Sequence 26, Application US/08477928A  
Patent No. 6207389  
GENERAL INFORMATION:  
APPLICANT: Dosch, Hans M.  
TITLE OF INVENTION: METHODS FOR CONTROLLING T  
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS  
STREET: 1299 Pennsylvania Avenue  
CITY: Washington D.C.

STATE: California  
COUNTRY: U.S.A.  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,928A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36902  
REFERENCE/DOCKET NUMBER: 19060-0105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 639 7700  
FAX: (202) 639 7890  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-928A-26

Query Match 35.4%; Score 29; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPPEKLAKEV 11  
|:|:|:|:|:  
Db 4 KNFDKDKMDV 13

RESULT 7  
US-09-369-364A-29  
Sequence 29, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apte, Suneel  
APPLICANT: Hurekainen, Tina L.  
APPLICANT: Hirohata, Satoshi  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
FILE REFERENCE: 26473/4007/10-30-00  
CURRENT APPLICATION NUMBER: US/09/369,364A  
CURRENT FILING DATE: 1999-08-06  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 14  
TYPE: PRT  
ORGANISM: synthetic construct  
US-09-369-364A-29

Query Match 34.1%; Score 28; DB 3; Length 14;  
Best Local Similarity 62.5%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPKXK 8  
|:|:|:|:|:  
Db 6 LKPPKXK 13

RESULT 8  
US-08-949-059A-7  
Sequence 7, Application US/08949059A  
Patent No. 6358921  
GENERAL INFORMATION:  
APPLICANT: Kondejewski, Leslie H.  
APPLICANT: Hodges, Robert S.

```
/ APPLICANT: Wishart, David S.
/ APPLICANT: Hancock, Robert E.W.
/ APPLICANT: McElhane, Ronald N.
/ APPLICANT: Premier, Elmar J.
/ APPLICANT: Lewis, Ruthven N.A.H
/ TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/949,059A
/ FILING DATE: 10-OCT-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 660081.412
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: cyclic
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 13
/ OTHER INFORMATION: /note="Residue is a D-Tyrosine"
/
US-08-949-059A-7

Query Match 33.5%; Score 27.5; DB 3; Length 14;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 LKPPKLVKVEVP 13
| | | | |
| | | | |
Db 3 LKVP-LKVKLP 14

RESULT 9
US-08-949-059A-14
/ Sequence 14, Application US/08949059A
/ Patent No. 6358921
/ GENERAL INFORMATION:
/ APPLICANT: Kondejewski, Leslie H.
/ APPLICANT: Hodges, Robert S.
/ APPLICANT: Wishart, David S.
/ APPLICANT: McElhane, Robert E.W.
/ APPLICANT: McElhane, Ronald N.
/ APPLICANT: Premier, Elmar J.
/ APPLICANT: Lewis, Ruthven N.A.H
/ TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
```

```
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/949,059A
/ FILING DATE: 10-OCT-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 660081.412
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: cyclic
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /note="Residue is a D-Tyrosine"
/
US-08-949-059A-14

Query Match 33.5%; Score 27.5; DB 3; Length 14;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 LKPPKLVKVEVP 13
| | | | |
| | | | |
Db 3 LKVP-LKVKLP 14

RESULT 10
US-08-347-198A-1
/ Sequence 1, Application US/08347198A
/ Patent No. 5747046
/ GENERAL INFORMATION:
/ APPLICANT: Munn, Edward A.
/ APPLICANT: Smith, Trevor S.
/ TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
/ TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP
/ STREET: 655 Fifteenth Street, N. W., Suite 330 - G
/ STREET: Street Lobby
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/347,198A
/ FILING DATE: 21-NOV-1994
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/020,526
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FILING DATE: 22-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/761,749  
FILING DATE: 17-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB90/00416  
FILING DATE: 19-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 89906156.8  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTIS, Monica C.  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P443-1289  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-347-198A-1

Query Match 32.9%; Score 27; DB 1; Length 11;  
Best Local Similarity 55.6%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVEF 12  
: : : : :  
Db 3 YPVVKEEF 11

RESULT 11  
US-08-335-844A-25  
Sequence 25, Application US/08335844A  
Patent No. 6066503  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, MARGARET  
APPLICANT: SMITH, TREVOR STANLEY  
APPLICANT: MUNN, EDWARD ALBERT  
APPLICANT: KNOX, DAVID PATRICK  
APPLICANT: OLIVER, JOANNA JANE  
APPLICANT: NEWTON, SUSAN ELIZABETH  
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Pig9, Ernst & Kurz  
STREET: Suite 701-E, 555 Thirteenth St., N.W  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,844A  
FILING DATE: 09-JAN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB PCT/GB93/00943  
FILING DATE: 06-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9209936  
FILING DATE: 08-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1181-241A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:

NAME: WALKER, Barbara W.  
REGISTRATION NUMBER: 35,400  
REFERENCE/DOCKET NUMBER: 1181-223A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-335-844A-25

Query Match 32.9%; Score 27; DB 3; Length 11;  
Best Local Similarity 55.6%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLKVVEF 12  
: : : : :  
Db 3 YPVVKEEF 11

RESULT 12  
US-09-129-366-25  
Sequence 25, Application US/09129366  
Patent No. 6534638  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, MARGARET  
APPLICANT: SMITH, TREVOR STANLEY  
APPLICANT: MUNN, EDWARD ALBERT  
APPLICANT: KNOX, DAVID PATRICK  
APPLICANT: OLIVER, JOANNA JANE  
APPLICANT: NEWTON, SUSAN ELIZABETH  
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Pig9, Ernst & Kurz  
STREET: Suite 701-E, 555 Thirteenth St., N.W  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/129,366  
FILING DATE: 05-AUG-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/335,844  
FILING DATE: 09-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB PCT/GB93/00943  
FILING DATE: 06-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9209936  
FILING DATE: 08-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1181-241A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-129-366-25

Query Match 32.9%; Score 27; DB 4; Length 11;  
Best Local Similarity 55.6%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPKLVEVF 12  
|:|:|:|:  
DB 3 YPVVKVEEF 11

RESULT 13  
US-09-095-639A-3  
Sequence 3, Application US/09095639A  
Patent No. 6750203

GENERAL INFORMATION:  
APPLICANT: POZZILI Paolo  
TITLE OF INVENTION: Product derived from milk  
TITLE OF INVENTION: substantially free of beta casein from non-human  
TITLE OF INVENTION: mammals and relative use.  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HEDMAN, GIBSON & COSTIGAN  
STREET: 1185 Avenue of the Americas  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC/2  
OPERATING SYSTEM: DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,639A  
FILING DATE: JUNE 6, 1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT RM 95 A 000850  
FILING DATE: 27-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Costigan, James V.  
REGISTRATION NUMBER: 25,669  
REFERENCE/DOCKET NUMBER: 515-4111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 302-8989  
TELEFAX: (212) 302-8998  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-095-639A-3

Query Match 32.9%; Score 27; DB 4; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPFP 15  
|:|:|:|:  
DB 3 YVPFP 7

RESULT 14  
US-09-095-639A-4  
Sequence 4, Application US/09095639A

Patent No. 6750203  
GENERAL INFORMATION:  
APPLICANT: POZZILI Paolo  
TITLE OF INVENTION: Product derived from milk  
TITLE OF INVENTION: substantially free of beta casein from non-human  
TITLE OF INVENTION: mammals and relative use.  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HEDMAN, GIBSON & COSTIGAN  
STREET: 1185 Avenue of the Americas  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC/2  
OPERATING SYSTEM: DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,639A  
FILING DATE: JUNE 6, 1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT RM 95 A 000850  
FILING DATE: 27-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Costigan, James V.  
REGISTRATION NUMBER: 25,669  
REFERENCE/DOCKET NUMBER: 515-4111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 302-8989  
TELEFAX: (212) 302-8998  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-095-639A-4

Query Match 32.9%; Score 27; DB 4; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPFP 15  
|:|:|:|:  
DB 3 YVPFP 7

RESULT 15  
US-09-092-000-1  
Sequence 1, Application US/09092000  
Patent No. 6339139  
GENERAL INFORMATION:  
APPLICANT: Gu, Jian-ren  
APPLICANT: Tian, Peikun  
TITLE OF INVENTION: Receptor-Mediated Gene Transfer System for Targeting  
TITLE OF INVENTION: Tumor Gene Therapy  
FILE REFERENCE: Gu  
CURRENT APPLICATION NUMBER: US/09/092,000  
CURRENT FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 96 116557.X  
EARLIER FILING DATE: 1996-10-31  
EARLIER APPLICATION NUMBER: PCT/CN97/00106  
EARLIER FILING DATE: 1997-10-27  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Ligand  
OTHER INFORMATION: oligopeptide for the receptor region of IGF I and  
OTHER INFORMATION: IGF II  
US-09-092-000-1

Query Match 32.9%; Score 27; DB 3; Length 14;  
Best Local Similarity 46.2%; Pred. No. 3.9e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 KPF--PKLVEVP 12  
:|||||:  
Db 1 BPFRRPKLALFTY 13

RESULT 16  
US-09-514-245-80

Sequence 80, Application US/09514245  
Patent No. 6703023

GENERAL INFORMATION:  
APPLICANT: JESTIN, Andre  
APPLICANT: ALBINA, Emanuel  
APPLICANT: Le CANN, Pierre  
APPLICANT: BLANCHARD, Philippe  
APPLICANT: HUTET, Evelyne  
APPLICANT: ARNAUD, Claire  
APPLICANT: TRUONG, Catherine  
APPLICANT: MAHE, Dominique  
APPLICANT: CARIOLET, Roland  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/09/514,245  
CURRENT FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 80  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type B PWD circovirus  
US-09-514-245-80

Query Match 32.9%; Score 27; DB 4; Length 15;  
Best Local Similarity 62.5%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KLVVEVP 13  
:|||||:  
Db 8 KLVVEFP 15

RESULT 17  
US-09-514-245-81

Sequence 81, Application US/09514245  
Patent No. 6703023

GENERAL INFORMATION:  
APPLICANT: JESTIN, Andre  
APPLICANT: ALBINA, Emanuel  
APPLICANT: Le CANN, Pierre  
APPLICANT: BLANCHARD, Philippe  
APPLICANT: HUTET, Evelyne  
APPLICANT: ARNAUD, Claire  
APPLICANT: TRUONG, Catherine  
APPLICANT: MAHE, Dominique  
APPLICANT: CARIOLET, Roland  
APPLICANT: MADOC, Francois  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/09/514,245  
CURRENT FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396

PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 81  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type B PWD circovirus  
US-09-514-245-81

Query Match 32.9%; Score 27; DB 4; Length 15;  
Best Local Similarity 62.5%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KLVVEVP 13  
:|||||:  
Db 4 KLVVEFP 11

RESULT 18  
US-09-774-639-257

Sequence 257, Application US/09774639  
Patent No. 6806351  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 90 Human Secreted Proteins  
FILE REFERENCE: P2013P  
CURRENT APPLICATION NUMBER: US/09/774,639  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
NUMBER OF SEQ ID NOS: 371  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 257  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-774-639-257

Query Match 32.9%; Score 27; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 KLVVEFP 15  
:|||||:  
Db 2 KLVVEFP 9

RESULT 19  
US-08-347-198A-16  
Sequence 16, Application US/08347198A  
Patent No. 5747046

GENERAL INFORMATION:  
APPLICANT: MUNN, Edward A.  
APPLICANT: SMITH, Trevor S.  
TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/347,198A  
FILING DATE: 21-NOV-1994

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/020,526  
FILING DATE: 22-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/761,749  
FILING DATE: 17-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB90/00416  
FILING DATE: 19-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 89906156.8  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTIS, Monica C.  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P443-1289  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-347-198A-16

Query Match 32.9%; Score 27; DB 1; Length 16;  
Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 FPKLKVEVF 12  
Db 3 YPVVKVEEF 11

RESULT 20  
US-08-335-844A-40  
Sequence 40, Application US/08335844A  
Patent No. 6066503  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, MARGARET  
APPLICANT: SMITH, TREVOR STANLEY  
APPLICANT: MUNN, EDWARD ALBERT  
APPLICANT: KNOX, DAVID PATRICK  
APPLICANT: OLIVER, JOANNA JANE  
APPLICANT: NEWTON, SUSAN ELIZABETH  
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figs, Ernst & Kurz  
STREET: Suite 701-E, 555 Thirteenth St., N.W  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,844A  
FILING DATE: 09-JAN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB PCT/GB93/00943  
FILING DATE: 06-MAY-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9209936  
FILING DATE: 08-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: WALKER, Barbara W.  
REGISTRATION NUMBER: 35,400  
REFERENCE/DOCKET NUMBER: 1181-223A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-335-844A-40

Query Match 32.9%; Score 27; DB 3; Length 16;  
Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 FPKLKVEVF 12  
Db 3 YPVVKVEEF 11

RESULT 21  
US-09-129-366-40  
Sequence 40, Application US/09129366  
Patent No. 6534658  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, MARGARET  
APPLICANT: SMITH, TREVOR STANLEY  
APPLICANT: MUNN, EDWARD ALBERT  
APPLICANT: KNOX, DAVID PATRICK  
APPLICANT: OLIVER, JOANNA JANE  
APPLICANT: NEWTON, SUSAN ELIZABETH  
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figs, Ernst & Kurz  
STREET: Suite 701-E, 555 Thirteenth St., N.W  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/129,366  
FILING DATE: 05-AUG-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/335,844  
FILING DATE: 09-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB PCT/GB93/00943  
FILING DATE: 06-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9209936  
FILING DATE: 08-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1181-241A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040

TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-129-366-40

Query Match 32.3%; Score 27; DB 4; Length 16;  
Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LKPKLVEVP 12  
DB 3 YPVVKEVP 11

## RESULT 22

US-08-915-314-22  
; Sequence 22, Application US/08915314  
; Patent No. 6180604  
; GENERAL INFORMATION:  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: Krieger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Eftle, Douglas  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915.314  
; FILING DATE: 20-AUG-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6180604tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 660081.405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-915-314-22

Query Match 32.3%; Score 26.5; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPKLVEVP 14  
DB 2 LKPKP-----FPFP 10

## RESULT 23

US-08-702-054B-28  
; Sequence 28, Application US/08702054B  
; Patent No. 6191254  
; GENERAL INFORMATION:  
; APPLICANT: Falls, Timothy J.  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha  
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702.054B  
; FILING DATE: 23-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/002,687  
; FILING DATE: 23-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07420/013001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-702-054B-28

Query Match 32.3%; Score 26.5; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 LKPKLVEVP 14  
DB 2 LKPKP-----FPFP 10

## RESULT 24

US-08-702-054B-29  
; Sequence 29, Application US/08702054B  
; Patent No. 6191254  
; GENERAL INFORMATION:  
; APPLICANT: Falls, Timothy J.  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha  
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,054B  
FILING DATE: 23-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/002,687  
FILING DATE: 23-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/013001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-702-054B-29

Query Match 32.3%; Score 26.5; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14  
|||  
Db 2 LKKFP-----FPPF 10

RESULT 25  
US-09-030-619-93  
Sequence 93, Application US/09030619B  
GENERAL INFORMATION:  
APPLICANT: Krieger, Timothy J.  
APPLICANT: Taylor, Robert  
APPLICANT: Erfile, Douglas  
APPLICANT: Fraser, Janet R.  
APPLICANT: West, Michael H.P.  
APPLICANT: McNicol, Patricia J.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
FILE REFERENCE: 660081.406  
CURRENT APPLICATION NUMBER: US/09/030,619B  
CURRENT FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 93  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Cationic Peptide Analogue  
US-09-030-619-93

Query Match 32.3%; Score 26.5; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14  
|||  
Db 2 LKKFP-----FPPF 10

RESULT 26  
US-09-030-619-100  
Sequence 100, Application US/09030619B  
Patent No. 6503881  
GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.  
APPLICANT: Taylor, Robert  
APPLICANT: Erfile, Douglas  
APPLICANT: Fraser, Janet R.  
APPLICANT: West, Michael H.P.  
APPLICANT: McNicol, Patricia J.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
FILE REFERENCE: 660081.406  
CURRENT APPLICATION NUMBER: US/09/030,619B  
CURRENT FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 100  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Cationic Peptide Analogue  
US-09-030-619-100

Query Match 32.3%; Score 26.5; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLVKVEVPPF 14  
|||  
Db 2 LKKFP-----FPPF 10

RESULT 27  
US-09-667-486-22  
Sequence 22, Application US/09667486  
Patent No. 6538106  
GENERAL INFORMATION:  
APPLICANT: Fraser, Janet R.  
APPLICANT: West, Michael H.P.  
APPLICANT: Krieger, Timothy J.  
APPLICANT: Taylor, Robert  
APPLICANT: Erfile, Douglas  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/667,486  
FILING DATE: 22-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,314  
FILING DATE: 20-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6538106tenburg Ph. D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 660081.405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-667-486-22

Query Match 32.3%; Score 26.5; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLKVEVPF 14  
|||  
Db 2 LKKFP-----FPPF 10

RESULT 28  
US-10-225-087-8  
Sequence 8, Application US/10225087  
Patent No. 6835536  
GENERAL INFORMATION:  
APPLICANT: Krieger, Timothy J.  
APPLICANT: McNicol, Patricia J.  
APPLICANT: Frazer, Janet R.  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND  
TITLE OF INVENTION: FORMULATIONS THEREOF  
FILE REFERENCE: 660081.417  
CURRENT APPLICATION NUMBER: US/10/225,087  
CURRENT FILING DATE: 2003-01-10  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Indolicidin analog  
US-10-225-087-8

Query Match 32.3%; Score 26.5; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPPKLKVEVPF 14  
|||  
Db 2 LKKFP-----FPPF 10

RESULT 29  
US-08-477-928A-46  
Sequence 46, Application US/08477928A  
Patent No. 6207389  
GENERAL INFORMATION:  
APPLICANT: Dosh, Hans M.  
TITLE OF INVENTION: METHODS FOR CONTROLLING T  
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS  
STREET: 1299 Pennsylvania Avenue  
CITY: Washington D.C.  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,928A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James  
REGISTRATION NUMBER: 36902  
REFERENCE/DOCKET NUMBER: 19060-0105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 639-7700  
TELEFAX: (202) 639-7890  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-928A-46

Query Match 31.7%; Score 26; DB 3; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.1e+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPKLKEV 11  
|||:  
Db 1 FDKLMKV 8

RESULT 30  
5459077-5  
Patent No. 5459077  
APPLICANT: MOORE, GRAHAM J.; MATSOUKAS, JOHN M.  
TITLE OF INVENTION: METHODS FOR MODELLING TERTIARY STRUCTURES  
OF BIOLOGICALLY ACTIVE LIGANDS AND FOR MODELLING AGONISTS AND  
ANTAGONISTS THEREO  
NUMBER OF SEQUENCES: 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/27,561  
FILING DATE: 05-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 458,926  
FILING DATE: 29-DEC-1989  
SEQ ID NO: 5;  
LENGTH: 8  
5459077-5

Query Match 31.7%; Score 26; DB 6; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KYEVPF 14  
:  
Db 2 RYIYRPF 8

RESULT 31  
5459077-5  
Patent No. 5459077  
APPLICANT: MOORE, GRAHAM J.; MATSOUKAS, JOHN M.  
TITLE OF INVENTION: METHODS FOR MODELLING TERTIARY STRUCTURES  
OF BIOLOGICALLY ACTIVE LIGANDS AND FOR MODELLING AGONISTS AND  
ANTAGONISTS THEREO  
NUMBER OF SEQUENCES: 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/27,561  
FILING DATE: 05-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 458,926  
FILING DATE: 29-DEC-1989  
SEQ ID NO: 5;  
LENGTH: 8  
5459077-5

Query Match 31.7%; Score 26; DB 6; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVEPF 14  
: |||||  
Db 2 RYVEPFP 8

## RESULT 32

US-08-347-198A-7  
; Sequence 7, Application US/08347198A  
; Patent No. 5747046  
; GENERAL INFORMATION:  
; APPLICANT: MUNN, Edward A.  
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC  
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIKAIKO, MARWELSTEIN, MURRAY & ORAM LLP  
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,198A  
; FILING DATE: 21-NOV-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER: US 08/020,526  
; FILING DATE: 22-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/761,749  
; FILING DATE: 17-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB90/00416  
; FILING DATE: 19-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 89906156.8  
; FILING DATE: 17-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KITTIS, Monica C.  
; REGISTRATION NUMBER: 36,105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/638-5000  
; TELEFAX: 202/638-4810  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-347-198A-7

Query Match 31.7%; Score 26; DB 1; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLKVVEP 12  
: |||||  
Db 3 PPLVTVVEAP 11

RESULT 33  
US-08-335-844A-31  
; Sequence 31, Application US/08335844A  
; Patent No. 6066503

; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figs, Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,844A  
; FILING DATE: 09-JAN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB PCT/GB93/00943  
; FILING DATE: 06-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9209936  
; FILING DATE: 08-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WALKER, Barbara W.  
; REGISTRATION NUMBER: 35,400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-335-844A-31

Query Match 31.7%; Score 26; DB 3; Length 12;  
Best Local Similarity 55.6%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLKVVEP 12  
: |||||  
Db 3 PPLVTVVEAP 11

RESULT 34  
US-09-129-366-31  
; Sequence 31, Application US/09129366  
; Patent No. 6534638  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; NUMBER OF SEQUENCES: 73



```

CORRESPONDENCE ADDRESS:
ADDRESSER: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,366
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6031
TELEFAX: (202)783-6040
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-129-366-31

Query Match      31.7%  Score 26; DB 4; Length 12;
Best Local Similarity 55.6%  Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4 PPKLYEVF 12
      ||: |||
Db      3 PFLVTVAF 11

RESULT 35
US-08-325-509-34
Sequence 34, Application US/08325509
Patent No. 5543308
GENERAL INFORMATION:
APPLICANT: MORGAN, RICHARD D.
TITLE OF INVENTION: ISOLATED DNA ENCODING THE FcE2
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR
PRODUCING THE SAME
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSER: GREGORY D. WILLIAMS, NEW ENGLAND
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,509
FILING DATE: 18-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-325-509-34

Query Match      31.7%  Score 26; DB 1; Length 13;
Best Local Similarity 66.7%  Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      10 EYVPPP 15
      ||: |||
Db      4 ELFPFP 9

RESULT 36
US-08-347-198A-19
Sequence 19, Application US/08347198A
Patent No. 5747046
GENERAL INFORMATION:
APPLICANT: MGN, Edward A.
APPLICANT: SMITH, Trevor S.
TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 - G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,198A
FILING DATE: 21-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/020,526
FILING DATE: 22-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,749
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P443-1289
TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-347-198A-19

Query Match 31.7% Score 26; DB 1; Length 15;  
Best Local Similarity 55.6%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLVEVP 12  
DB 3 PPLVTVEAP 11

RESULT 37  
US-09-552-802B-40  
Sequence 40, Application US/09552802B

Patent No. 6562943  
GENERAL INFORMATION:  
APPLICANT: Peakman, Mark  
APPLICANT: Chicz, Roman M.  
TITLE OF INVENTION: PEPTIDE BRITOPES RECOGNIZED BY DISEASE PROMOTING  
FILE REFERENCE: CD4+ T LYMPHOCYTES  
CURRENT APPLICATION NUMBER: US/09/552,802B  
CURRENT FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 09/295,868  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: US 60/130,355  
PRIOR FILING DATE: 1999-04-21  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 40  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-552-802B-40

Query Match 31.7% Score 26; DB 4; Length 17;  
Best Local Similarity 75.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 KLKVEVP 13  
DB 1 KLKVESSP 8

RESULT 38  
US-08-396-385-4  
Sequence 4, Application US/08396385

Patent No. 6001349  
GENERAL INFORMATION:  
APPLICANT: Schlom, Jeffrey  
APPLICANT: Panicali, Dennis  
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS  
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEWALL P. BRONSTEIN, DIKE, BRONSTEIN, ROBERTS  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/396,385  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44933  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRB UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-08-396-385-4

Query Match 30.5% Score 25; DB 3; Length 11;  
Best Local Similarity 55.6%; Pred. No. 6.4e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KLKVEVP 14  
DB 1 KLKVESSP 9

RESULT 39  
US-09-287-221-4  
Sequence 4, Application US/09287221

Patent No. 6319496  
GENERAL INFORMATION:  
APPLICANT: Schlom, Jeffrey  
APPLICANT: Panicali, Dennis  
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS  
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEWALL P. BRONSTEIN, DIKE, BRONSTEIN, ROBERTS  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/287,221  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/396,385  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44933  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRB UR  
INFORMATION FOR SEQ ID NO: 4:



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OM protein - protein search, using sw model

Run on: June 7, 2005, 23:00:52 ; Search time 67.5 Seconds  
(without alignments)  
85.185 Million cell updates/sec

Title: US-10-691-157-8  
Perfect score: 82  
Sequence: 1 LKPFKLVKVFPPF 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 38334425 residues

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Maximum Match 100%  
Listing first 100 summaries

Database :

Published Applications AA:\*

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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	82	100.0	15	US-10-691-157-8	Sequence 8, Appl1
3	82	100.0	15	US-10-691-330-8	Sequence 8, Appl1
4	37	45.1	18	US-09-864-761-40786	Sequence 40786, A
5	36	43.9	18	US-10-281-652-22	Sequence 22, Appl1
6	36	43.9	18	US-10-691-157-22	Sequence 22, Appl1
7	36	43.9	18	US-10-691-330-22	Sequence 22, Appl1
8	34.5	42.1	10	US-10-182-110-4	Sequence 4, Appl1
9	34	41.5	10	US-10-182-110-3	Sequence 3, Appl1
10	34	41.5	15	US-10-281-652-5	Sequence 5, Appl1
11	34	41.5	15	US-10-691-157-5	Sequence 5, Appl1

12	34	41.5	15	US-10-691-330-5	Sequence 5, Appl1
13	32	39.0	9	US-09-935-430-451	Sequence 451, App
14	32	39.0	9	US-09-935-430-555	Sequence 555, App
15	32	39.0	9	US-10-277-292-451	Sequence 451, App
16	32	39.0	9	US-10-277-292-555	Sequence 555, App
17	32	39.0	9	US-10-280-340-451	Sequence 451, App
18	32	39.0	9	US-10-280-340-555	Sequence 555, App
19	32	39.0	10	US-09-935-430-66	Sequence 66, Appl1
20	32	39.0	10	US-09-935-430-607	Sequence 607, App
21	32	39.0	10	US-10-277-292-66	Sequence 66, Appl1
22	32	39.0	10	US-10-277-292-607	Sequence 607, App
23	32	39.0	10	US-10-280-340-66	Sequence 66, Appl1
24	32	39.0	10	US-10-280-340-607	Sequence 607, App
25	32	39.0	16	US-10-225-667A-1110	Sequence 1110, Ap
26	32	39.0	17	US-10-474-955-64	Sequence 64, Appl1
27	31	37.8	13	US-09-766-412-39	Sequence 39, Appl1
28	30.5	37.2	18	US-10-226-007-1525	Sequence 1525, Ap
29	30	36.6	17	US-10-302-547-121	Sequence 121, App
30	29	35.4	9	US-10-884-862-93	Sequence 93, Appl1
31	29	35.4	12	US-09-281-717-31	Sequence 31, Appl1
32	29	35.4	12	US-09-281-717-35	Sequence 35, Appl1
33	28	34.1	12	US-10-333-235A-67	Sequence 67, Appl1
34	28	34.1	8	US-09-935-430-333	Sequence 333, App
35	28	34.1	9	US-10-277-292-333	Sequence 333, App
36	28	34.1	9	US-10-280-340-333	Sequence 333, App
37	28	34.1	9	US-10-884-862-63	Sequence 63, Appl1
38	28	34.1	9	US-10-884-862-146	Sequence 146, App
39	28	34.1	9	US-09-935-430-269	Sequence 269, App
40	28	34.1	10	US-09-935-430-356	Sequence 356, App
41	28	34.1	10	US-10-033-662-35	Sequence 35, Appl1
42	28	34.1	10	US-10-277-292-269	Sequence 269, App
43	28	34.1	10	US-10-280-340-269	Sequence 269, App
44	28	34.1	10	US-10-280-340-356	Sequence 356, App
45	28	34.1	10	US-09-918-111A-29	Sequence 29, Appl1
46	28	34.1	16	US-09-947-124-5	Sequence 5, Appl1
47	28	34.1	18	US-10-474-955-67	Sequence 67, Appl1
48	28	34.1	10	US-09-988-493-133	Sequence 133, App
49	27	32.9	10	US-10-014-340-427	Sequence 427, App
50	27	32.9	10	US-10-014-340-428	Sequence 428, App
51	27	32.9	10	US-10-203-334-2	Sequence 2, Appl1
52	27	32.9	10	US-10-601-837-131	Sequence 131, App
53	27	32.9	10	US-10-700-330-141	Sequence 140, App
54	27	32.9	10	US-10-100-049-25	Sequence 25, Appl1
55	27	32.9	11	US-10-340-458-24	Sequence 24, Appl1
56	27	32.9	12	US-10-500-804-24	Sequence 24, Appl1
57	27	32.9	12	US-10-474-955-110	Sequence 110, App
58	27	32.9	13	US-10-226-007-1513	Sequence 1513, App
59	27	32.9	14	US-09-969-730-339	Sequence 339, App
60	27	32.9	15	US-10-226-007-1514	Sequence 1514, App
61	27	32.9	15	US-10-226-007-1516	Sequence 1516, App
62	27	32.9	15	US-10-621-363-339	Sequence 339, App
63	27	32.9	15	US-10-682-420-80	Sequence 80, Appl1
64	27	32.9	15	US-10-682-420-81	Sequence 81, Appl1
65	27	32.9	15	US-10-409-613-80	Sequence 81, Appl1
66	27	32.9	15	US-10-409-613-81	Sequence 81, Appl1
67	27	32.9	15	US-10-442-180-80	Sequence 80, Appl1
68	27	32.9	15	US-10-442-180-81	Sequence 81, Appl1
69	27	32.9	15	US-10-474-955-109	Sequence 109, App
70	27	32.9	15	US-10-718-266-80	Sequence 80, Appl1
71	27	32.9	15	US-10-718-266-81	Sequence 81, Appl1
72	27	32.9	15	US-10-775-337-80	Sequence 80, Appl1
73	27	32.9	15	US-10-775-337-81	Sequence 81, Appl1
74	27	32.9	15	US-10-637-011-80	Sequence 80, Appl1
75	27	32.9	15	US-10-637-011-81	Sequence 81, Appl1
76	27	32.9	16	US-10-100-049-40	Sequence 40, Appl1
77	27	32.9	16	US-10-226-007-1515	Sequence 1515, App
78	27	32.9	16	US-10-226-007-1517	Sequence 1517, App
79	27	32.9	16	US-10-226-007-1519	Sequence 1519, App
80	27	32.9	17	US-09-754-831A-34	Sequence 34, Appl1
81	27	32.9	17		
82	27	32.9	10		
83	27	32.9	10		
84	27	32.9	10		

85	27	32.9	17	14	US-10-226-007-1518	Sequence 1518, Ap
86	27	32.9	17	14	US-10-226-007-1520	Sequence 1520, Ap
87	27	32.9	17	14	US-10-226-007-1522	Sequence 1522, Ap
88	27	32.9	17	16	US-10-302-547-120	Sequence 120, App
89	27	32.9	17	17	US-10-671-317-34	Sequence 34, Appl
90	27	32.9	18	14	US-10-226-007-1521	Sequence 1521, Appl
91	27	32.9	18	14	US-10-226-007-1523	Sequence 1523, Ap
92	26.5	32.3	13	9	US-09-030-619-93	Sequence 93, Appl
93	26.5	32.3	13	9	US-09-030-619-100	Sequence 100, App
94	26.5	32.3	13	14	US-10-229-368-8	Sequence 8, Appl
95	26.5	32.3	13	14	US-10-225-087-8	Sequence 93, Appl
96	26.5	32.3	13	15	US-10-277-232-93	Sequence 93, Appl
97	26.5	32.3	13	15	US-10-277-232-100	Sequence 100, App
98	26.5	32.3	13	15	US-10-277-233-93	Sequence 93, Appl
99	26.5	32.3	13	15	US-10-277-233-100	Sequence 100, App
100	26.5	32.3	13	15	US-10-351-985-22	Sequence 22, Appl

## ALIGNMENTS

## RESULT 1

US-10-281-652-8  
; Sequence 8, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265, 00220101  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-8

Query Match                      100.0%; Score 82; DB 14; Length 15;  
Best Local Similarity    100.0%; Pred. No. 3.2e-06;  
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY    1 LKPPKLVKVEVPPF 15

DB    1 LKPPKLVKVEVPPF 15

## RESULT 2

US-10-691-157-8  
; Sequence 8, Application US/10691157  
; Publication No. US2004026681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADIS, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUEL, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: 265, 00440101  
; CURRENT APPLICATION NUMBER: US/10/691,157  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-157-8

Query Match                      100.0%; Score 82; DB 16; Length 15;  
Best Local Similarity    100.0%; Pred. No. 3.2e-06;  
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY    1 LKPPKLVKVEVPPF 15

DB    1 LKPPKLVKVEVPPF 15

## RESULT 3

US-10-691-330-8  
; Sequence 8, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Bolodogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Krusel, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265,00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-8

Query Match                      100.0%; Score 82; DB 17; Length 15;  
Best Local Similarity    100.0%; Pred. No. 3.2e-06;  
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY    1 LKPPKLVKVEVPPF 15

DB    1 LKPPKLVKVEVPPF 15

## RESULT 4

US-09-864-761-40786  
; Sequence 40786, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

```

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40786
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC023296.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; US-09-864-761-40786

Query Match      45.1%; Score 37; DB 9; Length 18;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 KYEVPFP 15
       :|||
       3 REVAFPFP 10

RESULT 5
US-10-281-652-22
; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
```

```

; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265,00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-281-652-22

Query Match      43.9%; Score 36; DB 14; Length 18;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 PPKIKVEVF 12
       ||||
       5 PPKYVPEVF 14

RESULT 6
US-10-691-157-22
; Sequence 22, Application US/10691157
; Publication No. US2004026681A1
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: STANTON, G. John
; APPLICANT: GEORGIADIS, Jerzy
; APPLICANT: HUGHES, Thomas
; APPLICANT: KRUEZEL, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; FILE REFERENCE: 265,00440101
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
; US-10-691-157-22

Query Match      43.9%; Score 36; DB 16; Length 18;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 PPKIKVEVF 12
       ||||
       5 PPKYVPEVF 14

RESULT 7
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US-10-691-330-22  
; Sequence 22, Application US/10691330  
; Publication No. US20050042300A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldogh, Istvan  
; APPLICANT: Stanton, G. John  
; APPLICANT: Georgiades, Jerzy A.  
; APPLICANT: Hughes, Thomas K., Jr.  
; APPLICANT: Kruszal, Marian  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS  
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE  
; FILE REFERENCE: 265.00390101  
; CURRENT APPLICATION NUMBER: US/10/691,330  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US 60/420,369  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 22  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptides  
US-10-691-330-22

Query Match 43.9%; Score 36; DB 17; Length 18;  
Best Local Similarity 70.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKLKEVEF 12  
| | | | |  
DB 5 PPKLKEVEF 14  
| | | | |  
RESULT 8  
US-10-182-110-4  
; Sequence 4, Application US/10182110  
; Publication No. US20040171553A1  
; GENERAL INFORMATION:  
; APPLICANT: Regen Therapeutics plc  
; APPLICANT: Georgiades, Jerzy A.  
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use  
; FILE REFERENCE: AAT-14173  
; CURRENT APPLICATION NUMBER: US/10/182,110  
; PRIOR FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: GB0001825.9  
; PRIOR FILING DATE: 2000-01-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Truncated version of a peptide found in colostrinin  
US-10-182-110-4

Query Match 42.1%; Score 34.5; DB 16; Length 10;  
Best Local Similarity 81.8%; Pred. No. 69;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 5 PPLKVEVPPF 15  
| | | | |  
DB 1 PPLKVEV-PEP 10  
| | | | |  
RESULT 9  
US-10-182-110-3  
; Sequence 3, Application US/10182110  
; Publication No. US20040171553A1  
; GENERAL INFORMATION:  
; APPLICANT: Regen Therapeutics plc

; APPLICANT: Georgiades, Jerzy A  
; TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use  
; FILE REFERENCE: AAT-14173  
; CURRENT APPLICATION NUMBER: US/10/182,110  
; PRIOR FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: GB0001825.9  
; PRIOR FILING DATE: 2000-01-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Truncated version of a peptide found in colostrinin  
US-10-182-110-3

Query Match 41.5%; Score 34; DB 16; Length 10;  
Best Local Similarity 70.0%; Pred. No. 83;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PPLKVEVPPF 14  
| | | | |  
DB 1 PVLPEVPPF 10  
| | | | |  
RESULT 10  
US-10-281-652-5  
; Sequence 5, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-5

Query Match 41.5%; Score 34; DB 14; Length 15;  
Best Local Similarity 70.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PPLKVEVPPF 14  
| | | | |  
DB 5 PVLPEVPPF 14  
| | | | |  
RESULT 11  
US-10-691-157-5  
; Sequence 5, Application US/10691157  
; Publication No. US20040266681A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: STANTON, G. John  
; APPLICANT: GEORGIADES, Jerzy  
; APPLICANT: HUGHES, Thomas  
; APPLICANT: KRUSZAL, Marian



```

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS MODULATORS OF INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: 265, 00440101
; CURRENT APPLICATION NUMBER: US/10/691,157
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-157-5

Query Match          41.5%; Score 34; DB 16; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 PVLKVEVPPE 14
Db      5 PVLKVEVPPE 14

RESULT 12
US-10-691-330-5
; Sequence 5, Application US/10691330
; Publication No. US20050042300A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, G. John
; APPLICANT: Boldogh, Istvan
; APPLICANT: Georgiades, Terzy A.
; APPLICANT: Hughes, Thomas K., Jr.
; APPLICANT: Kruzel, Marian
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
; FILE REFERENCE: 265, 00390101
; CURRENT APPLICATION NUMBER: US/10/691,330
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US 60/420,369
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-5

Query Match          41.5%; Score 34; DB 17; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 PVLKVEVPPE 14
Db      5 PVLKVEVPPE 14

RESULT 13
US-09-935-430-451
; Sequence 451, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:

```

```

; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALIVITA-BID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050,00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-555

Query Match          39.0%; Score 32; DB 10; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 PPKLKLV 9
Db      2 PPKLKLV 8

RESULT 14
US-09-935-430-555
; Sequence 555, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALIVITA-BID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050,00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-555

Query Match          39.0%; Score 32; DB 10; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 PPKLKLV 9
Db      2 PPKLKLV 8

```

Db 2 PMPKLV 8

## RESULT 15

US-10-277-292-451  
; Sequence 451, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBYTZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/10/277,292  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 451  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-451

Query Match 39.0%; Score 32; DB 14; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLV 9  
| | | | |  
Db 2 PMPKLV 8

## RESULT 16

US-10-277-292-555  
; Sequence 555, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBYTZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/10/277,292  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 555  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-555

Query Match 39.0%; Score 32; DB 14; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLV 9  
| | | | |  
Db 2 PMPKLV 8

## RESULT 17

US-10-280-340-451  
; Sequence 451, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBYTZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/10/280,340  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 451  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-451

Query Match 39.0%; Score 32; DB 15; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLV 9  
| | | | |  
Db 2 PMPKLV 8

## RESULT 18

US-10-280-340-555  
; Sequence 555, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBYTZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7

;; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
;; OF INVENTION: OTHER CANCERS  
;; FILE REFERENCE: 51158-20050.00  
;; CURRENT APPLICATION NUMBER: US/10/280,340  
;; CURRENT FILING DATE: 2002-10-25  
;; PRIOR APPLICATION NUMBER: US/09/935,430  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/227,098  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/282,739  
;; PRIOR FILING DATE: 2001-04-10  
;; NUMBER OF SEQ ID NOS: 700  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 555  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-555

Query Match 39.0%; Score 32; DB 15; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLKV 9  
| | | | |  
Db 2 PMPKLV 8

RESULT 19  
US-09-935-430-66  
;; Sequence 66, Application US/09935430  
;; Publication No. US20030017466A1  
;; GENERAL INFORMATION:  
;; APPLICANT: PARIS, MARY  
;; APPLICANT: HUBERT, RENE  
;; APPLICANT: RAITANO, ARTHUR  
;; APPLICANT: AFAR, DANIEL  
;; APPLICANT: LEVIN, ELANA  
;; APPLICANT: CHALLITA-ELD, PIA  
;; APPLICANT: JAKOBOVITZ, AYA  
;; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
;; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
;; TITLE OF INVENTION: OTHER CANCERS  
;; FILE REFERENCE: 51158-20050.00  
;; CURRENT APPLICATION NUMBER: US/09/935,430  
;; CURRENT FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/227,098  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/282,739  
;; PRIOR FILING DATE: 2001-04-10  
;; NUMBER OF SEQ ID NOS: 700  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 66  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-935-430-66

Query Match 39.0%; Score 32; DB 10; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLKV 9  
| | | | |  
Db 2 PMPKLV 8

RESULT 20  
US-09-935-430-607

;; Sequence 607, Application US/09935430  
;; Publication No. US20030017466A1  
;; GENERAL INFORMATION:  
;; APPLICANT: PARIS, MARY  
;; APPLICANT: HUBERT, RENE  
;; APPLICANT: RAITANO, ARTHUR  
;; APPLICANT: AFAR, DANIEL  
;; APPLICANT: LEVIN, ELANA  
;; APPLICANT: CHALLITA-ELD, PIA  
;; APPLICANT: JAKOBOVITZ, AYA  
;; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
;; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
;; TITLE OF INVENTION: OTHER CANCERS  
;; FILE REFERENCE: 51158-20050.00  
;; CURRENT APPLICATION NUMBER: US/09/935,430  
;; CURRENT FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/227,098  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/282,739  
;; PRIOR FILING DATE: 2001-04-10  
;; NUMBER OF SEQ ID NOS: 700  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 607  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-935-430-607

Query Match 39.0%; Score 32; DB 10; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLKV 9  
| | | | |  
Db 2 PMPKLV 8

RESULT 21  
US-10-277-292-66  
;; Sequence 66, Application US/10277292  
;; Publication No. US20030199470A1  
;; GENERAL INFORMATION:  
;; APPLICANT: PARIS, MARY  
;; APPLICANT: HUBERT, RENE  
;; APPLICANT: RAITANO, ARTHUR  
;; APPLICANT: AFAR, DANIEL  
;; APPLICANT: LEVIN, ELANA  
;; APPLICANT: CHALLITA-ELD, PIA  
;; APPLICANT: JAKOBOVITZ, AYA  
;; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
;; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
;; TITLE OF INVENTION: OTHER CANCERS  
;; FILE REFERENCE: 51158-20050.00  
;; CURRENT APPLICATION NUMBER: US/10/277,292  
;; CURRENT FILING DATE: 2002-10-21  
;; PRIOR APPLICATION NUMBER: US/09/935,430  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/227,098  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/282,739  
;; PRIOR FILING DATE: 2001-04-10  
;; NUMBER OF SEQ ID NOS: 700  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 66  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-66

Query Match 39.0%; Score 32; DB 14; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9  
| | | | |  
DB 2 PMPKLKV 8

## RESULT 22

US-10-277-292-607  
; Sequence 607, Application US/10277292  
; Publication No. US2003019470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALILITA-EID, PIA  
; APPLICANT: JAKOBOWITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 607  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-607

Query Match 39.0%; Score 32; DB 14; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9  
| | | | |  
DB 2 PMPKLKV 8

## RESULT 23

US-10-280-340-66  
; Sequence 66, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALILITA-EID, PIA  
; APPLICANT: JAKOBOWITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-66

Query Match 39.0%; Score 32; DB 15; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9  
| | | | |  
DB 2 PMPKLKV 8

## RESULT 24

US-10-280-340-607  
; Sequence 607, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALILITA-EID, PIA  
; APPLICANT: JAKOBOWITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 607  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-607

Query Match 39.0%; Score 32; DB 15; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKLKV 9  
| | | | |  
DB 2 PMPKLKV 8

## RESULT 25

US-10-225-567A-1110  
; Sequence 110, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.

APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1930-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 1110  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-1110

Query Match 39.0%; Score 32; DB 14; Length 16;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPK 6  
DB 8 LKPPK 13

RESULT 26  
US-10-474-955-64  
Sequence 64, Application US/10474955  
Publication No. US20040241161A1  
GENERAL INFORMATION:  
APPLICANT: Drifhout, Jan W.  
APPLICANT: Konig, Frits  
APPLICANT: McAdam, Stephan N.  
APPLICANT: Ludwig, Solid Magne  
TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS  
FILE REFERENCE: 2799/71244-PCT-US  
CURRENT APPLICATION NUMBER: US/10/474,955  
CURRENT FILING DATE: 2003-10-13  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 64  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide sequence in pool 54  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (17)-(18)  
OTHER INFORMATION: "Y" on position 17 is P/S  
US-10-474-955-64

Query Match 39.0%; Score 32; DB 16; Length 17;  
Best Local Similarity 46.7%; Pred. No. 3e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

QY 1 LKPPKAKVEVPFP 15  
DB 3 LKPPKAKVEVPFP 13

RESULT 27  
US-09-766-412-39  
Sequence 39, Application US/09766412  
Patent No. US20020103129A1  
GENERAL INFORMATION:  
APPLICANT: GE, Rucwen et al.  
TITLE OF INVENTION: SMALL PEPTIDES HAVING ANTI-ANGIOGENIC AND ENDOTHELIAL CELL INHIBIT  
FILE REFERENCE: 1781-0215P  
CURRENT APPLICATION NUMBER: US/09/766,412  
CURRENT FILING DATE: 2001-01-11  
NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 39  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Mammalian  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: SHFLT2  
US-09-766-412-39

Query Match 37.8%; Score 31; DB 9; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKPPKAKVEVP 12  
DB 1 LKPPKAKVEVP 12

RESULT 28  
US-10-226-007-1525  
Sequence 1525, Application US/10226007  
Publication No. US20030105277A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
FILE REFERENCE: 5005.01  
CURRENT APPLICATION NUMBER: US/10/226,007  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: US 60/313,883  
PRIOR FILING DATE: 2001-08-21  
NUMBER OF SEQ ID NOS: 1673  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 1525  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Lymphocytic choriomeningitis virus  
US-10-226-007-1525

Query Match 37.2%; Score 30.5; DB 14; Length 18;  
Best Local Similarity 50.0%; Pred. No. 5.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 3 PFP-KLAKVEVPFP 15  
DB 1 PLPTKLKISTAPSP 14

RESULT 29  
US-10-302-547-121  
Sequence 121, Application US/10302547  
Publication No. US20040142448A1  
GENERAL INFORMATION:  
APPLICANT: MORPHY, BRIAN R.  
APPLICANT: COLLINS, PETER L.  
APPLICANT: SKIADOPOULOS, MARIO H.  
APPLICANT: NEWMAN, JASON T.  
TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE  
TITLE OF INVENTION: 1 (HPIV1) FROM CDNA AND USE OF RECOMBINANT HPIV1 IN  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT  
FILE REFERENCE: 2303-37-3  
CURRENT APPLICATION NUMBER: US/10/302,547  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: 60/331,961  
PRIOR FILING DATE: 2001-11-21  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO: 121  
LENGTH: 17

TYPE: PRT  
ORGANISM: Murine parainfluenza virus 1  
US-10-302-547-121

Query Match 36.6%; Score 30; DB 16; Length 17;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKPPKLKVEVPF 14  
DB 4 LKDFPKRYEYHVPY 17

RESULT 30  
US-10-884-862-93  
Sequence 93, Application US/10884862  
Publication No. US20050048071A1  
GENERAL INFORMATION:  
APPLICANT: BAE, Joo-eun  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES  
FILE REFERENCE: 047940-0239  
CURRENT APPLICATION NUMBER: US/10/884,862  
CURRENT FILING DATE: 2004-07-02  
PRIOR APPLICATION NUMBER: US 60/484689  
PRIOR FILING DATE: 2003-07-03  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 93  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-884-862-93

Query Match 35.4%; Score 29; DB 17; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKPPKLKY 9  
DB 1 LKPFKLKSL 9

RESULT 31  
US-09-281-717-31  
Sequence 31, Application US/09281717  
Patent No. US20020061539A1  
GENERAL INFORMATION:  
APPLICANT: Baxter, John D.  
APPLICANT: Dairmont, Beatrice  
APPLICANT: Feng, Weijun  
APPLICANT: Fletterick, Robert J.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: West, Brian  
APPLICANT: Yamamoto, Keith R.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
FILE REFERENCE: UCAL-253/02US  
CURRENT APPLICATION NUMBER: US/09/281,717  
CURRENT FILING DATE: 1999-03-30  
EARLIER APPLICATION NUMBER: US 60/079,956  
EARLIER FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (5)  
OTHER INFORMATION: Leu --> Arg (L454R)  
FEATURE:

NAME/KEY: MUTAGEN  
LOCATION: (7)  
OTHER INFORMATION: Leu --> Arg (L456R)  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (8)  
OTHER INFORMATION: Glu --> Lys (E457K)  
US-09-281-717-31

Query Match 35.4%; Score 29; DB 9; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPPLKVEVPF 12  
DB 2 PPPLFLVEVP 10

RESULT 32  
US-09-281-717-33  
Sequence 33, Application US/09281717  
Patent No. US20020061539A1  
GENERAL INFORMATION:  
APPLICANT: Baxter, John D.  
APPLICANT: Dairmont, Beatrice  
APPLICANT: Feng, Weijun  
APPLICANT: Fletterick, Robert J.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: West, Brian  
APPLICANT: Yamamoto, Keith R.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
FILE REFERENCE: UCAL-253/02US  
CURRENT APPLICATION NUMBER: US/09/281,717  
CURRENT FILING DATE: 1999-03-30  
EARLIER APPLICATION NUMBER: US 60/079,956  
EARLIER FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 33  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-281-717-33

Query Match 35.4%; Score 29; DB 9; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPPLKVEVPF 12  
DB 2 PPPLFLVEVP 10

RESULT 33  
US-09-281-717-35  
Sequence 35, Application US/09281717  
Patent No. US20020061539A1  
GENERAL INFORMATION:  
APPLICANT: Baxter, John D.  
APPLICANT: Dairmont, Beatrice  
APPLICANT: Feng, Weijun  
APPLICANT: Fletterick, Robert J.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: West, Brian  
APPLICANT: Yamamoto, Keith R.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
FILE REFERENCE: UCAL-253/02US  
CURRENT APPLICATION NUMBER: US/09/281,717  
CURRENT FILING DATE: 1999-03-30

EARLIER APPLICATION NUMBER: US 60/079,956  
EARLIER FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-281-717-35

Query Match 35.4%; Score 29; DB 9; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PPKLKEVF 12  
Db 2 PPKLKEVF 10

RESULT 34  
US-10-333-235A-67  
Sequence 67, Application US/10333235A  
Publication No. US20040132007A1  
GENERAL INFORMATION:  
APPLICANT: COT-A-GENE AB  
APPLICANT: Leif, Lindholm  
APPLICANT: Karin, Nord  
APPLICANT: Pierre, Boulanger  
APPLICANT: Rebecca, Gardner  
TITLE OF INVENTION: Modified Virus  
FILE REFERENCE: 9.7.72728/001  
CURRENT APPLICATION NUMBER: US/10/333,235A  
CURRENT FILING DATE: 2003-12-04  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 67  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Linker peptide  
US-10-333-235A-67

Query Match 34.1%; Score 28; DB 16; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEVPP 13  
Db 2 KVEVPP 7

RESULT 35  
US-09-935-430-333  
Sequence 333, Application US/09935430  
Publication No. US20030017466A1  
GENERAL INFORMATION:  
APPLICANT: PARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALITA-ETD, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/09/935,430  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739

PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 333  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-935-430-333

Query Match 34.1%; Score 28; DB 10; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLX 8  
Db 4 PPKLX 9

RESULT 36  
US-10-277-292-333  
Sequence 333, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: PARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALITA-ETD, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 333  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-333

Query Match 34.1%; Score 28; DB 14; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPKLX 8  
Db 4 PPKLX 9

RESULT 37  
US-10-280-340-333  
Sequence 333, Application US/10280340  
Publication No. US20030207835A1  
GENERAL INFORMATION:  
APPLICANT: PARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA

```

; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-333

```

```

Query Match          34.1%; Score 28; DB 15; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 PPKPKL 8
        |||||
DB      4 PMPKPK 9

```

```

RESULT 38
; Sequence 63, Application US/10884862
; Publication No. US20050048071A1
; GENERAL INFORMATION:
; APPLICANT: BAE, JOO-eun
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0238
; CURRENT APPLICATION NUMBER: US/10/884,862
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/484689
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-862-63

```

```

Query Match          34.1%; Score 28; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 LKPPKLT 7
        |||||
DB      3 LKPFLKL 9

```

```

RESULT 39
US-10-884-862-146
; Sequence 146, Application US/10884862
; Publication No. US20050048071A1
; GENERAL INFORMATION:
; APPLICANT: BAE, JOO-eun
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0238
; CURRENT APPLICATION NUMBER: US/10/884,862
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: US 60/484689

```

```

; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-862-146

```

```

Query Match          34.1%; Score 28; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 LKPPKLT 7
        |||||
DB      2 LKPFLKL 8

```

```

RESULT 40
US-09-935-430-269
; Sequence 269, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARRIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-269

```

```

Query Match          34.1%; Score 28; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 PPKPKL 8
        |||||
DB      5 PMPKPK 10

```

```

Search completed: June 7, 2005, 23:31:41
Job time : 69.5 secs

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: June 7, 2005, 22:55:36 ; Search time 13.9091 Seconds  
(without alignments)  
103.763 Million cell updates/sec

Title: US-10-691-157-8  
Perfect score: 82  
Sequence: 1 LKPPFKLKEVFPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	40.2	18	2	A60915
2	24	28.3	17	2	S78756
3	23.5	28.7	18	2	S04229
4	23	28.0	9	2	PC7073
5	22	26.8	13	2	CS3275
6	22	26.8	17	2	G85956
7	22	26.8	18	2	A42576
8	22	26.8	18	2	A61220
9	21.5	26.2	16	2	A48301
10	21	25.6	8	2	S66646
11	21	25.6	11	1	XASNBA
12	21	25.6	15	2	PS0452
13	21	25.6	15	2	PA0060
14	21	25.6	16	2	PH0758
15	21	25.6	16	2	I40065
16	20.5	25.0	14	2	H64008
17	20	24.4	6	2	A61049
18	20	24.4	10	2	A60624
19	20	24.4	10	2	A60410
20	20	24.4	10	2	A90917
21	20	24.4	10	2	A90345
22	20	24.4	11	2	PA0028
23	20	24.4	11	2	S07207
24	20	24.4	13	2	S32475
25	20	24.4	14	2	PH1566
26	20	24.4	15	1	LRECP
27	20	24.4	15	2	PA0026
28	20	24.4	15	2	PA0024
29	20	24.4	15	2	PA0088

30	20	24.4	15	2	PD0444	coupling factor 6
31	20	24.4	16	2	A53337	regulatory protein
32	20	24.4	17	2	A37823	dihydroliponamide S
33	20	24.4	18	2	S14661	photosystem I prot
34	20	24.4	18	2	S09731	photosystem I prot
35	20	24.4	18	2	A61392	brain-associated s
36	20	24.4	18	2	H75063	hypothetical prote
37	19	23.2	9	2	S66635	alpha-2-macroglobu
38	19	23.2	10	2	S65432	angiotensin I - ho
39	19	23.2	10	2	A61218	alpha-gliadin 4Ha
40	19	23.2	10	2	B61218	alpha-gliadin 6Ha
41	19	23.2	12	2	C20907	Ig kappa-1 chain J
42	19	23.2	13	2	S32474	lymadpamide 4 - g
43	19	23.2	14	2	A01250	angiotensin I prec
44	19	23.2	15	2	A60834	angiotensin I prec
45	19	23.2	15	2	S29207	avenin gamma-4 - O
46	19	23.2	15	2	C61511	milk band B protei
47	19	23.2	16	2	S33590	beta-crystallin A3
48	19	23.2	16	2	A20190	hypodermin B - ear
49	19	23.2	18	2	PN0149	beta-gliadin 13 -
50	18.5	22.6	17	2	S59481	hydroxyproline-ric
51	18	22.0	8	2	A46306	spasmogenic toxin
52	18	22.0	9	2	I46023	growth hormone rec
53	18	22.0	10	2	S74147	glyceroldehyde-3-p
54	18	22.0	11	2	S78026	ribosomal protein
55	18	22.0	11	2	PC2254	cytochrome P450 3A
56	18	22.0	11	2	S33519	probable secreted
57	18	22.0	12	2	PA0098	ribosomal protein
58	18	22.0	12	2	PH1567	cerebrin 28 - huma
59	18	22.0	13	2	A60458	protocatechuate 3,
60	18	22.0	13	2	B44957	protein I7 - commo
61	18	22.0	13	2	S23640	Ig kappa chain J s
62	18	22.0	13	2	S21152	tryptophyltin-rela
63	18	22.0	15	2	B31061	hypothetical prote
64	18	22.0	15	2	A28965	ribulose-bisphosph
65	18	22.0	16	2	D45193	zinc finger protei
66	18	22.0	17	2	S29165	quinadine oxide
67	18	22.0	17	2	I55612	thyroid hormone re
68	17.5	21.3	15	2	A41436	alpha-macroglobuli
69	17	20.7	9	2	S35338	ribosomal protein
70	17	20.7	9	2	A4873	caldesmon - rabbit
71	17	20.7	10	1	XASNPC	angiotensin-conver
72	17	20.7	10	2	JC1367	thryoliberin poten
73	17	20.7	10	2	H28027	protein p11 - curi
74	17	20.7	10	2	A60476	S-layer protein -
75	17	20.7	10	2	B31143	pneumadin - huma
76	17	20.7	10	2	A33143	proteasome endope
77	17	20.7	11	2	G42762	substance P - Atla
78	17	20.7	11	2	S23306	ranacthykinin A -
79	17	20.7	11	2	A61033	glutathione transf
80	17	20.7	11	2	D61033	histone H2B - huma
81	17	20.7	12	2	S17869	enterotoxin C-1 -
82	17	20.7	12	2	A60757	Ig kappa chain J1
83	17	20.7	12	2	S67540	hypothetical prote
84	17	20.7	12	2	A20907	lymadpamide 2 - g
85	17	20.7	13	2	S32472	Ig kappa chain J s
86	17	20.7	13	2	S23638	223K exoantigen -
87	17	20.7	14	2	S33098	superoxide dismuta
88	17	20.7	16	2	B58503	calmodulin kinase
89	17	20.7	16	2	T44936	glutathione transf
90	17	20.7	17	2	C37520	chlorophyll a/b-bi
91	17	20.7	17	2	S50901	extensin - maize (
92	17	20.7	17	2	S33609	T-cell receptor be
93	17	20.7	17	2	C49255	proteasome endope
94	17	20.7	17	2	PC2319	neurofibromatosis-
95	17	20.7	18	2	B35910	thrombopoietin rec
96	17	20.7	18	2	I78841	arsenite oxidase I
97	17	20.7	18	2	A45138	locustamyotropin I
98	17	20.7	18	2	A61620	ubiquitin thioleat
99	16.5	20.1	15	2	S10891	
100	16.5	20.1	15	2	S10891	

## ALIGNMENTS

## RESULT 1

A60915 enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)

N:Alternate names: aminoenkephalinase; aminopeptidase MII  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004C:Accession: A60915  
R:Dyer, S.H.; Slaughter, C.A.; Orth, K.; Noonan, C.R.; Hersh, L.B.  
J. Neurochem. 54, 547-554, 1990A:Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive  
A:Reference number: A60915; PMID:90132681; PMID:2299352  
A:Accession: A60915

A:Molecule type: protein

A:Residues: 1-18 &lt;DYE&gt;

A:Cross-references: UNIPROT:Q7M076

A>Note: this sequence represents the N-terminus of both soluble and membrane-associated  
C:Superfamily: membrane alanyl aminopeptidase

C:Keywords: hydrolase

## Query Match

Best Local Similarity 40.2%; Score 33; DB 2; Length 18;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPFPKLKVEVP 13

Db 4 PPFERLPTVSP 15

## RESULT 2

S78756 ribosomal protein MRP-15, mitochondrial - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999C:Accession: S78756  
R:Grack, H.R.submitted to the Protein Sequence Database, May 1999  
A:Reference number: S78756

A:Accession: S78756

A:Molecule type: protein

A:Residues: 1-12/13-17 &lt;GRA&gt;

C:Keywords: mitochondrion

## Query Match

Best Local Similarity 29.3%; Score 24; DB 2; Length 17;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PFPKLKVE 10

Db 3 PFELEVE 10

## RESULT 3

S04229 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24k chain - rat (fragment)

N:Alternate names: glycosylasparaginase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993C:Accession: S04229  
R:Tollersrud, O.K.; Aronson Jr., N.N.  
Biochem. J. 260, 101-108, 1989A:Title: Purification and characterization of rat liver glycosylasparaginase.  
A:Reference number: S04228; PMID:89374025; PMID:2775174

A:Accession: S04229

A:Molecule type: protein

A:Residues: 1-18 &lt;TOL&gt;

C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase

C:Keywords: hydrolase

## Query Match

Best Local Similarity 28.7%; Score 23.5; DB 2; Length 18;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 PFPKLKVEVP 14

Db 3 PFPKLKVEVP 13

## RESULT 4

PC7073 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004C:Accession: PC7073  
R:Tangita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Matsui, T.; Watanabe, Y.

Electrophoresis 21, 1853-1871, 2000

A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t

A:Reference number: PC7072

A:Accession: PC7073

A:Molecule type: protein

A:Residues: 1-9 &lt;TSU&gt;

A:Cross-references: UNIPROT:O9CVK7

C:Keywords: brain; core protein; oxidoreductase

## Query Match

Best Local Similarity 28.0%; Score 23; DB 2; Length 9;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

## RESULT 5

CS3275 Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-1996C:Accession: CS3275  
R:Avadi, H.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.  
A:Reference number: A53275; PMID:91372868; PMID:1909995

A:Accession: CS3275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 &lt;DNA&gt;

A>Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:56164)  
C:Comment: This J3 segment may not be functional because of substitutions in the 7 mer a

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 26.8%; Score 22; DB 2; Length 13;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PFKLVVVP 13

Db 5 PFKLVVVP 13

## RESULT 6

G85956 hypothetical protein 24331 [imported] - Escherichia coli (strain O157:H7, substrain EDLs

C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004C:Accession: G85956  
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, B.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; PMID:21074935; PMID:11206551  
A:Accession: G85956  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 7  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 8  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 9  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 10  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 11  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

RESULT 12  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:O8X4A4; GB:AE005174; NID:G12517539; PIDN:AGS8115.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:GeneID:8  
A:Gene: 24331

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 17;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VFPP 15  
DB 4 VSPFP 8

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C:Accession: A48301  
R:Grimm, B.; Bull, A.; Welinder, K.G.; Gough, S.P.; Kannangara, C.G.  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998  
C:Accession: A42576  
R:Yem, A.W.; Tomasselli, A.G.; Heinrikson, R.L.; Zurcher-Neely, H.; Ruff, V.A.; Johnson, J. Biol. Chem. 267, 2868-2871, 1992  
A:Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 and A:Reference number: A42576; MUID:92147620; PMID:1371107  
A:Accession: A42576  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <YEM>  
A:Experimental data: thymus  
A:Note: sequence extracted from NCBI backbone (NCBI:80696)  
C:Superfamily: human FK506-binding protein FKBP51; BGBP-type peptidylprolyl isomerase hc C:Keywords: steroid hormone receptor

Query Match  
Best Local Similarity 57.1%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVPP 14  
DB 11 EVELFEP 17

RESULT 8  
A:Residues: 1-18 <YEM>  
A:Cross-references: UNIPROT:Q7M060  
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23 C:Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFP 6  
DB 2 KPAP 6

RESULT 9  
A:Residues: 1-18 <YEM>  
A:Cross-references: UNIPROT:Q7M060  
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23 C:Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFP 6  
DB 2 KPAP 6

RESULT 10  
A:Residues: 1-18 <YEM>  
A:Cross-references: UNIPROT:Q7M060  
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23 C:Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFP 6  
DB 2 KPAP 6

RESULT 11  
A:Residues: 1-18 <YEM>  
A:Cross-references: UNIPROT:Q7M060  
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23 C:Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFP 6  
DB 2 KPAP 6

RESULT 12  
A:Residues: 1-18 <YEM>  
A:Cross-references: UNIPROT:Q7M060  
A:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23 C:Keywords: hydrolase; serine proteinase

Query Match  
Best Local Similarity 80.0%; Score 22; DB 2; Length 18;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFP 6  
DB 2 KPAP 6

RESULT 12  
 PS0452  
 32K protein 3306 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C:Accession: PS0452  
 R:Tsugita, A.; Miyatake, N.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0208  
 A:Accession: PS0452  
 A:Molecule type: protein  
 A:Residues: 1-15 <TSU>  
 A:Experimental source: bran, strain Nihonbare  
 C:Comment: molecular weight 32K, pI 5.3.

Query Match 25.6%; Score 21; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPKKL 7  
 |||  
 Db 6 PPKL 10

RESULT 13  
 PA0060  
 protein QP200037 - fungus (Fusarium sporotrichioides) (fragment)  
 C:Species: Fusarium sporotrichioides  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0060  
 R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A:Reference number: PA0051  
 A:Accession: PA0060  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>

Query Match 25.6%; Score 21; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPK 6  
 |||  
 Db 2 LRPLPE 7

RESULT 14  
 PH0758  
 T-cell receptor beta chain (E22) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C:Accession: PH0758  
 R:Caesnova, J.L.; Romero, P.; Wiemann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A:Reference number: PH0746; MUID:92078846; PMID:1836010  
 A:Accession: PH0758  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <CAS>  
 A:Cross-references: EMBL:X60853; NID:G50743; PID:CAA43243.1; PID:G50744  
 A:Experimental source: T lymphocyte  
 C:Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPKKLVEVF 12  
 |||  
 Db 5 PTKGSNTVEVF 14

RESULT 15  
 I40065  
 Shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
 C:Species: Buchnera aphidicola  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I40065  
 R:Roubaksh, D.; Baumann, P.  
 Gene 155, 107-112, 1995  
 A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont)  
 A:Reference number: I40061; MUID:95212914; PMID:7535281  
 A:Accession: I40065  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: UNIPROT:Q44610; EMBL:U10499; NID:G854717; PIDN:AAA79128.1; PID:G8547  
 C:Genetics:  
 A:Gene: aroL  
 C:Keywords: oxidoreductase

Query Match 25.6%; Score 21; DB 2; Length 16;  
 Best Local Similarity 60.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPKLK 8  
 |||  
 Db 9 PPKLR 13

RESULT 16  
 H64008  
 hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
 C:Accession: H64008  
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
 R:Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: H64000; MUID:95350630; PMID:7542800  
 A:Accession: H64008  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-14 <TRIG>  
 A:Cross-references: GB:U02731; GB:L42023; NID:G1573465; PID:G1573478; TIGR:HI0492

Query Match 25.0%; Score 20.5; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
 Matches 4; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 LKP-PPKL 7  
 |||  
 Db 1 MKPKTPKM 8

RESULT 17  
 A61049  
 halo-toxin - Pseudomonas syringae pv. mori  
 C:Species: Pseudomonas syringae pv. mori  
 C:Date: host mulberry tree  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
 C:Accession: A61049  
 R:Kajimoto, T.; Yokomizo, K.; Yabito, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;  
 Chem. Lett. 00, 679-680, 1989  
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri  
 A:Reference number: A61049  
 A:Accession: A61049  
 A:Molecule type: protein  
 A:Residues: 1-6 <KAJ>  
 A>Note: sequence confirmed by synthesis  
 C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry

C:Keywords: toxin

Query Match 24.4%; Score 20; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5  
|||  
DB 1 PFP 3

RESULT 18

A60624

angiotensin I - Japanese quail

C:Species: Coturnix coturnix japonica (Japanese quail)

C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 09-Jul-2004

C:Accession: A60624

R:Takei, Y.; Hasegawa, Y.

Gen. Comp. Endocrinol. 79, 12-22, 1990

A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of the

A:Reference number: A60624; MUID:90284684; PMID:2191893

A:Accession: A60624

A:Molecule type: protein

A:Residues: 1-10 <TR>

A:Cross-references: UNIPROT:P01018

C:Superfamily: Serpin

C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 24.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYEVPFP 14  
:|:|:|  
DB 2 RYVYVFP 8

RESULT 19

A60410

beta-neoendorphin / dynorphin precursor - guinea pig

N:Alternate names: alpha-neoendorphin; proenkephalin B precursor

C:Species: Cavia porcellus (guinea pig)

C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 21-Jan-2000

C:Accession: A60410

R:Murphy, R.; Turner, C.A.

Peptides 11, 65-68, 1990

A:Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.

A:Reference number: A60410; MUID:90259864; PMID:2342931

A:Accession: A60410

A:Molecule type: protein

A:Residues: 1-10 <MR>

C:Superfamily: proenkephalin

C:Keywords: neuropeptide; opioid peptide

Query Match 24.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPK 6  
||:|  
DB 5 LRYVFP 10

RESULT 20

A90917

angiotensin precursor - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 09-Jul-2004

C:Accession: A90917; A01250

R:Nakayama, T.; Nakajima, T.; Sokabe, H.

Chem. Pharm. Bull. 21, 2085-2087, 1973

A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its

A:Reference number: A90917; MUID:74127845; PMID:4361802

A:Accession: A90917

A:Molecule type: protein

A:Residues: 1-10 <NA>

A:Cross-references: UNIPROT:P01018

C:Keywords: blood pressure control; hormone; vasoconstrictor

F:1-10/Product: angiotensin I #status experimental <AN1>

F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYEVPFP 14  
:|:|:|  
DB 2 RYVYVFP 8

RESULT 21

A90345

angiotensin precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 09-Jul-2004

C:Accession: A90345; A01250

R:Elliot, D.F.; Peart, W.S.

Biochem. J. 65, 246-254, 1957

A:Title: The amino acid sequence in a hypertensin.

A:Reference number: A90345

A:Accession: A90345

A:Molecule type: protein

A:Residues: 1-10 <EL>

A:Cross-references: UNIPROT:P01017

C:Keywords: blood pressure control; hormone; vasoconstrictor

F:1-10/Product: angiotensin I #status experimental <AN1>

F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KYEVPFP 14  
:|:|:|  
DB 2 RYVYVFP 8

RESULT 22

PA0028

protein QA30042 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C:Accession: PA0028

R:Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JRPD, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona

A:Reference number: PA0001

A:Accession: PA0028

A:Molecule type: protein

A:Residues: 1-11 <AM>

A:Experimental source: seed

Query Match 24.4%; Score 20; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5  
|||  
DB 6 PFP 8

RESULT 23

S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C:Species: Crinia georgiana

C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Aug-2004  
 C/Accession: S07207  
 R:Erpamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.  
 Experimentia 35, 1132-1133, 1979  
 A>Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1  
 A/Reference number: S07207; MUID:80024575; PMID:488254  
 A/Accession: S07207  
 A/Molecule type: protein  
 A/Residues: 1-11 <ERS>  
 A/Cross-references: UNIPROT:P09037

Query Match 24.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 PRLKVEVFP 14  
 | : : | | |  
 DB 2 PDRIVHPF 11

RESULT 24  
 S32475  
 LymadFamide 5 - great pond snail  
 C/Species: Lymnaea stagnalis (great pond snail)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S32475  
 R:Johnsen, A.H.; Rehfeld, J.F.  
 Eur. J. Biochem. 213, 875-879, 1993  
 A>Title: LymadFamide, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
 A/Reference number: S32475; MUID:93238777; PMID:8477756  
 A/Accession: S32475  
 A/Molecule type: protein  
 A/Residues: 1-13 <IOH>  
 A/Cross-references: UNIPROT:P80182; PIDN:AMB26366.1; PID:g299833  
 A/Experimental source: ganglia  
 C/Keywords: amidated carboxyl end; neuropeptide  
 F/13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 24.4%; Score 20; DB 2; Length 13;  
 Best Local Similarity 30.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 PPKLVEVFP 12  
 | : : |  
 DB 1 PDRISSAF 10

RESULT 25  
 PH1566  
 cerebrin 30 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
 C/Accession: PH1566  
 R:Deone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
 J. Neurochem. 61, 533-540, 1993  
 A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance  
 A/Reference number: PH1566; MUID:93329419; PMID:8336140  
 A/Accession: PH1566  
 A/Molecule type: protein  
 A/Residues: 1-14 <LEO>

Query Match 24.4%; Score 20; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 3.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 PRLKVEVFP 13  
 | : : | | |  
 DB 2 PRAQVSVQP 10

RESULT 26  
 LFECF  
 phe operon leader peptide - Escherichia coli (strain K-12)

N/Alternate names: attenuator peptide  
 C/Species: Escherichia coli  
 C/Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
 C/Accession: A03593; B36494; A65038  
 R:Zurawski, G.; Brown, K.; Kittingly, D.; Yanofsky, C.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978  
 A>Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli  
 A/Reference number: A03593; MUID:79033820; PMID:360214  
 A/Accession: A03593  
 A/Molecule type: DNA  
 A/Residues: 1-15 <ZUR>  
 A/Cross-references: UNIPROT:P03057; GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1; P  
 R:Gavin, N.; Davidson, B.E.  
 J. Biol. Chem. 265, 21532-21535, 1990  
 A>Title: pheAO mutants of Escherichia coli have a defective pheA attenuator.  
 A/Reference number: A36494; MUID:91072346; PMID:2254312  
 A/Accession: B36494  
 A/Molecule type: DNA  
 A/Residues: 1-15 <GAV>  
 A/Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1; PID:g147180  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A>Title: The complete genome sequence of Escherichia coli K-12.  
 A/Reference number: A64720; MUID:97426617; PMID:9278503  
 A/Accession: A65038  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Accession: A65038  
 A/Molecule type: DNA  
 A/Residues: 1-15 <BLAT>  
 A/Cross-references: GB:A0000346; GB:U00096; NID:g2367141; PIDN:AAC75647.1; PID:g178950;  
 A/Experimental source: strain K-12, substrain MG1655  
 C/Genetics:  
 A/Gene: pheA; pheA  
 A/Map position: 56 min  
 C/Superfamily: pheA leader peptide

Query Match 24.4%; Score 20; DB 1; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 4e+03;  
 Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 LKPPKLVVFP 15  
 | : | | | |  
 DB 1 MKHDPFPAFPPTFP 15

RESULT 27  
 PA0026  
 protein QA300027 - Arabidopsis thaliana (fragment)  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C/Accession: PA0026  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.  
 submitted to JIPID, July 1994  
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
 A/Reference number: PA0001  
 A/Accession: PA0026  
 A/Molecule type: protein  
 A/Residues: 1-15 <KAM>  
 A/Experimental source: leaf

Query Match 24.4%; Score 20; DB 2; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 4e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 LKVEVFP 14  
 | | | | |  
 DB 2 LKVYGVXP 9

RESULT 28  
 PA0024  
 protein QA300050 - Arabidopsis thaliana (fragment)  
 C/Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0024  
R:Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions  
A:Reference number: PA0001  
A:Accession: PA0024  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Experimental source: seed

Query Match 24.4%; Score 20; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5  
|||  
Db 6 PFP 8

## RESULT 29

PA0088  
Protein QP200051 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0088  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0088  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>

Query Match 24.4%; Score 20; DB 2; Length 15;  
Best Local Similarity 27.3%; Pred. No. 4e+03;  
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 PRLKVEVFP 15  
|:|:|  
Db 3 PDIPXDYPAP 13

## RESULT 30

PD0444  
Coupling factor 6 mitochondrial - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999  
C:Accession: PD0444  
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, August 1998  
A:Description: Proteome analysis of mouse brain.  
A:Reference number: PD0441  
A:Contents: Striatum  
A:Accession: PD0444  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
C:Keywords: mitochondrion

Query Match 24.4%; Score 20; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKPPKLYVE 10  
|:|:|  
Db 4 LDPVQKLFVD 13

## RESULT 31

AS3337  
regulatory protein tyrR - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C>Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 07-May-1999

C:Accession: AS3337  
R:Arguet, V.P.; Wilson, T.J.; Davidson, B.E.  
J. Biol. Chem. 269: 5171-5178, 1994  
A>Title: Purification of the Escherichia coli regulatory protein TyrR and analysis of it  
A:Reference number: AS3337; MUID:94148980; PMID:8106498  
A:Accession: AS3337  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <ARG>

Query Match 24.4%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVEVF 12  
::|:|  
Db 1 MRLVVF 6

## RESULT 32

A37823  
dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 09-Jul-2004  
C:Accession: A37823  
R:Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.  
J. Biol. Chem. 265: 14512-14517, 1990  
A>Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon select  
A:Reference number: A37823; MUID:90354445; PMID:2167319  
A:Accession: A37823  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <RAH>  
A:Cross-references: UNIPROT:Q7M2M8  
C:Keywords: acyltransferase; coenzyme A

Query Match 24.4%; Score 20; DB 2; Length 17;  
Best Local Similarity 55.6%; Pred. No. 4.6e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PRLKVEVFP 13  
||:|:|  
Db 2 PKGRVFPVSP 10

## RESULT 33

S14661  
photosystem I protein psaa - maize (fragment)  
C:Species: Zea mays (maize)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S14661  
R:Kangasjarvi, J.; Gengenbach, B.G.  
submitted to the EMBL Data Library, March 1991  
A:Description: Nucleotide sequence of maize plastid genome BamHI 14 fragment.  
A:Reference number: S14660  
A:Accession: S14661  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-18 <KAN>  
A:Cross-references: EMBL:X58080; NID:g12429; PIDN:CAA41109.1; PID:g12431  
C:Superfamily: photosystem I P700 apoprotein

Query Match 24.4%; Score 20; DB 2; Length 18;  
Best Local Similarity 42.9%; Pred. No. 4.9e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PRLKVEV 11  
|:|:|  
Db 8 PEVKIIV 14

## RESULT 34

S09731

photosystem I protein psal - spinach chloroplast (fragment)  
C:Species: chloroplast Spinacia oleracea (spinach)  
C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 19-Jan-1996  
C:Accession: S09731  
R:Ikemuchi, M.; Hirano, A.; Hiyaama, T.; Inoue, Y.  
FEBS Lett. 263, 274-278, 1990  
A>Title: Polypeptide composition of higher plant photosystem I complex. Identification o  
A:Reference number: S09730; MUID:90242987; PMID:2185953  
A:Accession: S09731  
A:Molecule type: protein  
A:Residues: 1-18 <IRK>  
A:Genetics:  
A:Gene: psal  
A:Genome: chloroplast  
C:Superfamily: photosystem I protein psal  
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; th  
  
Query Match 24.4%; Score 20; DB 2; Length 18;  
Best Local Similarity 42.9%; Pred. No. 4.9e+03;  
Matches 6; Conservative 1; Mismatches 3; Indels 4; Gaps 1;  
  
QY 4 FPKLVE---VFP 13  
|||  
Db 3 FPSIFVPLVGLVFP 16  
  
RESULT 35  
A61392  
brain-associated small cell lung cancer antigen - human (fragment)  
N:Alternate names: BASCA  
C:Species: Homo sapiens (man)  
C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Sep-1994  
C:Accession: A61392  
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shitai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.  
Jpn. J. Clin. Oncol. 21, 251-255, 1991  
A>Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1  
A:Reference number: A61392; MUID:92046737; PMID:1719260  
A:Accession: A61392  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <DME>  
  
Query Match 24.4%; Score 20; DB 2; Length 18;  
Best Local Similarity 42.9%; Pred. No. 4.9e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 LKVEVFP 13  
|:|:|  
Db 1 IQVDIVP 7  
  
RESULT 36  
H75063  
hypothetical protein PAB7382 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: H75063  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: H75063  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-18 <KAW>  
A:Cross-References: UNIPROT:Q9UYK7; GB:AJ248287; GB:AL096836; NID:95458657; PIDD:CBM5040  
A:Experimental source: strain Orsay  
A:Genetics:  
A:Gene: PAB7382  
  
Query Match 24.4%; Score 20; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 4.9e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVKE 10  
|||  
Db 2 KLVKE 6  
  
RESULT 37  
S66635  
alpha-2-macroglobulin isoform 1 - bovine (fragment)  
C:Species: Bos primigenius indicus (zebu cattle)  
C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66635  
R:Doimer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottru  
FEBS Lett. 372, 93-95, 1995  
A>Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o  
A:Reference number: S66634; MUID:96032553; PMID:7556651  
A:Accession: S66635  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <DOL>  
A:Cross-References: UNIPROT:Q7M2N8  
  
Query Match 23.2%; Score 19; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 FPF 14  
|||  
Db 4 FPF 6  
  
RESULT 38  
S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Ridding, G.; Elyin, C.; Kemp, D.; Willadsen, P  
Eur. J. Biochem. 237, 414-423, 1996  
A>Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran  
A:Reference number: S65431; MUID:96215437; PMID:8647080  
A:Accession: S65432  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WID>  
A>Note: the source is designated as Haematobia irritans exigua  
  
Query Match 23.2%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.9e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 8 KVEVFPF 14  
|:|:|  
Db 2 RYTHPF 8  
  
RESULT 39  
A61218  
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Dasypyrum villosum  
C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: A61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A>Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
A:Reference number: A61218; MUID:91315394; PMID:1855356  
A:Accession: A61218  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHE>  
A:Cross-References: UNIPROT:Q7M1F7  
C:Keywords: seed; storage protein



Query Match 23.2%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPKLK 8  
| | | | |  
Db 5 PVPOLQ 10

## RESULT 40

B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Dasyphyum villosum  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #ext\_change 09-Jul-2004  
C:Accession: B61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia  
A:Reference number: A61218; MUID:91315394; PMID:1859356  
A:Accession: B61218  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHS>  
A:Cross-references: UNIPROT:Q7M1P6  
C:Keywords: seed; storage protein

Query Match 23.2%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPKLK 8  
| | | | |  
Db 4 PVPOLQ 9

Search completed: June 7, 2005, 23:20:42  
Job time : 13.9091 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 22:55:46 ; Search time 66 Seconds  
(without alignments)  
116.382 Million cell updates/sec

Title: US-10-691-157-8  
Perfect score: 82  
Sequence: 1 LKPFKLVKVEPPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 9318

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	40.2	18	2	07M076 rattus norv
2	30	36.6	14	2	P82435 piactodum
3	29	35.4	11	2	07RBB2 glycine max
4	29	35.4	15	2	09B929 glycine max
5	29	35.4	16	2	09B929 glycine max
6	26	31.7	15	2	06LAI1 drosophila
7	26	31.7	18	2	09QV11 rattus sp.
8	25	30.5	17	2	09JIA7 mus musculi
9	25	29.3	10	2	06QV66 phaseolus v
10	24	29.3	15	2	06LC13 homo sapien
11	24	29.3	16	2	06QVE1 arthropode
12	24	29.3	16	2	09R4J0 arthropode
13	24	29.3	17	2	09T529 pinelodelia
14	23	28.0	8	2	06R408 bubalus bub
15	23	28.0	11	1	PVK3_BACR bladerus cr
16	23	28.0	11	1	PVK3_BIADU bladerus cr
17	23	28.0	11	1	PVK3_GROPO bladerus cr
18	23	28.0	11	1	PVK3_LEUMA bladerus cr
19	23	28.0	11	1	PVK3_NAUCI bladerus cr
20	23	28.0	16	1	FOR2_MYRGU myrmecia gu
21	23	28.0	17	2	09TRH5 bos taurus
22	23	28.0	18	2	006711 saccharomyc
23	23	28.0	18	2	067216 mus musculi
24	23	28.0	11	2	09QV66 mus musculi
25	22	26.8	16	2	08LVE0 mus musculi
26	22	26.8	16	2	08LVE1 mus musculi
27	22	26.8	16	2	08LVE2 mus musculi
28	22	26.8	16	2	08MC15 mus musculi
29	22	26.8	16	2	08MC17 mus musculi
30	22	26.8	16	2	08MC19 mus musculi
31	22	26.8	16	2	08MC21 mus musculi

32	22	26.8	16	2	08MC23 sonneratia
33	22	26.8	16	2	08MC25 sonneratia
34	22	26.8	16	2	08MC27 sonneratia
35	22	26.8	16	2	08MC29 sonneratia
36	22	26.8	16	2	08MC31 sonneratia
37	22	26.8	16	2	08MC33 sonneratia
38	22	26.8	16	2	08MC35 sonneratia
39	22	26.8	16	2	08MC37 sonneratia
40	22	26.8	16	2	08MC39 sonneratia
41	22	26.8	16	2	08MC41 sonneratia
42	22	26.8	16	2	08MC43 sonneratia
43	22	26.8	16	2	08MC45 sonneratia
44	22	26.8	16	2	08MC47 sonneratia
45	22	26.8	16	2	08MC49 sonneratia
46	22	26.8	16	2	08MC51 sonneratia
47	22	26.8	16	2	08MC53 sonneratia
48	22	26.8	16	2	08MC58 sonneratia
49	22	26.8	16	2	08MC60 sonneratia
50	22	26.8	16	2	08MC62 sonneratia
51	22	26.8	16	2	08MC64 sonneratia
52	22	26.8	16	2	08MC66 sonneratia
53	22	26.8	16	2	08MC68 sonneratia
54	22	26.8	16	2	08MC70 sonneratia
55	22	26.8	16	2	08MC72 sonneratia
56	22	26.8	16	2	08MC74 sonneratia
57	22	26.8	16	2	08MC76 sonneratia
58	22	26.8	16	2	08MC78 sonneratia
59	22	26.8	16	2	08MC80 sonneratia
60	22	26.8	16	2	08MC82 sonneratia
61	22	26.8	16	2	08MC84 sonneratia
62	22	26.8	16	2	08MC86 sonneratia
63	22	26.8	16	2	08MC88 sonneratia
64	22	26.8	16	2	08MC90 sonneratia
65	22	26.8	16	2	08MC92 sonneratia
66	22	26.8	16	2	08MC94 sonneratia
67	22	26.8	16	2	08MC96 sonneratia
68	22	26.8	16	2	08MC98 sonneratia
69	22	26.8	16	2	08MC100 sonneratia
70	22	26.8	16	2	08MC102 sonneratia
71	22	26.8	16	2	08MC104 sonneratia
72	22	26.8	16	2	08MC106 sonneratia
73	22	26.8	16	2	08MC108 sonneratia
74	22	26.8	16	2	08MC110 sonneratia
75	22	26.8	16	2	08MC112 sonneratia
76	22	26.8	16	2	08MC114 sonneratia
77	22	26.8	16	2	08MC116 sonneratia
78	22	26.8	16	2	08MC118 sonneratia
79	22	26.8	16	2	08MC120 sonneratia
80	22	26.8	16	2	08MC122 sonneratia
81	22	26.8	16	2	08MC124 sonneratia
82	22	26.8	16	2	08MC126 sonneratia
83	22	26.8	16	2	08MC128 sonneratia
84	22	26.8	16	2	08MC130 sonneratia
85	22	26.8	16	2	08MC132 sonneratia
86	22	26.8	16	2	08MC134 sonneratia
87	22	26.8	16	2	08MC136 sonneratia
88	22	26.8	16	2	08MC138 sonneratia
89	22	26.8	16	2	08MC140 sonneratia
90	22	26.8	16	2	08MC142 sonneratia
91	22	26.8	16	2	08MC144 sonneratia
92	22	26.8	16	2	08MC146 sonneratia
93	22	26.8	16	2	08MC148 sonneratia
94	22	26.8	16	2	08MC150 sonneratia
95	22	26.8	16	2	08MC152 sonneratia
96	22	26.8	16	2	08MC154 sonneratia
97	22	26.8	16	2	08MC156 sonneratia
98	22	26.8	16	2	08MC158 sonneratia
99	22	26.8	16	2	08MC160 sonneratia
100	22	26.8	16	2	08MC162 sonneratia

## ALIGNMENTS

## RESULT 1

Q7M076 PRELIMINARY; PRT; 18 AA.  
 ID Q7M076  
 AC Q7M076  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP MEDLINE=90132681; PubMed=2289352;  
 RX Dyer S.H., Slaughter C.A., Orth K., Moosaw C.R., Hersh L.B.;  
 RA "Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enkephalin-degrading aminopeptidases from rat."  
 RT J. Neurochem. 54:547-554(1990).  
 RL PIR: A60915; A60915.  
 DR NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2172 MW; 100BA083239CC3 CRC64;

Query Match 40.2%; Score 33; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPFPKLVKVEVP 13  
 :|||:  
 Db 4 RPFERLPTVEVP 15

## RESULT 2

P82435 PRELIMINARY; PRT; 14 AA.  
 ID P82435  
 AC P82435  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE 29 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Stabas A.R.,  
 RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 DR CO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1645 MW; CA0D490EF7F851B2 CRC64;

Query Match 36.6%; Score 30; DB 2; Length 14;  
 Best Local Similarity 45.5%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKLVKVEVP 14  
 :|||:  
 Db 2 YRKVDVDFTF 12

## RESULT 3

Q7RBB2 PRELIMINARY; PRT; 11 AA.  
 ID Q7RBB2  
 AC Q7RBB2  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY06234;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=17XNL;  
 RX PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Anguilo S.V., Suh B.B., Kooli T.W., Pertea M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M.,  
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."  
 RL Nature 419:512-519(2002).  
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBO whole genome shotgun (WGS) entry which is preliminary data.  
 DR EMBL; AABL01002084; EAA18412.1; -.  
 CC Hypothetical protein.  
 SQ SEQUENCE 11 AA; 1326 MW; 59A5901B69D5B337 CRC64;

Query Match 35.4%; Score 29; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKPPKTK 8  
 :|||:  
 Db 4 LKSPKSK 11

## RESULT 4

Q9S929 PRELIMINARY; PRT; 15 AA.  
 ID Q9S929  
 AC Q9S929  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Pyruvate-5-carboxylate reductase, PSOR (Fragment).  
 OS Glycine max (soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Euphorbia; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=91378472; PubMed=1898034;  
 RA Chilson O.P., Kelly-Chilson A.B., Siegel N.R.;  
 RT "Pyruvate-5-carboxylate reductase in soybean nodules: isolation/partial primary structure/evidence for isozymes."  
 RL Arch. Biochem. Biophys. 288:350-357(1991).  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1715 MW; D9821F773FD5F524 CRC64;

Query Match 35.4%; Score 29; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEVFPFP 15  
 :|||:

Db 1 MEIPPIP 7

## RESULT 5

Q9BG68 PRELIMINARY; PRT; 16 AA.  
AC Q9BG68;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Thyroid hormone receptor alpha (Fragment).  
GN Name=TRHAI;  
OS Sorex araneus (Eurasian common shrew) (European shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.  
OX NCBI\_TaxId=42254;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Larkin D., Serov O., Zhdanova N.;  
RT "Mapping of five genes from human chromosome 17 to chromosome hn of the common shrew (Sorex araneus).";  
RL Acta Theriol. 45:143-146(2000).  
DR EMBL; AF314827; AAK13419.1; -  
DR GO; GO:0004872; P.receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1951 MW; 775166E3BE5F52E2 CRC64;

Query Match 35.4%; Score 29; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PPKLXVEP 12  
Db 3 PPKLLEVP 11

## RESULT 6

Q6LAI1 PRELIMINARY; PRT; 15 AA.  
AC Q6LAI1;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Andropin (Fragment).  
GN Name=And;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Montemayor;  
RX MEDLINE=98393576; PubMed=9725836;  
RA Ramos-Onsins S., Aguade M.;

RT "Molecular Evolution of the Cecropin multigene family in Drosophila: functional genes vs pseudogenes.";  
RL Genetics 150:157-171(1998).  
DR EMBL; Y16853; CAA76430.1; -  
DR EMBL; Y16854; CAA76436.1; -  
DR EMBL; Y16855; CAA76442.1; -  
DR EMBL; Y16856; CAA76448.1; -  
DR EMBL; Y16857; CAA76454.1; -  
DR EMBL; Y16858; CAA76460.1; -  
DR EMBL; Y16859; CAA76466.1; -  
DR EMBL; Y16861; CAA76476.1; -  
DR EMBL; Y16862; CAA76477.1; -  
FT NON\_TER 1 1  
SQ SEQUENCE 15 AA; 1659 MW; C86F9313DEE241B2 CRC64;

Query Match 31.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 2.7e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFPKL 7  
Db 6 KPFPKL 11

## RESULT 7

Q9QV11 PRELIMINARY; PRT; 18 AA.  
AC Q9QV11;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92031479; PubMed=1931964;  
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;  
RT "Structural and functional correlates of sucrase-alpha-dextrinase in intact brush border membranes.";  
RL Biochemistry 30:10399-10408(1991).  
FT NON\_TER 1 1  
SQ SEQUENCE 18 AA; 2122 MW; 68F1AB87B24E49 CRC64;

Query Match 31.7%; Score 26; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 3.3e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLXVEP 11  
Db 7 PPKLLEVP 15

## RESULT 8

Q9JIA7 PRELIMINARY; PRT; 17 AA.  
AC Q9JIA7;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE Fibroblast growth factor homologous factor 3 isoform 1B (Fragment).  
GN Name=FHR-3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20112823; PubMed=10644718; DOI=10.1074/jbc.275.4.2589;  
RA Munoz-Sauvan I., Smallwood P.M., Natchans U.;  
RT "Isoform diversity among fibroblast growth factor homologous factors is generated by alternative promoter usage and differential splicing.";  
RL J Biol Chem. 275:2589-2597(2000).  
DR EMBL; AF199604; AAF31391.1; -  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1870 MW; 9A0E0364E96D949 CRC64;

Query Match 30.5%; Score 25; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 4.5e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPPPLK 8  
Db 3 LKPPPLK 10

## RESULT 9

06QV6 PRELIMINARY; PRT; 10 AA.

AC 06QV6; 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Ribonuclease H (Fragment).  
 OS Name=RNase H;  
 OS Phaseolus vulgaris (kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 NCBI\_TaxID=3885;

RP SEQUENCE FROM N.A.  
 RX PubMed=15060605; DOI=10.1139/g03-102;  
 RA Galindo L.M., Galtan E., Baccam P., Tohme J.;  
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia  
 retrotransposons in common bean (Phaseolus vulgaris L.).";  
 RL Genome 47:84-95(2004).  
 DR EMBL; AY524233; AAS18550.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1113 MW; AE2362376321A726 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6  
 Db 6 KPFPK 10

## RESULT 10

06LC13 PRELIMINARY; PRT; 15 AA.

AC 06LC13; 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Na<sup>+</sup>-phosphate cotransporter type II (Fragment).  
 GN Name=NP2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=93317607; PubMed=8327470;  
 RA Maggiani S., Werner A., Markovich D., Sorribas V., Strange G.,  
 RA Biber U., Murer H.;  
 RT "Expression cloning of human and rat renal cortex Na/Pi cotransport.",  
 RT Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983(1993).  
 [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=96293539; PubMed=8693007; DOI=10.1073/pnas.93.14.7409;  
 RA Hartman C.M., Hewson A.S., Kos C.H., Hilfinger H., Sounounou Y.,  
 RA Murer H., Tenenhouse H.S.;  
 RT "Structure of murine and human renal type II Na<sup>+</sup>-phosphate  
 cotransporter genes (Npt2 and NPT2).";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414(1996).  
 DR EMBL; U56684; AAD14856.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1770 MW; 23810E2056D88BAB CRC64;

Query Match 29.3%; Score 24; DB 2; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 5.8e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPFPK 10  
 Db 7 KPFPK 15

## RESULT 11

06QV6 PRELIMINARY; PRT; 16 AA.

AC 06QV6; 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Ribonuclease H (Fragment).  
 OS Name=RNase H;  
 OS Phaseolus vulgaris (kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 NCBI\_TaxID=3885;

RP SEQUENCE FROM N.A.  
 RX PubMed=15060605; DOI=10.1139/g03-102;  
 RA Galindo L.M., Galtan E., Baccam P., Tohme J.;  
 RT "Isolation and characterization of RNase-LTR sequences of Ty1-copia  
 retrotransposons in common bean (Phaseolus vulgaris L.).";  
 RL Genome 47:84-95(2004).  
 DR EMBL; AY524258; AAS18555.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 16 AA; 1935 MW; 3E60812E8E2D6A23 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 6.2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6  
 Db 6 KPFPK 10

## RESULT 12

09R4J0 PRELIMINARY; PRT; 16 AA.

AC 09R4J0; 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE LIMONATE dehydrogenase (Fragment).

OS Arthrobacter globiformis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococciaceae; Micrococcaceae; Arthrobacter.  
 NCBI\_TaxID=1665;

RP SEQUENCE.  
 RX MEDLINE=96045380; PubMed=7546548; DOI=10.1016/0031-9422(94)00953-Q;  
 RA Sunayda C.G., Omura M., Hasegawa S.;  
 RT "Limonate dehydrogenase from Arthrobacter globiformis: the native  
 enzyme and its N-terminal sequence.";  
 RT Phytochemistry 40:17-20(1995).  
 SQ SEQUENCE 16 AA; 1759 MW; 514B2B906FD5984 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 16;  
 Best Local Similarity 55.6%; Pred. No. 6.2e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPFPK 11  
 Db 2 KPFPK 10

## RESULT 13

09T5Z9 PRELIMINARY; PRT; 17 AA.

AC 09T5Z9;

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DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATPase8;
OS Pimelodella chagresi.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pimelodidae; Pimelodella.
OK NCBI_TaxID=71257;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98291472; PubMed=9628002;
RA Berningham E., Martin A.P.;
RT "Comparative mtDNA phylogeography of neotropical freshwater fishes:
RT testing shared history to infer the evolutionary landscape of lower
RT Central America."
RL Mol. Ecol. 7:499-517(1998).
DR EMBL; AF040423; AAC77594.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 17 AA; 2113 MW; 40325B578612222A CRC64;

Query Match 29.3%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 KLRKEVFPP 15
DB 6 KLRKEVFPP 15

RESULT 14
O6R408 PRELIMINARY; PRT; 8 AA.
AC O6R408;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Alpha-Si-casein (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OK NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RA Mishra S.S., Bhattacharya T.K., Sharma A., Dayal S., Vohra V.,
RA Shelkh F.D., Kumar P.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF514427; AAS00439.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 920 MW; 633879D2CB0769D7 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 3 PPKKLVFP 12
DB 1 PPP---EVF 6

RESULT 15
PVK3 BLACR STANDARD; PRT; 11 AA.
AC P83933; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Periviscerokinin-3 (Iem-PVK-3).
OS Blaberus craniifer (Beach's head cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Blaberus.
OK NCBI_TaxID=6982;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphatic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES
FT MOD RES
SQ SEQUENCE 11 AA; 1147 MW; 2FAD9FF2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKKL 7
DB 7 PPKRV 11

RESULT 16
PVK3 BLADU STANDARD; PRT; 11 AA.
AC P83934; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Periviscerokinin-3 (Iem-PVK-3).
OS Blaptica dubia (Argentinian wood cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Blaptica.
OK NCBI_TaxID=132935;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphatic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES
FT MOD RES
SQ SEQUENCE 11 AA; 1147 MW; 2FAD9FF2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKKL 7
DB 7 PPKRV 11

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RESULT 17
PVK3 GROPO STANDARD; PRT; 11 AA.
AC P83935; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Gromphadorina portentosa (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Gromphadorhina.
OX NCBI_TaxId=36953;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 18
PVK3 LEUMA STANDARD; PRT; 11 AA.
AC P83931; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxId=6988;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 19
PVK3 NAUCI STANDARD; PRT; 11 AA.
AC P83932; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Nauphoeta.
OX NCBI_TaxId=6990;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 20
FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Formacin 2.
OS Myrmecia gillosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmecinae; Myrmecini; Myrmecia.
OX NCBI_TaxId=36170;
RN [1]
RN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332; DOI=10.1074/jbc.273.11.6139;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gillosa of two inducible O-glycosylated
RT proline-rich antibacterial peptides."
RL J. Biol. Chem. 273:6139-6143(1998).

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SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 17
PVK3 GROPO STANDARD; PRT; 11 AA.
AC P83935; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Gromphadorina portentosa (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Gromphadorhina.
OX NCBI_TaxId=36953;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 18
PVK3 LEUMA STANDARD; PRT; 11 AA.
AC P83931; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxId=6988;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 19
PVK3 NAUCI STANDARD; PRT; 11 AA.
AC P83932; P82700;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Periviscerokinin-3 (Lem-PVK-3).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Nauphoeta.
OX NCBI_TaxId=6990;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steimetz T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI; RANGE=1-11;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the periviscerokinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 11 Valine amide.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9F2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPKL 7
DB 7 PPRV 11

RESULT 20
FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Formacin 2.
OS Myrmecia gillosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmecinae; Myrmecini; Myrmecia.
OX NCBI_TaxId=36170;
RN [1]
RN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332; DOI=10.1074/jbc.273.11.6139;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gillosa of two inducible O-glycosylated
RT proline-rich antibacterial peptides."
RL J. Biol. Chem. 273:6139-6143(1998).

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CC -1- FUNCTION: Antibacterial peptide. Has activity against E.coli but  
 CC none against other Gram-negative bacteria and Gram-positive  
 CC bacteria.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- INDUCTION: By bacterial infection.  
 CC -1- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide, O-  
 CC glycosylation is essential for full biological activity.  
 CC Antibiotic; Direct protein sequencing; Glycoprotein; Hemolymph;  
 KW Insect immunity.  
 FT CARBOHYD 11 11 O-linked (GalNAc...)  
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 28.0%; Score 23; DB 1; Length 16;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEPKLV 7  
 Db 12 PYPRL 16

## RESULT 21

Q9TRH5 PRELIMINARY; PRT; 17 AA.  
 AC Q9TRH5;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
 DE Alpha-S1-casein homolog (Fragment).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovinae; Bos.  
 OC NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93231344; PubMed=1299613; DOI=10.1016/0014-5793(92)80664-3;  
 RA Neubom B., Giuffrida M.G., Conti A.;  
 RT "Isolation of a new ligand-carrying casein fragment from bovine  
 RT mammary gland microsomes";  
 RL FEBS Lett. 305:189-191(1992).  
 SQ SEQUENCE 17 AA; 1950 MW; 8690EF0685A0537F CRC64;

Query Match 28.0%; Score 23; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 9.6e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 3 PEPKLV 12  
 Db 4 PEP---EVF 9

## RESULT 22

Q06711 PRELIMINARY; PRT; 18 AA.  
 AC Q06711;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Ubiquitin (Fragment).  
 GN Name=UB1;  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OC NCBI\_Taxid=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YPH1;  
 RX MEDLINE=94024010; PubMed=8211183;  
 RA Ota I.M., Vazhnevsky A.;  
 RT "A yeast protein similar to bacterial two-component regulators";  
 RL Science 262:566-569(1993).  
 DR EMBL; U01835; AAC48913.1; -.

FT NON TER 1 1  
 SQ SEQUENCE 18 AA; 2249 MW; D13E4F7C1DBBFD1 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 1e+04;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPPKLV 8  
 Db 11 LRPKGLK 18

## RESULT 23

O67216 PRELIMINARY; PRT; 18 AA.  
 AC O67216;  
 DT 25-OCT-2004 (TRENBLrel. 28, Created)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE Photosystem I apoprotein A1 (Fragment).  
 GN Name=psaa;  
 OS Pennisetum americanum (Pearl millet).  
 OG Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACAD clade; Panicoideae; Paniceae; Pennisetum.  
 OC NCBI\_Taxid=4543;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nallal S.C., Nekkalaipudi S.C., Podile A.R.;  
 RT "Pennisetum glaucum clone PGB788 coding for IRP170.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY694132; AAU2166.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2111 MW; 008E617FE6845893 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 1e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PEPKLV 11  
 Db 6 PEPVKIV 14

## RESULT 24

O90YF6 PRELIMINARY; PRT; 11 AA.  
 AC O90YF6;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DE Pancreas transcription factor1 p48 subunit (Fragment).  
 GN Name=PTFP48;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129sv;  
 RX MEDLINE=21219338; PubMed=11318877;  
 RA Obata J., Yano M., Mimura H., Goto T., Nakayama R., Mibu Y., Oka C.,  
 RA Kawauchi M.;  
 RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the  
 RT intracellular mediator of Notch signalling, and is expressed in the  
 RT neural tube of early stage embryos";  
 RL Genes Cells 6:345-360(2001).  
 DR EMBL; AB035674; BAA88247.1; -.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKPPK 6  
 |||:  
 Db 6 LKPPK 11

## RESULT 25

Q8LVE0 PRELIMINARY; PRT; 16 AA.

AC Q8LVE0; 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Trapa maximowiczii.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Trapa.  
 OX NCBI\_TaxID=162053;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035729; AAL14139.1; -;  
 DR EMBL; AY035730; AAL14141.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPVKILV 14

## RESULT 26

Q8LVE1 PRELIMINARY; PRT; 16 AA.

AC Q8LVE1; 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Punica granatum (Pomegranate).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Punica.  
 OX NCBI\_TaxID=22663;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035724; AAL14129.1; -;  
 DR EMBL; AY035742; AAL14165.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast. 16  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPVKILV 14

## RESULT 27

Q8LVE2 PRELIMINARY; PRT; 16 AA.

AC Q8LVE2; 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Lythrum salicaria (Purple loosestrife).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lythrum.  
 OX NCBI\_TaxID=13129;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035727; AAL14135.1; -;  
 DR EMBL; AF421495; AAM45853.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPVKILV 14

## RESULT 28

Q8MC15 PRELIMINARY; PRT; 16 AA.

AC Q8MC15; 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Fuchsia hybrid cultivar.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Onagraceae; Fuchsia.  
 OX NCBI\_TaxID=133545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035746; AAL14173.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match  
Best Local Similarity 26.8%; Score 22; DB 2; Length 16;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKIKVEV 11  
| | | | |  
| | | | |  
DB 6 PEPKIKLIV 14

## RESULT 29

Q8MC17 PRELIMINARY; PRT; 16 AA.  
ID Q8MC17;  
AC Q8MC17;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE psaa (Fragment).  
GN Name=psaa;  
OS Ludwigia hyssopifolia.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Onagraceae; Ludwigia.  
OC NCBI\_TaxID=155013;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035745; AAL14171.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match  
Best Local Similarity 26.8%; Score 22; DB 2; Length 16;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKIKVEV 11  
| | | | |  
| | | | |  
DB 6 PEPKIKLIV 14

## RESULT 30

Q8MC19 PRELIMINARY; PRT; 16 AA.  
ID Q8MC19;  
AC Q8MC19;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE psaa (Fragment).  
GN Name=psaa;  
OS Quisqualis indica (Rangoon creeper).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Combretaceae; Quisqualis.  
OC NCBI\_TaxID=3956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";

RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035744; AAL14169.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match  
Best Local Similarity 26.8%; Score 22; DB 2; Length 16;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKIKVEV 11  
| | | | |  
| | | | |  
DB 6 PEPKIKLIV 14

## RESULT 31

Q8MC21 PRELIMINARY; PRT; 16 AA.  
ID Q8MC21;  
AC Q8MC21;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE psaa (Fragment).  
GN Name=psaa;  
OS Combretum wallichii.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Combretaceae; Combretum.  
OC NCBI\_TaxID=131243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035743; AAL14167.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match  
Best Local Similarity 26.8%; Score 22; DB 2; Length 16;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPKIKVEV 11  
| | | | |  
| | | | |  
DB 6 PEPKIKLIV 14

## RESULT 32

Q8MC23 PRELIMINARY; PRT; 16 AA.  
ID Q8MC23;  
AC Q8MC23;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE psaa (Fragment).  
GN Name=psaa;  
OS Sonneratia alba.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OC NCBI\_TaxID=122812;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";

RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035741; AAL14163.1; "-  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPEVKILV 14

## RESULT 33

Q8MC25 PRELIMINARY; PRT; 16 AA.

AC Q8MC25;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Sonneratia apetala.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Sonneratia.  
 OX NCBI\_TaxID=122813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035740; AAL14161.1; "-  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPEVKILV 14

## RESULT 34

Q8MC27 PRELIMINARY; PRT; 16 AA.

AC Q8MC27;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Lagerstroemia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=162025;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based

RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035739; AAL14159.1; "-  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPEVKILV 14

## RESULT 35

Q8MC29 PRELIMINARY; PRT; 16 AA.

AC Q8MC29;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Duabanga grandiflora.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Duabanga.  
 OX NCBI\_TaxID=122808;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035738; AAL14157.1; "-  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPKLKVEV 11  
 |:::|  
 Db 6 PEPEVKILV 14

## RESULT 36

Q8MC31 PRELIMINARY; PRT; 16 AA.

AC Q8MC31;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Psaa (Fragment).  
 GN Name=psaa;  
 OS Lagerstroemia speciosa (Queen crape myrtle).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=122810;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;

RT "Phylogenetics of *Lythraceae sensu lato*: A Preliminary Analysis Based  
 on Chloroplast *rbcL* Gene, *psaA-psc3* Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences";  
 RL Int. J. Plant Sci. 163:215-225 (2002).  
 DR EMBL, AY053737; AAL14155.1; -.  
 KM GO: GO:0009507; C:chloroplast; IEA.  
 DR Chloroplast.  
 FT NON TER 16  
 SEQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match	26.8%	Score 22	DB 2	Length 16
Best Local Similarity	44.4%	Pred. No. 1.3e+04		
Matches	4	Conservative	3	Mismatches 2
				Indels 0
				Gaps 0

Qy	3	PEPKLKVEV	11
		:   :	
Db	6	PEPEVKILV	14

**RESULT 37**

ID	OBMC33;	PRELIMINARY;	PRT;	16 AA.
AC	OBMC33;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	PsaA (Fragment).			
CN	Name=psaA;			
OS	Rotula indica.			
OC	Chloroplast.			
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	Myrtales; Myrtaceae; Rotula.			
OX	NCBI_taxid=162024;			

Query Match	26.8%;	Score 22;	DB 2;	Length 16;
Best Local Similarity	44.4%;	Pred. No. 1.3e+04;		
Matches	4;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy	3	PEPKLKEV	11
		::	
Db	6	PEPEVKILV	14

**RESULT 38**

ID	OBMC35	PRELIMINARY;	PRT;	16 AA.
AC	OBMC35;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Peaa (Fragment).			
CN	Name=peaa;			
OS	Helimia myrtifolia.			
OC	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	Myrtales; Myrtaceae; Helimia.			
OX	NCBI_TaxID=135798;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

RA Huang Y., Shi S.: "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psal-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225 (2002).  
R DR EMBL; AY005735; AL14151.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT 16 16  
SQ NON TER 16  
SEQUENCE 16 AA; 1895 MW; 517FBE918B9355B9 CRC64;

Query Match	26.8%;	Score 22;	DB 2;	Length 16;
Best Local Similarity	44.4%;	Pred. No. 1.3e+04;		
Matches	4;	Conservative	3;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	3	PPFKLKVEV	11
		: :	
Db	6	PEPEVKILV	14

**RESULT 39**

ID	QBKC37	PRELIMINARY;	PRT,	16 AA.
AC	QBKC37			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Psaa (Fragment).			
CN	Name=psaa;			
OS	Lawsonia inermis.			
OG	Chloroplast.			
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids,			
OC	Mytales; Lythraceae; Lawsonia.			
OX	NCBI_taxid=141191;			

Query Match	26.8%;	Score 22;	DB 2;	Length 16;
Best Local Similarity	44.4%;	Pred. No. 1.3e+04;		
Matches	4;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy	3	P	P	P	K	L	K	V	E	V	11
				:	:						
Db	6	P	P	P	V	K	L	V			14

**RESULT 40**

ID	Q8WBC3;	PRELIMINARY;	PRT;	16 AA.
AC	Q8WBC3;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	PsaA (Fragment).			
GN	Name=PsaA;			
OS	Ammannia baccifera.			
OC	Chloroplast.			
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	Myrtales; Myrtaceae; Ammannia.			
OX	NCBI_TaxID=162022;			
RN	[1]			

RP SEQUENCE FROM N.A.  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psal-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035733; AAL14147.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
Query Match 26.8%; Score 22; DB 2; Length 16;  
Best Local Similarity 44.4%; Pred. No. 1.3e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PEPKIKVEY 11  
DB 6 PEPVKILV 14

Search completed: June 7, 2005, 23:19:04  
Job time : 67 secs